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OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 58.6907 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVVMTQSLPLVTLGQPAS.....CQQTHTFPYFGQTRLRIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	112	4	Aae06949 Humanised
2	590	100.0	112	4	Aau09921 Humanised
3	590	100.0	112	5	Abg75530 Humanised
4	590	100.0	112	5	Aao14973 Humanised
5	590	100.0	112	5	Adf98233 Humanised
6	590	100.0	112	8	Adq89234 Humanised
7	590	100.0	112	9	Aeb09507 Humanised
8	584	99.0	114	4	Aae07035 Humanised
9	584	99.0	114	8	Adq89328 Humanised
10	584	99.0	114	9	Aeb09601 Humanised
11	577	97.8	112	4	Aae06950 Humanised
12	577	97.8	112	4	Aau09922 Humanised
13	577	97.8	112	5	Abg75531 Humanised
14	577	97.8	112	5	Adf98234 Humanised
15	577	97.8	112	8	Adq89235 Humanised
16	577	97.8	112	9	Aeb09508 Humanised
17	572	96.9	112	4	Aae07036 Humanised
18	572	96.9	112	4	Aau09925 Humanised
19	572	96.9	112	5	Abg75534 Humanised
20	572	96.9	112	5	Adf98237 Humanised
21	572	96.9	112	8	Adq89329 Humanised
22	572	96.9	112	9	Aeb09602 Humanised
23	572	96.6	112	4	Aae06951 Humanised
24	572	96.6	112	4	Aau09923 Humanised

25	570	96.6	112	5	Abg75532 Humanised
26	570	96.6	112	5	Adf98235 Humanised
27	570	96.6	112	8	Adq89236 Humanised
28	570	96.6	112	9	Aeb09509 Humanised
29	569	96.4	112	8	Adq31290 Humanised
30	566	95.9	112	8	Adq31289 Humanised
31	565	95.8	112	4	Aae06952 Humanised
32	565	95.8	112	4	Aau09924 Humanised
33	565	95.8	112	5	Abg75533 Humanised
34	565	95.8	112	5	Aao14976 Humanised
35	565	95.8	112	5	Adf98236 Humanised
36	565	95.8	112	8	Adq89237 Humanised
37	565	95.8	112	9	Aeb09510 Humanised
38	559	94.7	113	6	Abp58270 Humanised
39	559	94.7	219	6	Abp58272 Humanised
40	559	94.7	239	6	Abp58274 Humanised
41	557.5	94.5	111	5	Aao14977 Humanised
42	554.5	94.0	111	5	Aao14975 Humanised
43	549	93.1	110	5	Aao14974 Humanised
44	542	91.9	132	5	Abg76931 Humanised
45	542	91.9	132	8	Adr88415 Humanised

#### ALIGNMENTS

##### RESULT 1

AAE06949  
ID AAE06949 standard; protein; 112 AA.

XX AC AAE06949;

XX DT 11-SEP-2003 (revised)

XX DT 16-OCT-2001 (first entry)

XX DE Humanised murine ID9 antibody kappa light chain variable region, ID9RKA.  
 XX KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; stenosis; allograft rejection;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention; ID9 antibody;  
 KW neointimal hyperplasia; VK; kappa light chain variable region; ID9RKA.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

XX Region 23..39 /label= CDR1

XX Region 55..61 /note= "Complementarity determining region 1"

XX Region 94..102 /label= CDR2

XX Region 94..102 /note= "Complementarity determining region 2"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX Region 94..102 /note= "Complementarity determining region 3"

XX Region 94..102 /label= CDR3

XX WPI; 2001-48888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated

XX disorder in a patient, comprises a binding specificity for CCR2, and a

XX non-human antigen binding region and human immunoglobulin.

XX Claim 61; Fig 11; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding

XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),

XX comprising an antigen binding region of non-human origin and at least a

XX portion of an immunoglobulin of human origin. The humanised antibodies

XX are useful for inhibiting the interaction of a cell expressing CCR2. They

XX are useful for inhibiting or treating HIV infection. The proteins of the

XX CCR2-mediated disorders such as inflammatory disorder, autoimmune

XX disorders such as rheumatoid arthritis and multiple sclerosis,

XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They

XX are useful in therapy or diagnosis, and in the manufacture of a

XX medicament for treating CCR-2 mediated disease. They are also useful for

XX treating allergy, anaphylaxis, malignancy, chronic and acute

XX inflammation, histamine and IgE-mediated allergic reaction, shock,

XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory

XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis

XX associated with vascular intervention, including angioplasty and/or stent

XX placement in a mammal. Humanised antibodies are also useful for

XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting

XX neointimal hyperplasia of a vessel in a mammal, preferably associated

XX with vascular intervention. The present sequence is humanised murine 1D9

XX antibody kappa light chain variable (VK) region, 1D9KA. (Updated on 11-

XX SEP-2003 to standardise OS field)

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 4; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60

Db 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGTTHFPYFGQGTLEIK 112

Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGTTHFPYFGQGTLEIK 112

RESULT 2

AAU09921

ID AAU09921 standard; protein; 112 AA.

AC AAU09921;

DT 18-JUN-2002 (first entry)

XX Humanised 1D9 light chain variable region, 1D9KA protein sequence.

XX Human; mouse; 1D9 light chain variable region; vasotropic;

XX anti-inflammatory; collagen disease; immunosuppressive; antiasthmatic;

XX insulin-dependent diabetes mellitus; inflammatory bowel disease;

XX ulcerative colitis; HF-21/28; graft rejection; allergic disease;

XX antipsoriatic; 1D9KA; anti-arthritic; nephrotropic; antithyroid;

XX restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;

XX vascular injury; autoimmune disease; immunoglobulin;

XX complementarity determining region; CDR; CD18; CCR2; atherosclerosis;

XX mutant; mutein.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

OS Chimeric.

XX

PH Key Location/Qualifiers

FT Region 24..39

FT /note= "Complementarity determining region 1 (CDR1),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Region 55..61

FT /note= "Complementarity determining region 2 (CDR2),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Region 94..102

FT /note= "Complementarity determining region 3 (CDR3),

FT grafted from mouse mAb 1D9 light chain sequence

FT (AAU09918)"

FT Misc-difference 112

FT /note= "Addition of Lys residue normally present in mouse

FT mAb 1D9 sequence and absent in human antibody HF-21/28

FT sequence (AAU09920)"

PN WO200170266-A2.

PD 27-SEP-2001.

XX 15-MAR-2001; 2001WO-US008266.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CV, Rao PE;

XX WPI; 2001-607511/69.

XX Inhibiting stenosis or restenosis of a blood vessel following vascular

XX injury or angioplasty in a subject by administering agent which inhibits

XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.

XX Claim 32; Fig 17; 108pp; English.

XX The present invention relates to a new method of inhibiting stenosis or

XX restenosis of a blood vessel following vascular injury in a subject. The

XX new method comprises administering to the subject agents which inhibit

XX the adhesion and/or recruitment of neutrophils and mononuclear cells to a

XX site of vascular injury by binding CD18 or CCR2. The method of the

XX invention inhibits stenosis or restenosis of a blood vessel following

XX vascular injury arising from a vascular intervention procedure such as

XX vascular by-pass or transplantation surgery. The method is also useful

XX for treating a subject having an inflammatory disease or condition

XX mediated by neutrophil and mononuclear cell activity e.g. asthma and

XX graft versus host disease. Chronic inflammatory diseases of the lung,

XX collagen diseases, and insulin-dependent diabetes mellitus can also be

XX treated. The method is further useful for treating inflammatory bowel

XX diseases, such as ulcerative colitis. Additional diseases or conditions

XX include inflammatory or allergic diseases and conditions, including

XX systemic anaphylaxis of hypersensitivity responses, drug allergies,

XX psoriasis and inflammatory dermatoses, autoimmune diseases such as

XX arthritis, graft rejection and other diseases including atherosclerosis.

XX The present sequence represents the variable region of one of several

XX humanised 1D9 light chains (AAU09921-AAU09925). These light chains were

XX used in the invention for the production of anti-CCR2 antibody or antigen

XX -binding fragment

XX SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 4; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60

Db 1 DVNMTQSLPLVTLGQPASISCKSSQSLDSDGKTFNLNWFQRPQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCQGTTHFPYFGQGTLEIK 112



Db 61 SGVDPFRSGSGTDTFTLKISRVEADVGVYCWQGTHTFPYTFGGQTRLEIK 112

# RESULT 3

ABG75530  
ID ABG75530 standard; protein; 112 AA.

AC ABG75530;

DT 16-APR-2003 (first entry)

DE Humanised mouse mAb 1D9 light chain variable region, 1D9RKAVK.

XX Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
KW antigen binding fragment; cellular adhesion molecule; adhesion;  
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
KW percutaneous transluminal coronary angioplasty; PTCA; stent; angioplasty;  
KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
KW endovascular stenting; prosthetic valve; transplantation;  
KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
KW chronic bronchitis; asthma; graft-versus-host disease;  
KW chronic inflammatory disease; hypersensitivity pneumonitis;  
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RKAVK;  
KW light chain variable region; VK; complementarity determining region; CDR;  
KW mutant; mutein.

XX Mus sp.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Region 24..39 /note= "Mouse complementarity determining region 1 (CDR1)"

FT Region 55..61 /note= "Mouse complementarity determining region 2 (CDR2)"

FT Region 94..102 /note= "Mouse complementarity determining region 3 (CDR3)"

FT Misc-difference 112

FT /note= "Lys derived from the mouse 1D9 mAb sequence"

XX US2002106369-A1.

XX 08-AUG-2002.

XX 15-MAR-2001; 2001US-00809739.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Rao PE;

XX WPI; 2002-697861/75.

XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
PT administering first and second agents that inhibit adhesion and/or  
PT recruitment of neutrophils and mononuclear cells, respectively to site of  
PT vascular injury.

XX Claim 32; Fig 17; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of  
CC a blood vessel following vascular injury in a subject. The method  
CC involves administering to the subject a first therapeutic agent, which  
CC comprises an antibody or its antigen binding fragment which binds a  
CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment

CC of neutrophils to a site of vascular injury and a second therapeutic  
CC agent, which comprises an antagonist of CCR2 function, that inhibits  
CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
CC injury. The vascular injury arises from a vascular intervention procedure  
CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
CC stenting, insertion of a prosthetic valve and transplantation of organs,  
CC tissues or cells. The method is also useful for treating inflammatory  
CC diseases or conditions mediated by early neutrophil activity and later  
CC mononuclear cell activity. Preferably, the method is useful for treating  
CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
CC asthma and graft-versus-host disease, chronic inflammatory disease of  
CC lung, hypersensitivity pneumonitis, pancreatitis and insulin dependent diabetes  
CC other idiopathic conditions, collagen diseases, sarcoidosis and  
CC mellitus. The method is also useful for treating inflammatory bowel  
CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
CC psoriasis, atopic dermatitis and allergic rhinitis), graft rejection,  
CC (such as arthritis and multiple sclerosis), atherectomy, atherectomy,  
CC atherosclerosis and myositis. The method enables simultaneous inhibition  
CC of neutrophil and mononuclear cell participation in response to vascular  
CC injury or inhibition of neutrophil participation followed by inhibition  
CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
CC chain variable region (VK), 1D9RKAVK, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human HP-21/28  
CC mAb VK regions with a mouse derived Lys at position 112  
XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 5; Length 112;

Best Local Similarity 100.0%; Pred. No. 2.4e-46;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60

DB 1 DVWMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFNLNWFQQRPGQSPRLIYLVSKLD 60

QY 61 SGVDPFRSGSGTDTFTLKISRVEADVGVYCWQGTHTFPYTFGGQTRLEIK 112

DB 61 SGVDPFRSGSGTDTFTLKISRVEADVGVYCWQGTHTFPYTFGGQTRLEIK 112

## RESULT 4

AAO14973

ID AAO14973 standard; protein; 112 AA.

XX AC AAO14973;

XX DT 05-SEP-2002 (first entry)

XX DE Humanised murine light chain variable region (1D9Rka V<sub>k</sub>).

XX Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
KW bowel transplant; heart transplant; graft-versus host disease;  
KW chronic graft rejection; antibody light chain variable region; 1D9Rka V<sub>k</sub>.

XX OS Mus musculus.

XX OS Synthetic.

XX US2002042370-A1.

XX PD 11-APR-2002.

XX PF 13-APR-2001; 2001US-00835087.

XX PR 14-APR-2000; 2000US-00549448.

XX PA (MILL-) MILLENNIUM PHARM INC.

PI Hancock WW;  
 XX WPI; 2002-351265/38.  
 XX Inhibiting graft rejection, graft versus host disease or chronic  
 PT rejection of a transplanted graft, involves administering a CCR2  
 PT antagonist.  
 XX  
 XX Claim 26; Fig 1; 16pp; English.  
 XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody light chain variable region (1D9Rka Vκ)  
 XX  
 XX Sequence 112 AA;  
 SQ  
 Query Match 100.0%; Score 590; DB 5; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVSCLD 60  
 Db 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVSCLD 60  
 Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112  
 RESULT 5  
 ADF98233  
 ID ADF98233 standard; protein; 112 AA.  
 XX  
 AC ADF98233;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Humanised 1D9 light chain variable region, 1D9Rka V kappa, SEQ ID 3.  
 XX  
 KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
 KW graft versus host disease; CC chemokine receptor 2; CCR2;  
 KW anti-CCR2 antibody.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 OS Homo sapiens.  
 XX  
 FN WO200178653-A2.  
 XX  
 XX 25-OCT-2001.  
 XX  
 XX 13-APR-2001; 2001WO-US012139.  
 XX  
 XX 14-APR-2000; 2000US-00549448.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 PI Hancock WW;  
 XX  
 XX WPI; 2002-017543/02.  
 XX  
 XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
 PT involves use of CC chemokine receptor 2 inhibitor.  
 PT

XX Claim 26; Fig 1; 44pp; English.  
 XX The present invention relates to a method for inhibiting graft rejection  
 CC or graft versus host diseases. The method comprises administration of a  
 CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADF98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft versus host disease for a bone marrow graft.  
 XX  
 XX Sequence 112 AA;  
 SQ  
 Query Match 100.0%; Score 590; DB 5; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVSCLD 60  
 Db 1 DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTFLNWFQQRPGQSPRLIYLVSCLD 60  
 Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112  
 Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTFFPYTFGGQTRLEIK 112  
 RESULT 6  
 ADQ89234  
 ID ADQ89234 standard; protein; 112 AA.  
 XX  
 AC ADQ89234;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Humanised immunoglobulin protein #1.  
 XX  
 KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 KW inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.  
 XX  
 OS Synthetic.  
 XX  
 XX US2004151721-A1.  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 10-DEC-2003; 2003US-00733563.  
 XX  
 XX 19-OCT-2001; 2001US-0350166P.  
 XX  
 XX 26-JUN-2002; 2002US-0392364P.  
 XX  
 XX 17-OCT-2002; 2002US-00272899.  
 XX  
 XX (OKEE/) O'KEEFE T.  
 XX (PONA/) PONATH P.  
 XX  
 XX O'keefe T, Ponath P;  
 XX  
 XX WPI; 2004-580175/56.  
 XX  
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.  
 XX  
 XX Claim 5; SEQ ID NO 12; 128pp; English.  
 XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised

CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.

XX  
SQ Sequence 112 AA;

Query Match 100.0%; Score 590; DB 8; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2.4e-46;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQPLSLPVTLGPASISCKSSQLSDSGKTFILNWFQQRPQGSPRLIYLVS KLD 60  
DB 1 DVVMTQPLSLPVTLGPASISCKSSQLSDSGKTFILNWFQQRPQGSPRLIYLVS KLD 60  
QY 61 SGVPDRPSGSGGDFTLKISRVEADGVVYCWQGTTHPPYFGQGRLEIK 112  
DB 61 SGVPDRPSGSGGDFTLKISRVEADGVVYCWQGTTHPPYFGQGRLEIK 112

RESULT 7  
AEB09507  
ID AEB09507 standard; protein; 112 AA.  
XX AC AEB09507;  
DT 08-SEP-2005 (first entry)  
XX Humanized 129 kappa light chain variable region SEQ ID NO 12.  
DE anti-inflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
XX antibody engineering; therapeutic; diagnosis; inflammation;  
KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
KW light chain variable region.  
OS Homo sapiens.  
XS Mus musculus.  
OS Synthetic.  
XX WO2005060368-A2.  
XX 07-JUL-2005.  
XX 10-DEC-2003; 2003WO-US039599.  
PF 10-DEC-2003; 2003WO-US039599.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Okeefe T, Ponath P;  
PI WPI; 2005-488561/49.  
XX  
XX New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.  
XX  
XX Claim 1; SEQ ID NO 12; 192pp; English.  
XX  
XX The invention describes a humanized immunoglobulin (I) or its antigen  
CC binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
PT disorder in a patient, comprises a binding specificity for CCR2, and a  
PT non-human antigen binding region and human immunoglobulin.  
XX Disclosure; Fig 24; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
CC comprising an antigen binding region of non-human origin and at least a  
CC portion of an immunoglobulin of human origin. The humanised antibodies  
CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
CC are useful for inhibiting or treating HIV infection. The proteins of the  
CC invention are useful for inhibiting leukocyte trafficking, for treating  
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
CC disorders such as rheumatoid arthritis and multiple sclerosis,  
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
CC are useful in therapy or diagnosis, and in the manufacture of a  
CC medicament for treating CCR-2 mediated disease. They are also useful for  
CC treating allergy, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
CC associated with vascular intervention, including angioplasty and/or stent  
CC placement in a mammal. Humanised antibodies are also useful for  
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
CC with vascular intervention. The present sequence is humanised murine  
CC antibody light chain region, 1D9RKA. (Updated on 11-SEP-2003 to  
CC standardise OS field)

XX Sequence 114 AA;  
SQ

Query Match 99.0%; Score 584; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFILNWFQQRPGQSPRLIYLVSKLDS 61  
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFILNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTFTLKISRVEAEDGIVYYCWQGTTHPPYFGQGTLEIK 112  
Db 62 GVPDRFSGSGGTFTLKISRVEAEDGIVYYCWQGTTHPPYFGQGTLEIK 112

RESULT 9  
ADQ89328  
ID ADQ89328 standard; protein; 114 AA.  
AC ADQ89328;  
XX  
XX 21-OCT-2004 (first entry)  
XX Humanised immunoglobulin protein #10.  
XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
XX Synthetic.  
XX  
XX US2004151721-A1.  
XX  
XX 05-AUG-2004.  
XX  
XX 10-DEC-2003; 2003US-00733563.  
XX  
XX 19-OCT-2001; 2001US-0350166P.  
XX 26-JUN-2002; 2002US-0392364P.  
XX 17-OCT-2002; 2002US-00272899.  
XX

PA (OKEE/) O'KEEFE T.  
PA (PONA/) PONATH P.  
XX O'Keefe T, Ponath P;  
XX WPI; 2004-580175/56.  
XX N-PSDB; ADQ89320.  
XX  
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
XX Disclosure; SEQ ID NO 106; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.

XX Sequence 114 AA;  
SQ

Query Match 99.0%; Score 584; DB 8; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFILNWFQQRPGQSPRLIYLVSKLDS 61  
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLSDSGKTFILNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTFTLKISRVEAEDGIVYYCWQGTTHPPYFGQGTLEIK 112  
Db 62 GVPDRFSGSGGTFTLKISRVEAEDGIVYYCWQGTTHPPYFGQGTLEIK 112

RESULT 10  
AEB09601  
ID AEB09601 standard; protein; 114 AA.  
XX  
XX AEB09601;  
XX  
XX 08-SEP-2005 (first entry)  
XX Humanized light chain 1D9RKA.  
XX  
XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
KW antibody engineering; therapeutic; diagnosis; inflammation;  
KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
KW light chain variable region.  
XX  
XX Synthetic.  
XX  
XX WO2005060368-A2.  
XX  
XX 07-JUL-2005.  
XX  
XX 10-DEC-2003; 2003WO-US039599.  
XX  
XX 10-DEC-2003; 2003WO-US039599.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Okeefe T, Ponath P;  
XX WPI; 2005-488561/49.  
XX N-PSDB; AEB09593.  
XX

XX New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.  
XX  
XX Disclosure; SEQ ID NO 106; 192pp; English.  
XX  
XX The invention describes a humanized immunoglobulin (I) or its antigen  
CC binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
CC immunoglobulin light chain, or its antigen binding fragment, having  
CC binding specificity for CCR2 and comprising the amino acid sequence of  
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
CC sequence, given in specification. The following are disclosed: isolated  
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
CC construct comprising nucleic acid molecule encoding (I); and host cell  
CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response, for use in the treatment of diseases  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of humanized light  
CC chain 1D9RKA.  
XX  
XX Sequence 114 AA;

Query Match 99.0%; Score 584; DB 9; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-46;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVMTQSPVLPVLTGQPASISCKSSQSLDSDGKTFLNWFQORPQSPRLIYLVSKLDS 61  
DB 2 VVMTQSPVLPVLTGQPASISCKSSQSLDSDGKTFLNWFQORPQSPRLIYLVSKLDS 61  
QY 62 GVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWOGTHPPYTFGQGTGLEIK 112  
DB 62 GVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWOGTHPPYTFGQGTGLEIK 112

RESULT 11  
AAE06950  
ID AAE06950 standard; protein; 112 AA.

XX  
XX AAE06950;  
XX  
XX 11-SEP-2003 (revised)  
XX 16-OCT-2001 (first entry)  
XX  
XX Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKB.  
XX  
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
KW neointimal hyperplasia; VK; kappa light chain variable region; 1D9RKB.  
XX  
XX Mus sp.

OS Homo sapiens.  
OS Chimeric.  
XX  
XX Key  
XX Region  
XX Location/Qualifiers  
XX 23..39  
XX /label= CDR1  
XX /note= "Complementarity determining region 1"  
XX 55..61  
XX /label= CDR2  
XX /note= "Complementarity determining region 2"  
XX 94..102  
XX /label= CDR3  
XX /note= "Complementarity determining region 3"  
XX  
XX WO200157226-A1.  
XX  
XX 09-AUG-2001.  
XX  
XX 02-FEB-2001; 2001WO-US003537.  
XX  
XX 03-FEB-2000; 2000US-00497625.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T,  
XX WPI; 2001-48888/53.  
XX  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX  
XX Claim 61; Fig 11; 183pp; English.  
XX  
XX The patent discloses a humanised antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
XX comprising an antigen binding region of non-human origin and at least a  
XX portion of an immunoglobulin of human origin. The humanised antibodies  
XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
XX are useful for inhibiting or treating HIV infection. The proteins of the  
XX invention are useful for inhibiting leukocyte trafficking, for treating  
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune  
XX disorders such as rheumatoid arthritis and multiple sclerosis,  
XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
XX are useful in therapy or diagnosis, and in the manufacture of a  
XX medicament for treating CCR-2 mediated disease. They are also useful for  
XX treating allergy, anaphylaxis, malignancy, chronic and acute  
XX inflammation, histamine and Igs-mediated allergic reaction, shock,  
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
XX associated with vascular intervention, including angioplasty and/or stent  
XX placement in a mammal. Humanised antibodies are also useful for  
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
XX neointimal hyperplasia of a vessel in a mammal, preferably associated  
XX with vascular intervention. The present sequence is humanised murine 1D9  
XX antibody kappa light chain variable (VK) region, 1D9RKB. (Updated on 11-  
XX SEP-2003 to standardise OS field)  
XX  
XX Sequence 112 AA;

Query Match 97.8%; Score 577; DB 4; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVMTQSPVLPVLTGQPASISCKSSQSLDSDGKTFLNWFQORPQSPRLIYLVSKLD 60  
DB 1 DVMTQSPVLPVLTGQPASISCKSSQSLDSDGKTFLNWFQORPQSPRLIYLVSKLD 60  
QY 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWOGTHPPYTFGQGTGLEIK 112  
DB 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWOGTHPPYTFGQGTGLEIK 112

RESULT 12  
AAU09922  
ID AAU09922 standard; protein; 112 AA.  
XX AC  
XX AAU09922;  
DT 18-JUN-2002 (first entry)  
XX  
DE Humanised ID9 light chain variable region, ID9RKB protein sequence.  
XX  
KW Human; mouse; ID9 light chain variable region; vasotropic;  
KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;  
KW insulin-dependent diabetes mellitus; inflammatory bowel disease;  
KW ulcerative colitis; HF-21/28; graft rejection; allergic disease;  
KW antipsoriatic; ID9RKB; antiarthritic; nephrotropic; antichyroid;  
KW restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;  
KW vascular injury; autoimmune disease; immunoglobulin;  
KW complementarity determining region; CDR; CD18; CCR2; atherosclerosis;  
KW mutant; mutein.  
XX  
OS Homo sapiens.  
OS Mus sp.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Region 24. .39  
FT /note= "Complementarity determining region 1 (CDR1),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 41  
FT /note= "Substitution of Phe residue normally present in  
FT human HF-21/28 sequence (AAU09920) by Leu residue  
FT normally present in mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 42  
FT /note= "Substitution of Gln residue normally present in  
FT human HF-21/28 sequence (AAU09920) by Leu residue  
FT normally present in mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Region 55. .61  
FT /note= "Complementarity determining region 2 (CDR2),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Region 94. .102  
FT /note= "Complementarity determining region 3 (CDR3),  
FT grafted from mouse mAb ID9 light chain sequence  
FT (AAU09918)"  
FT  
FT Misc-difference 112  
FT /note= "Addition of Lys residue normally present in mouse  
FT mAb ID9 sequence and absent in human antibody HF-21/28  
FT sequence (AAU09920)"  
FT  
FT WO200170266-A2.  
XX  
PD 27-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US008266.  
XX  
XX 17-MAR-2000; 2000US-00528267.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Horvath CJ, Rao PE;  
XX  
XX WPI; 2001-607511/69.  
XX  
XX Inhibiting stenosis or restenosis of a blood vessel following vascular  
XX injury or angioplasty in a subject by administering agent which inhibits  
XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.  
XX  
XX Claim 32; Fig 17; 108pp; English.

CC The present invention relates to a new method of inhibiting stenosis or  
CC restenosis of a blood vessel following vascular injury in a subject. The  
CC new method comprises administering to the subject agents which inhibit  
CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
CC site of vascular injury by binding CD18 or CCR2. The method of the  
CC invention inhibits stenosis or restenosis of a blood vessel following  
CC vascular injury arising from a vascular intervention procedure such as  
CC vascular by-pass or transplantation surgery. The method is also useful  
CC for treating a subject having an inflammatory disease or condition  
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
CC graft versus host disease. Chronic inflammatory diseases of the lung,  
CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
CC treated. The method is further useful for treating inflammatory bowel  
CC diseases, such as ulcerative colitis. Additional diseases or conditions  
CC include inflammatory or allergic diseases and conditions, including  
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,  
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
CC arthritis, graft rejection and other diseases including atherosclerosis.  
CC The present sequence represents the variable region of one of several  
CC humanised ID9 light chains (AAU09921-AAU09925). These light chains were  
CC used in the invention for the production of anti-CCR2 antibody or antigen  
CC -binding fragment  
XX  
XX Sequence 112 AA;  
SQ  
Query Match 97.8%; Score 577; DB 4; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DVVMTQPLSLPVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQSPGSPRLIYLVSKLD 60  
DB 1 DVVMTQPLSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRLIYLVSKLD 60  
QY 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVVYCWQGHFPTFGQGRLEIK 112  
DB 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVVYCWQGHFPTFGQGRLEIK 112  
RESULT 13  
ABG75531  
ID ABG75531 standard; protein; 112 AA.  
XX  
AC ABG75531;  
XX  
DT 16-APR-2003 (first entry)  
XX  
DE Humanised mouse mAb ID9 light chain variable region, ID9RKBVK.  
XX  
KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
KW antigen binding fragment; cellular adhesion molecule; adhesion;  
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
KW endovascular stenting; prosthetic valve; transplantation;  
KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
KW chronic bronchitis; asthma; graft-versus-host disease;  
KW chronic inflammatory disease; hypersensitivity pneumonitis;  
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;  
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
KW graft rejection; atherosclerosis; myositis; therapy; ID9; ID9RKBVK;  
KW light chain variable region; VK; complementarity determining region; CDR;  
KW mutant; mutein.  
XX  
XX Mus sp.  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Region 24. .39  
XX /note= "Mouse complementarity determining region 1  
XX (CDR1)"  
FT  
FT



FT Misc-difference 41..42  
 FT /note= "Leu's derived from the mouse 1D9 mAb sequence"  
 FT 55..61  
 FT /note= "Mouse complementarity determining region 2  
 FT (CDR2)"  
 FT 94..102  
 FT /note= "Mouse complementarity determining region 3  
 FT (CDR3)"  
 FT Misc-difference 112  
 FT /note= "Lys derived from the mouse 1D9 mAb sequence"  
 FT  
 FT  
 PN US2002106369-A1.  
 XX  
 XX 08-AUG-2002.  
 XX  
 PF 15-MAR-2001; 2001US-00809739.  
 XX  
 PR 17-MAR-2000; 2000US-00528267.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Horvath CJ, Rao PE;  
 XX  
 XX WPI; 2002-697861/75.  
 XX  
 DR Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 XX administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.  
 PT  
 PS Claim 32; Fig 17; 59pp; English.  
 XX  
 CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
 CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
 CC asthma and graft-versus-host disease, chronic inflammatory disease of  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
 CC chain variable region (VK), 1D9K3VK, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human HP-21/28  
 CC positions 41 and 42  
 XX  
 SQ Sequence 112 AA;  
 Query Match 97.8%; Score 577; DB 5; Length 112;  
 Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQSPVLPVITLGPASISCKSSQSLDSDGKTFLNWFQQRFGQSPRRILYLVSKLD 60  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 RESULT 14  
 ADF98234  
 ID ADF98234 standard; protein; 112 AA.  
 XX  
 AC ADF98234;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Humanised 1D9 light chain variable region, 1D9KB V kappa, SEQ ID 4.  
 XX  
 KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
 KW graft verses host disease; CC chemokine receptor 2; CCR2;  
 KW anti-CCR2 antibody.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 OS Homo sapiens.  
 XX  
 PN WO200178653-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 13-APR-2001; 2001WO-US012139.  
 XX  
 PR 14-APR-2000; 2000US-00549448.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Hancock WW;  
 XX  
 DR WPI; 2002-017543/02.  
 XX  
 FT Inhibition of rejection of graft e.g. heart or graft verses host disease  
 FT involves use of CC chemokine receptor 2 inhibitor.  
 XX  
 PS Claim 26; Fig 1; 4pp; English.  
 XX  
 CC The present invention relates to a method for inhibiting graft rejection  
 CC or graft verses host diseases. The method comprises administration of a  
 CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADP98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft verses host disease for a bone marrow graft.  
 XX  
 SQ Sequence 112 AA;  
 Query Match 97.8%; Score 577; DB 5; Length 112;  
 Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
 Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DVVMTQSPVLPVITLGPASISCKSSQSLDSDGKTFLNWFQQRFGQSPRRILYLVSKLD 60  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 QY 61 SGVPRFSGSGSGTDFTLKISRVEAEDVGVYVCWQGTTHFPYTFGGQTRLEIK 112  
 DB |||||  
 RESULT 15  
 ADQ89235



ID ADQ89235 standard; protein; 112 AA.  
XX  
AC ADQ89235;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Humanised immunoglobulin protein #2.  
XX  
KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
OS Synthetic.  
XX  
FN US2004151721-A1.  
XX  
PD 05-AUG-2004.  
XX  
PF 10-DEC-2003; 2003US-00733563.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
PR 17-OCT-2002; 2002US-00272899.  
XX  
PA (OKEE/) O'KEEFE T.  
PA (PONA/) PONATH P.  
XX  
FI O'Keefe T, Ponath P;  
XX  
XX WPI; 2004-580175/56.  
XX  
PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
PS Example 2; SEQ ID NO 13; 128pp; English.  
XX  
CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX  
SQ Sequence 112 AA;  
  
Query Match 97.8%; Score 577; DB 8; Length 112;  
Best Local Similarity 98.2%; Pred. No. 3.7e-45;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 DVNVTQSPSLPVTILGPASISCKSSQSLSDSGKTFILNWFQRPQSPRLIYLVSKLD 60  
Db 1 DVNVTQSPSLPVTILGPASISCKSSQSLSDSGKTFILNWFQRPQSPRLIYLVSKLD 60  
  
Qy 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYCWGTHPPYTFGQGTLEIK 112  
Db 61 SGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYCWGTHPPYTFGQGTLEIK 112

Search completed: January 28, 2006, 09:38:12  
Job time : 58.6907 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 11.4354 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-12  
Perfect score: 590  
Sequence: 1 DVVMTQSLPLSVTLGQPAS.....CWQGTTHPPYTFGGTRLEIK 112  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PTR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	90.0	113	2 F30560	Ig kappa chain V r
2	530	89.8	132	2 C32513	Ig kappa chain pre
3	526	88.2	133	2 S23230	Ig kappa chain pre
4	526	89.2	142	2 S22902	Ig kappa chain V r
5	517	87.6	112	2 A36259	Ig kappa chain V r
6	514	87.1	133	1 K2HURP	Ig kappa chain pre
7	513.5	87.0	114	2 S49572	Ig kappa chain pre
8	512	86.8	111	2 S20709	Ig kappa chain V r
9	512	86.8	112	2 A53491	proteolytic antibo
10	506	85.8	133	1 A24452	Ig kappa chain pre
11	505.5	85.7	140	2 S22658	Ig kappa chain pre
12	505	85.6	133	2 S40324	Ig kappa chain V r
13	503	85.3	131	2 S31577	Ig kappa chain - m
14	501	84.9	112	2 PL0273	Ig kappa chain V r
15	501	84.9	133	2 S42611	HUNVK protein prec
16	499	84.6	118	2 S40374	Ig kappa chain - h
17	499	84.6	122	2 S40338	Ig kappa chain - h
18	496.5	84.2	114	2 B49002	Ig kappa chain V r
19	491	83.2	132	2 A30322	Ig kappa chain - h
20	488	82.7	101	2 A33730	Ig kappa chain V r
21	477	80.8	126	2 S40312	Ig kappa chain - h
22	470	79.7	120	2 S42268	Ig kappa chain V r
23	470	79.7	120	2 S42267	Ig kappa chain V r
24	461.5	78.2	134	2 S40376	Ig kappa chain - h
25	457	77.5	103	2 PH1056	Ig light chain V r
26	457	77.5	112	2 A31807	Ig kappa chain V r
27	456	77.3	103	2 PH1055	Ig light chain V r
28	456	77.3	219	2 S16112	Ig kappa chain V r
29	454	76.9	115	2 S38715	Ig kappa chain V r

30	452	76.6	131	2 B39276	Ig light chain pre
31	450	76.3	113	1 K2HUTW	Ig kappa chain V-I
32	449	76.1	113	1 K2HUFH	Ig kappa chain V-I
33	448.5	76.0	130	2 S40321	Ig kappa chain - h
34	448	75.9	113	2 PL0203	anti-DNA autoantib
35	447	75.8	114	2 A32967	Ig kappa chain V-I
36	446	75.6	112	2 E27887	Ig kappa chain V r
37	445	75.4	91	2 S42186	Ig kappa chain V r
38	445	75.4	131	2 B32513	Ig kappa chain pre
39	444.5	75.3	115	1 K2HUCM	Ig kappa chain V-I
40	444	75.3	219	2 S52028	Ig kappa chain - m
41	443	75.1	111	2 PL0257	Ig kappa chain V r
42	443	75.1	112	2 S58207	Ig light chain V r
43	443	75.1	131	2 B30577	Ig kappa chain pre
44	443	75.1	136	2 S40357	Ig kappa chain V-J
45	442	74.9	115	2 S60066	Ig kappa chain V r

ALIGNMENTS

RESULT 1

F30560  
Ig kappa chain V region (28.4.10A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C:Accession: F30560  
R:Matsuda, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonor  
A:Reference number: A30560; MUID:89110062; PMID:2464028  
A:Accession: F30560  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-113 <MAT>  
A:Cross-references: UNIPARC:UPI0000114E24; GB:M24273; NID:G197081; PIDN:AAA63370.1; PID:G  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:16-95/Domain; immunoglobulin homology <IMM>

Query Match

Best Local Similarity 90.0%; Score 531; DB 2; Length 113;  
Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY	1	DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTFLNWFOORPGQSPRRLLYLVS	60
DB	1	DVVMTQSLPLSVTLGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPRRLLYLVS	60
QY	61	SGVPRFSGSGSGTDFTLKISRVEAEDVGVYCWQGTTHPPYTFGGTRLEIK	112
DB	61	SGVPRFSGSGSGTDFTLKISRVEAEDLVGVYCWQGTTHPPYTFGGTKLEIK	112

RESULT 2

C32513  
Ig kappa chain precursor V region (BXW14) - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: C32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988  
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID:88331394; PMID:3138286  
A:Accession: C32513  
A:Molecule type: DNA  
A:Residues: 1-132 <KOF>  
A:Cross-references: UNIPARC:UPI0000114D99; GB:M20830; NID:G196939; PIDN:AAA38844.1; PID:G  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:36-115/Domain; immunoglobulin homology <IMM>

Query Match 89.8%; Score 530; DB 2; Length 132;



```
Query Match      87.1%; Score 514; DB 1; Length 133;
Best Local Similarity 87.5%; Pred. No. 3.3e-41;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKNRD 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEIK 132
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
S49572
Ig kappa chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C:Accession: S49572
R:Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A:Description: k+1+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49572
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <GIA>
A:CROSS-references: UNIPARC:UPI0000116709; EMBL:246626; NID:G575261; PIDN:CAA86596.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      87.0%; Score 513.5; DB 2; Length 114;
Best Local Similarity 87.6%; Pred. No. 3.1e-41;
Matches 99; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKNRD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFP-YTFGGQTRLEIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEIK 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
S20709
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20709
R:Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Carr, F.J.; Oeb
submitted to the EMBL Data Library, April 1992
A:Description: Binding specificity and variable region sequences of two monoclonal anti
A:Reference number: S20706
A:Accession: S20709
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <BRE>
A:CROSS-references: UNIPARC:UPI00001163E1; EMBL:211917; NID:G52655; PIDN:CAA77975.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      86.8%; Score 512; DB 2; Length 111;
Best Local Similarity 85.6%; Pred. No. 4.2e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQLTQSPPLTSLVTIGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEI 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Db 61 SGVPRFRFGSGSGTDFTLKISRVEADLGYYVCMQGTHTFPQTFGGQTKLEI 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
A55491
proteolytic antibody light chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55491
R:Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.;
J. Biol. Chem. 269, 32389-32393, 1994
A>Title: Molecular cloning of a proteolytic antibody light chain.
A:Reference number: A55491; MUID:95096089; PMID:7798238
A:Accession: A55491
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <GRO>
A:CROSS-references: UNIPROT:Q8K0F8; UNIPARC:UPI0000176CCE; GB:I34775
A>Note: authors translated the codon TAT for residue 37 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match      86.8%; Score 512; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 4.2e-41;
Matches 96; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRFRFGSGSGTDFTLKISRVEADLGYYVCMQGTHTFPQTFGGQTKLEIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
A24452
Ig kappa chain precursor V-II region (RPMI 6410) - human
C:Species: Homo sapiens (man)
C>Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: A24452
R:Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A>Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A:Reference number: A24452; MUID:86232631; PMID:3086847
A:Accession: A24452
A:Molecule type: DNA
A:Residues: 1-133 <WEI>
A:CROSS-references: UNIPARC:UPI0000113B46; GB:M36859; NID:G185932; PIDN:AAA58920.1; PID:
C:Genetics:
A>Note: this sequence was determined from the differentiated gene
A:Gene: GDB:IGKV2
A:CROSS-references: GDB:I36265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match      85.8%; Score 506; DB 1; Length 133;
Best Local Similarity 86.6%; Pred. No. 1.8e-40;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTFNLNWFQORPGQSPRLIYLVSKLD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DVWMTQSPSLPVTLGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKNRD 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRFRFGSGSGTDFTLKISRVEADVGYYVCMQGTHTFPYTFGGQTRLEIK 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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|||||
81 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTWSWTFGQGTKEIK 132

RESULT 11
S22658
Ig kappa chain precursor V region (0-81VL) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C/Accession: S22658
R/Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A/Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a
A/Reference number: S22657; MUID:92285150; PMID:1598223
A/Accession: S22658
A/Molecule type: mRNA
A/Residues: 1-140 <HIR>
A/Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI00001769CF; EMBL:X59135
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 505.5; DB 2; Length 140;
Best Local Similarity 87.6%; Pred. No. 2.2e-40; Mismatches 8; Indels 1; Gaps 1;
Matches 99; Conservative 5;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSCLD 60
Db 21 DVVMTQSPVLTIGQPASISCKSSQSLVHSDGNTYLNWFQQRPGQSPRLIYVSNRD 80

Qy 61 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTF-PYTFGQGTREIK 112
Db 81 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTWSWTFGQGTREIK 133

RESULT 12
S40324
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C/Accession: S40324
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40324
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-133 <KLE>
A/Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI0000176CAA; EMBL:X72434
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 505; DB 2; Length 133;
Best Local Similarity 84.8%; Pred. No. 2.3e-40; Mismatches 10; Indels 0; Gaps 0;
Matches 95; Conservative 10;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSCLD 60
Db 18 DVVMTQSPVLTIGQPASISCKSSQSLVSDGNTYLNWFQQRPGQSPRLIYKVSNRD 77

Qy 61 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTF-PYTFGQGTREIK 112
Db 78 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTWSWTFGQGTKEIK 129

RESULT 13
S31577
Ig kappa chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
```

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C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31577
R/Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, January 1993
A/Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antic
A/Reference number: S31577
A/Accession: S31577
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-131 <REC>
A/Cross-references: UNIPARC:UPI000011469C; EMBL:Z19575; NID:G53983; PIDN:CAA79627.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 503; DB 2; Length 131;
Best Local Similarity 84.8%; Pred. No. 3.5e-40; Mismatches 8; Indels 0; Gaps 0;
Matches 95; Conservative 8;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSCLD 60
Db 20 DVVMTQAPLTLSVTIGQPASISCKSSHSLSDGKTYLNMLLQRPQSPKRLIYLVSCLD 79

Qy 61 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTF-PYTFGQGTREIK 112
Db 80 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTFPITFGGTLEMK 131

RESULT 14
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C/Accession: PL0273
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0273
A/Molecule type: mRNA
A/Residues: 1-112 <SHL>
A/Cross-references: UNIPROT:Q8K0F8; UNIPARC:UPI0000115487
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

Query Match 84.9%; Score 501; DB 2; Length 112;
Best Local Similarity 84.8%; Pred. No. 4.5e-40; Mismatches 10; Indels 0; Gaps 0;
Matches 95; Conservative 10;

Qy 1 DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFNLNWFQQRPGQSPRLIYLVSCLD 60
Db 1 DVVMTQTPLTLSVTIGQPASISCKSSQSLVYRNKTYLNMLLQRPQSPKRLIYLVSCLD 60

Qy 61 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTF-PYTFGQGTREIK 112
Db 61 SGVDFRFGSGSGDFTLKISRVEADVGVIYCMQGTHTFPWTFGGTLEIK 112

RESULT 15
S42611
HUNK protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C/Accession: S42611
R/Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
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Search completed: January 28, 2006, 09:45:38  
Job time : 12.4354 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 59.3634 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVNMTQSLSLPVLGQPAS.....CWOQTHPTPTFGQTRLEIK I12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	87.1	133	1 KV2F HUMAN	P06310 homo sapien
2	511	86.6	239	2 Q8TCD0 HUMAN	Q8Tcd0 homo sapien
3	496.5	84.2	114	2 Q9UL80 HUMAN	Q9ul80 homo sapien
4	491	83.2	239	2 Q58EU8 MOUSE	Q58eu8 mus musculus
5	459	77.8	239	2 Q8P491 HUMAN	Q8p491 homo sapien
6	450	76.3	113	1 KV2D HUMAN	P01617 homo sapien
7	449	76.1	113	1 KV2B HUMAN	P01615 homo sapien
8	447	75.8	239	2 Q8NEK0 HUMAN	Q8nek0 homo sapien
9	445	75.4	248	2 Q65ZQ7 9MURI	Q65zq7 mus sp. b3(
10	444.5	75.3	115	1 KV2A HUMAN	P01614 homo sapien
11	438	74.2	117	1 KV2E HUMAN	P08309 homo sapien
12	430.5	73.0	115	2 Q5F2I0 MOUSE	Q5f2i0 mus musculus
13	430	72.9	113	1 KV2G MOUSE	P01631 mus musculus
14	428	72.5	112	2 Q53VP8 MOUSE	Q53vp8 mus musculus
15	418	70.8	219	2 Q65ZC0 MOUSE	Q65zc0 mus musculus
16	417.5	70.8	240	2 Q6PIH6 HUMAN	Q6pih6 homo sapien
17	411	69.7	234	2 Q5XKG4 MOUSE	Q5xkg4 mus musculus
18	405.5	68.7	112	1 KV2C HUMAN	P01616 homo sapien
19	402	68.1	113	1 KV2E MOUSE	P03976 mus musculus
20	397	67.3	113	1 KV2C MOUSE	P01628 mus musculus
21	396	67.1	112	1 KV2D MOUSE	P01629 mus musculus
22	396	67.1	113	1 KV2F MOUSE	P01630 mus musculus
23	390	66.1	112	1 KV2A MOUSE	P01626 mus musculus
24	390	66.1	112	2 Q6LEM8 MOUSE	Q6lem8 mus musculus
25	386.5	65.5	134	1 KV4C HUMAN	P06314 homo sapien
26	385.5	65.3	108	1 KV1 CANFA	P01618 canis famil
27	380.5	64.5	114	1 KV4A HUMAN	P01625 homo sapien
28	378.5	64.2	111	1 KV2L MOUSE	P01664 mus musculus
29	378.5	64.2	111	1 KV3M MOUSE	P01665 mus musculus
30	377.5	64.0	111	1 KV3O MOUSE	P01667 mus musculus
31	372.5	63.1	111	1 KV3Q MOUSE	P01669 mus musculus

32	371.5	63.0	111	1 KV3N MOUSE	P01666 mus musculus
33	371	62.9	110	1 KV3P MOUSE	P01668 mus musculus
34	370	62.7	86	2 Q7Z3Y5 HUMAN	Q7z3y5 homo sapien
35	369.5	62.6	111	2 Q811U6 MOUSE	Q811u6 mus musculus
36	368.5	62.5	111	1 KV3H MOUSE	P01660 mus musculus
37	365.5	61.9	111	1 KV3J MOUSE	P01662 mus musculus
38	363	61.5	120	1 KV2B MOUSE	P01627 mus musculus
39	361.5	61.3	111	2 Q920B9 MOUSE	Q920e9 mus musculus
40	360.5	61.1	131	1 KV3I MOUSE	P01661 mus musculus
41	360.5	61.1	255	2 Q6KB05 MOUSE	Q6kb05 mus musculus
42	359	60.8	133	1 KV4B HUMAN	P06313 homo sapien
43	356.5	60.4	111	1 KV3K MOUSE	P01663 mus musculus
44	356.5	60.4	111	1 KV3U MOUSE	P01673 mus musculus
45	355.5	60.3	240	2 Q52L64 MOUSE	Q52l64 mus musculus

ALIGNMENTS

RESULT 1					
KV2F HUMAN					
ID KV2F HUMAN	STANDARD;	PRT;	133 AA.		
AC P06310;					
DT 01-JAN-1988 (Rel. 06, Created)					
DT 01-JAN-1988 (Rel. 06, Last sequence update)					
DT 10-MAY-2005 (Rel. 47, Last annotation update)					
DE IG kappa chain V-II region RPMI 6410 precursor.					
OS Homo sapiens (Human)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC Homo.					
OX NCBI_TaxID=9606;					
RP NUCLEOTIDE SEQUENCE					
RX MEDLINE=86041852; PubMed=2997711;					
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;					
RT "Human immunoglobulin kappa light chain genes of subgroups II and III. ";					
RL Nucleic Acids Res. 13:6499-6513(1985).					
CC -----					
CC This Swiss-Prot entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC the European Bioinformatics Institute. There are no restrictions on its					
CC use as long as its content is in no way modified and this statement is not					
CC removed.					
CC -----					
DR EMBL; Z00020; CAA77315.1; -; Genomic_DNA.					
DR PIR; A01890; K2HURP.					
DR HSSP; Q99M37; 1191.					
DR SMR; P06310; 21-133.					
DR Ensembl; ENSG00000173758; Homo sapiens.					
DR GO; GO:0005576; C:extracellular region; NAS.					
DR GO; GO:0003823; F:antigen binding; NAS.					
DR GO; GO:0006955; P:immune response; NAS.					
DR InterPro; IPR007110; IG-like.					
DR SMART; SM00406; IGV; 1.					
DR PROSITE; PS50835; IG_Like; 1.					
KW Immunoglobulin domain; Immunoglobulin V region; Signal.					
FT SIGNAL	1	20			
FT CHAIN	21	133			
FT REGION	21	43			
FT REGION	44	59			
FT REGION	60	74			
FT REGION	75	81			
FT REGION	82	113			
FT REGION	114	122			
FT REGION	123	132			
FT REGION	133	133			
FT DISULFID	43	113			
FT NON_TER	133	133			
SQ SEQUENCE	133 AA;	14707 MW;	513CCAF3673009EE	CRC64;	
Query Match	87.1%;	Score 514;	DB 1;	Length 133;	

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Best Local Similarity 87.5%; Pred. No. 5,3e-45;
Matches 98; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQPSLSPVTLGPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSCLD 60
Db 21 DVVMTQPSLSPVTLGPASISCKSSQSLVYSDGNTYLNWFQQRPGQSPRLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYFCMQGTHFPYTFQGTGLEIK 112
Db 81 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYFCMQGTHSWTFQGTGLEIK 132

RESULT 2
Q8TCD0_HUMAN
ID Q8TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarathne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.F., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
RL nephritis-associated idiotype.";
RL Nucleic Acids Res. 20:2601-0(1992).
[4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiebe R., Zocher I., Zachau H.G.;
RT "The human immunoglobulin kappa locus. Characterization of the
RL duplicated A regions.";
RL Eur. J. Immunol. 22:1023-1029(1992).
[5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;

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"Expressed human immunoglobulin kappa genes and their hypermutation.";
RL Eur. J. Immunol. 23:3248-3262(1993).
[6]
RP NUCLEOTIDE SEQUENCE.
RX Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; BC022362; AAH22362.1; -; mRNA.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR SMR; Q8TCD0; 21-237.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26235 MW; FAGEDC3A3B03871D CRC64;

Query Match 86.6%; Score 511; DB 2; Length 239;
Best Local Similarity 86.6%; Pred. No. 2.1e-44;
Matches 97; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVVMTQPSLSPVTLGPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSCLD 60
Db 21 DVVMTQPSLSPVTLGPASISCKSSQSLVYSDGNTYLNWFQQRPGQSPRLIYKVSNRD 80

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYFCMQGTHFPYTFQGTGLEIK 112
Db 81 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYFCMQGTHSWTFQGTGLEIK 132

RESULT 3
Q9UL80_HUMAN
ID Q9UL80_HUMAN PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1322670;
RA Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA Gaskin F., Fu S.M.;
RT "A rheumatoid factor from a normal individual encoded by VH2 and V
RT kappa II gene segments.";
RT Arthritis Rheum. 35:900-904(1992).

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[3]
RA NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RT Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
[4]
RA NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint.";
RL Eur. J. Immunol. 22:1561-1565(1992).
DR EMBL; AF035034; AAD56270.1; -; mRNA.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; P01625; 1LVE.
DR SMR; Q9UL80; 1-114.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 84.2%; Score 496.5; DB 2; Length 114;
Best Local Similarity 85.8%; Pred. No. 2.9e-43;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 1 DVWMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRGQSPRLIYLVS KLD 60
Db 1 DVWMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRGQSPRLIYLVS NRD 60

Qy 61 SGVPRFSGSGSGTDFTLKISRVAEDVGVYVCWGTHF-PVTFQGTGLEIK 112
Db 61 SGVPRFSGSGSGTDFTLKISRVAEDVGVYVCWGTHF-PVTFQGTGLEIK 113

RESULT 4
ID Q58EUB MOUSE PRELIMINARY; PRT; 239 AA.
AC Q58EUB;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RA NUCLEOTIDE SEQUENCE.
RX STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Mnt1 model.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RA NUCLEOTIDE SEQUENCE.
RX STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Mnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR SMR; Q58EUB; 21-239.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS02290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 239 AA; 26302 MW; 98FC4BA8EB404215 CRC64;

Query Match 83.2%; Score 491; DB 2; Length 239;
Best Local Similarity 83.9%; Pred. No. 2.4e-42;
Matches 94; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DVWMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRGQSPRLIYLVS KLD 60
Db 21 DVWMTQSLPSLVTLGQPASISCKSSQSLSDSGKTFNLWFQQRGQSPRLIYLVS KLE 80

Qy 61 SGVPRFSGSGSGTDFTLKISRVAEDVGVYVCWGTHF-PVTFQGTGLEIK 112
Db 81 SGVPRFSGSGSGTDFTLKISRVAEDVGVYVCWGTHF-PVTFQGTGLEIK 132

RESULT 5
Q6P491 HUMAN PRELIMINARY; PRT; 239 AA.
ID Q6P491 HUMAN PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RA NUCLEOTIDE SEQUENCE.
RX TISSUE=Skin;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=52020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q652Q7; 4-247.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248
FT SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;
Query Match 75.4%; Score 445; DB 2; Length 248;
Best Local Similarity 74.1%; Pred.No.1.4e-37;
Matches 83; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
QY 1 DVVMTQPSLSPLVTLGQPASISCKSSQSLDSDGKTFLNWFQRPQGSPRLIYLYSKLD 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 136 DVLMTQPSLSPLVSLGQASISCKSSQIIVHSNGNTYLEYLOKPGQSPKLLIKVSNRF 195
QY 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYQCWQTHFPYTFQGGYRLRIK 112
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 196 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYCYFQGSHPVTFGSGTKLEIK 247
RESULT 10
KV2A HUMAN STANDARD; PRT; 115 AA.
ID ID KV2A HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RN PROTEIN SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hlischmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RX MEDLINE=70063440; PubMed=4186189;
RA Hlischmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; B91639; K2HUCM.
CC HSSP; P01751; INQB.
CC SMR; P01614; 2-115.

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FT REGION 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match
Best Local Similarity 74.2%; Score 438; DB 1; Length 117;
Matches 85; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDGKTFNLNFWFOORPQSPRRLLIYLVSKLD 60
DB 5 DIVMTQSLPLPVTGPEPASISCRSSQLHNSGNYLWDYIQKQPSQLLIYLVSNRA 64

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQGTTHPPYTFGQGTLEIK 112
DB 65 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQGLQTPQTFGGQTKVEIK 116

RESULT 12
QSF210 MOUSE
ID QSF210 MOUSE PRELIMINARY; PRT; 115 AA.
AC QSF210.
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DE Kappa light chain variable region (Fragment)
GN Name=IGL1 anti-TS1 VL;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.; Holm P.; Ullen A.; Stigbrand T.; Sundstrom B.E.;
RT "Studies of the interactions between the anticytokerin 8 monoclonal
antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1."
RL J. Mol. Recognit. 16:157-163(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ884575; CAI56337.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 1
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match
Best Local Similarity 74.3%; Score 430.5; DB 2; Length 115;
Matches 84; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDGKTFNLNFWFOORPQSPRRLLIYLVSKLD 60
DB 1 DVVMTQSLPLPVLGDAQASISCRSSQLVHNSGNYLHWYIQKQSPKLLIYKVSNRF 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQGTTHP-PYTFGQGTLEIK 112
DB 61 SGVPRFSGSGGTDTFTLKISRVEADLGVPFCSTTHVPYTFGGQTKLEMK 113

RESULT 13
KV2G MOUSE
ID KV2G MOUSE STANDARD; PRT; 113 AA.
AC F01631;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J.; Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody."
RL Biochemistry 22:1153-1158(1983).
CC 1- MISCELLANEOUS: This chain was isolated from an IGG2a hybridoma
protein that binds digoxin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HSP; A01914; KVMG26.
DR HSP; O99M37; I19I.
DR Ensembl; ENSMUSG00000055315; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Complementarity-determining-2.
FT REGION 55 61 Complementarity-determining-3.
FT REGION 62 93 Complementarity-determining-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 72.9%; Score 430; DB 1; Length 113;
Matches 83; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDGKTFNLNFWFOORPQSPRRLLIYLVSKLD 60
DB 1 DVVMTQSLPLPVLGDAQASISCRSSQLVHNSGNYLHWYIQKQSPKLLIYKVSNRF 60

QY 61 SGVPRFSGSGGTDTFTLKISRVEADVGYYCQGTTHPPYTFGQGTLEIK 112
DB 61 SGVPRFSGSGGTDTFTLKISRVEADLGVPFCSTTHVPYTFGGQTKLEIK 112

RESULT 14
Q53VP8 MOUSE
ID Q53VP8 MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8.
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., There J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RL antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 108-109.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
RL EMBL; X03386; CAA27113.1; -; mRNA.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;

Query Match 72.5%; Score 428; DB 2; Length 112;
Best Local Similarity 72.3%; Pred. No. 3.3e-36;
Matches 81; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 DVNMTQSPLSVLTIGQPASISCKSSQSLSDSGKTFNWFQORPGQSPRLIYLVS KLD 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DVNMTQSPLSVLTIGQPASISCKSSQSLSDSGKTFNWFQORPGQSPRLIYLVS KLD 60
EMBO J. 4:3681-3688(1985).

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112

RESULT 15
Q652C0_MOUSE PRELIMINARY; PRT; 219 AA.
ID Q652C0_MOUSE PRELIMINARY; PRT; 219 AA.
AC Q652C0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi thummi major
RT allergen Chi t.I.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -; mRNA.
DR SMR; Q652C0; 1-219.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAP845 CRC64;

Query Match 70.8%; Score 418; DB 2; Length 219;
Best Local Similarity 71.4%; Pred. NO. 7.6e-35;
Matches 80; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DVNMTQSPLSVLTIGQPASISCKSSQSLSDSGKTFNWFQORPGQSPRLIYLVS KLD 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DVNMTQSPLSVLTIGQPASISCKSSQSLSDSGKTFNWFQORPGQSPRLIYLVS KLD 60
EMBO J. 4:3681-3688(1985).

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112
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Db 1 ELVMTQSPLSVLTIGQPASISCKSSQSLSDSGKTFNWFQORPGQSPRLIYLVS NRF 60
Qy 61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGVDPDRFSGSGGTDFTLKISRVEADVGVVYCWQGHFPYTFGGGTREIK 112
EMBO J. 4:3681-3688(1985).

Search completed: January 28, 2006, 09:44:18
Job time : 60.3634 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 16.4805 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVWMTQSLPLVTLGQPAS.....CWQGHFFPYTGGTGLEIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	590	100.0	112	2	US-09-809-739-14	Sequence 14, Appl
2	590	100.0	112	2	US-09-840-459-12	Sequence 12, Appl
3	590	100.0	112	2	US-09-497-625A-12	Sequence 12, Appl
4	584	99.0	114	2	US-09-840-459-106	Sequence 106, Appl
5	584	99.0	114	2	US-09-497-625A-106	Sequence 106, Appl
6	577	97.8	112	2	US-09-809-739-15	Sequence 15, Appl
7	577	97.8	112	2	US-09-840-459-13	Sequence 13, Appl
8	577	97.8	112	2	US-09-497-625A-13	Sequence 13, Appl
9	572	96.9	112	2	US-09-809-739-18	Sequence 18, Appl
10	572	96.9	112	2	US-09-840-459-107	Sequence 107, Appl
11	570	96.6	112	2	US-09-809-739-16	Sequence 16, Appl
12	570	96.6	112	2	US-09-840-459-14	Sequence 14, Appl
13	570	96.6	112	2	US-09-497-625A-14	Sequence 14, Appl
14	565	95.8	112	2	US-09-809-739-17	Sequence 17, Appl
15	565	95.8	112	2	US-09-840-459-15	Sequence 15, Appl
16	565	95.8	112	2	US-09-497-625A-15	Sequence 15, Appl
17	536	90.8	112	2	US-09-809-739-11	Sequence 11, Appl
18	536	90.8	112	2	US-09-840-459-9	Sequence 9, Appl
19	536	90.8	112	2	US-09-497-625A-9	Sequence 9, Appl
20	536	90.8	142	2	US-09-840-459-102	Sequence 102, Appl
21	536	90.8	142	2	US-09-497-625A-102	Sequence 102, Appl
22	527	89.3	257	2	US-09-419-788-113	Sequence 113, Appl
23	526	89.2	111	2	US-09-809-739-13	Sequence 13, Appl
24	526	89.2	111	2	US-09-840-459-59	Sequence 59, Appl
25	526	89.2	111	2	US-09-497-625A-11	Sequence 11, Appl
26	526	89.2	111	2	US-09-497-625A-59	Sequence 59, Appl
27	526	89.2	112	1	US-08-477-877B-89	Sequence 89, Appl

28	526	89.2	112	1	US-08-472-281A-89	Sequence 89, Appl
29	526	89.2	112	1	US-08-477-989B-89	Sequence 89, Appl
30	526	89.2	112	2	US-09-462-140D-97	Sequence 97, Appl
31	524	88.8	113	2	US-09-698-705-7	Sequence 7, Appl
32	524	88.8	218	2	US-09-698-705-12	Sequence 12, Appl
33	521	88.3	112	2	US-09-840-459-54	Sequence 54, Appl
34	521	88.3	112	2	US-09-497-625A-54	Sequence 54, Appl
35	521	88.3	112	2	US-09-254-180C-8	Sequence 8, Appl
36	521	88.3	353	2	US-09-203-958A-4	Sequence 4, Appl
37	520	88.1	111	2	US-09-840-459-11	Sequence 11, Appl
38	520	88.1	112	2	US-09-840-459-58	Sequence 58, Appl
39	520	88.1	112	2	US-09-497-625A-58	Sequence 58, Appl
40	518	87.8	112	2	US-09-647-468-149	Sequence 149, Appl
41	518	87.8	112	2	US-09-647-468-150	Sequence 150, Appl
42	518	87.8	131	2	US-09-647-468-163	Sequence 163, Appl
43	518	87.8	131	2	US-09-647-468-164	Sequence 164, Appl
44	518	87.8	243	2	US-09-297-181-2	Sequence 2, Appl
45	516	87.5	535	2	US-08-983-035A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-14

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Best Local Similarity	100.0%	Pred. No. 3.1e-51;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	DVWMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORQSPRLIYLVSKLD 60		
Db	1	DVWMTQSLPLVTLGQPASISCKSSQSLDSDGKTFLNWFQORQSPRLIYLVSKLD 60		
Qy	61	SGVDPFRFSGSGTGDTFLKISRVEADGVVYCWGTHFPVTFGGTGLEIK 112		
Db	61	SGVDPFRFSGSGTGDTFLKISRVEADGVVYCWGTHFPVTFGGTGLEIK 112		

RESULT 2  
US-09-840-459-12  
; Sequence 12, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran H.  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; METHODS OF USE THEREFOR



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; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-497-625A-106

Query Match
Best Local Similarity 99.0%; Score 584; DB 2; Length 114;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRRILIYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRRILIYLVSKLDS 61

QY 62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112

RESULT 6
US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112

RESULT 7
US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112

RESULT 8
US-09-497-625A-13
; Sequence 13, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-13

Query Match
Best Local Similarity 97.8%; Score 577; DB 2; Length 112;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1' DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRRILIYLVSKLD 60
Db 1 DVVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWLLQRPQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112
Db 61 SGVPRFSGSGGTDFTLKISRVEADVGVYVCWQGHFPPYTFGGQTRLEIK 112
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RESULT 9
US-09-809-739-18
; Sequence 18, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-18

Query Match      96.9%; Score 572; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.9e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60
    |||||
Db 1 DVVMTQSLPLPVTLGHPASISCKSSQSLSDSGKTFNLWLLQRPQSPRLIYLVSKLD 60
    |||||

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
    |||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
    |||||

RESULT 10
US-09-840-459-107
; Sequence 107, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-107

Query Match      96.9%; Score 572; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.9e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLNWFQORPGQSPRLIYLVSKLD 60
    |||||
Db 1 DVVMTQSLPLPVTLGHPASISCKSSQSLSDSGKTFNLWLLQRPQSPRLIYLVSKLD 60
    |||||

Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
    |||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
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RESULT 11
US-09-809-739-16
; Sequence 16, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-16

Query Match      96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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    |||||
Db 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWLLQRPQSPRLIYLVSKLD 60
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Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
    |||||
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHFFPTFGQGTGLEIK 112
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RESULT 12
US-09-840-459-14
; Sequence 14, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
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; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60
DB 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60

QY 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112
DB 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112

RESULT 13
US-09-497-625A-14
; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

Query Match          96.6%; Score 570; DB 2; Length 112;
Best Local Similarity 97.3%; Pred. No. 3e-49;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60
DB 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60

QY 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112
DB 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112

RESULT 14
US-09-809-739-17
; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-17

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 9.3e-49;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60
DB 1 DVVMTQSPFLSPVTLGHPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60

QY 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112
DB 61 SGVPRFSGSGGTDTTLKISRVEADVGVYVCWQTHPPYTFGGGTRLEIK 112

RESULT 15
US-09-840-459-15
; Sequence 15, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-15

Query Match          95.8%; Score 565; DB 2; Length 112;
Best Local Similarity 96.4%; Pred. No. 9.3e-49;
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPFLSPVTLGQPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60
DB 1 DVVMTQSPFLSPVTLGHPASISCKSSQSLDSDGKTFNLNWFQORQSPRRLIYLVSKLD 60
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Qy 61 SGVPDRFSGSGTDTTLKISRVEADVGYYVCWGTHPPYTFGGTRLEIK 112  
Db 61 SGVPDRFSGSGTDTTLKISRVEADVGYYVCWGTHPPYTFGGTRLEIK 112

Search completed: January 28, 2006, 09:47:28  
Job time : 17.4805 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 47.7598 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-12  
Perfect score: 590  
Sequence: 1 DVVMTQSPVLTIGQPAS.....CWSQTHFPYTFGGTRLEIK 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	112	3	US-09-835-087-3
2	590	100.0	112	3	US-09-809-739-14
3	590	100.0	112	3	US-09-840-459-12
4	590	100.0	112	4	US-10-766-773-12
5	590	100.0	112	4	US-10-766-610-12
6	590	100.0	112	4	US-10-733-563-12
7	590	100.0	112	5	US-10-662-061-14
8	584	99.0	114	3	US-09-840-459-106
9	584	99.0	114	4	US-10-766-773-106
10	584	99.0	114	4	US-10-766-610-106
11	584	99.0	114	4	US-10-733-563-106
12	577	97.8	112	3	US-09-835-087-4
13	577	97.8	112	3	US-09-809-739-15
14	577	97.8	112	3	US-09-840-459-13
15	577	97.8	112	4	US-10-766-773-13
16	577	97.8	112	4	US-10-766-610-13
17	577	97.8	112	4	US-10-733-563-13
18	577	97.8	112	5	US-10-662-061-15
19	572	96.9	112	3	US-09-835-087-7
20	572	96.9	112	3	US-09-809-739-18
21	572	96.9	112	3	US-09-840-459-107
22	572	96.9	112	4	US-10-766-610-107
23	572	96.9	112	4	US-10-733-563-107
24	572	96.9	112	5	US-10-662-061-18
25	570	96.6	112	3	US-09-835-087-5
26	570	96.6	112	3	US-09-809-739-16
27	570	96.6	112	3	US-09-840-459-14

28	570	96.6	112	4	US-10-766-773-14	Sequence 14, Appl
29	570	96.6	112	4	US-10-766-610-14	Sequence 14, Appl
30	570	96.6	112	4	US-10-733-563-14	Sequence 14, Appl
31	570	96.6	112	5	US-10-662-061-16	Sequence 16, Appl
32	565	95.8	112	3	US-09-835-087-6	Sequence 6, Appl
33	565	95.8	112	3	US-09-809-739-17	Sequence 17, Appl
34	565	95.8	112	3	US-09-840-459-15	Sequence 15, Appl
35	565	95.8	112	4	US-10-766-773-15	Sequence 15, Appl
36	565	95.8	112	4	US-10-766-610-15	Sequence 15, Appl
37	565	95.8	112	4	US-10-733-563-15	Sequence 15, Appl
38	565	95.8	112	5	US-10-662-061-17	Sequence 17, Appl
39	559	94.7	113	5	US-10-476-265-9	Sequence 9, Appl
40	559	94.7	219	5	US-10-476-265-11	Sequence 11, Appl
41	559	94.7	239	5	US-10-476-265-19	Sequence 19, Appl
42	542	91.9	132	4	US-10-010-942B-11	Sequence 11, Appl
43	542	91.9	132	4	US-10-388-389-11	Sequence 11, Appl
44	542	91.9	132	4	US-10-703-713-11	Sequence 11, Appl
45	542	91.9	132	4	US-10-704-070-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-835-087-3  
; Sequence 3, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; TITLE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-3

Query Match	100.0%	Score 590;	DB 3;	Length 112;
Best Local Similarity	100.0%	Pred. No. 2.8e-47;		
Matches 112;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFELNWFQORPQSPRLIYLVSKLD	60	
Db	1	DVVMTQSPVLTIGQPASISCKSSQSLSDSGKTFELNWFQORPQSPRLIYLVSKLD	60	
Qy	61	SGVPRPFGSGSGTDTLTKISRVEADVGYYCWQTHFPYTFGGTRLEIK	112	
Db	61	SGVPRPFGSGSGTDTLTKISRVEADVGYYCWQTHFPYTFGGTRLEIK	112	

RESULT 2  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; TITLE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGQTRLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGQTRLEIK 112

RESULT 3
US-09-840-459-12
; Sequence 12, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12

Query Match      100.0%; Score 590; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60
Db 1 DVVMTQSLPLPVTLGQPASISCKSSQSLSDSGKTFNLWFQQRPGQSPRLIYLVSKLD 60

Qy 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGQTRLEIK 112
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDVGVYVCWQGTTHPPYTFGGQTRLEIK 112

RESULT 4
US-10-766-773-12
; Sequence 12, Application US/10766773
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-610-12

Query Match      100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60
   |||||
Db 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112
   |||||
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 6
US-10-733-563-12
; Sequence 12, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12

Query Match      100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60
   |||||
Db 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112
   |||||
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
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; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-662-061-14

Query Match      100.0%; Score 590; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60
   |||||
Db 1 DVVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLD 60

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112
   |||||
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 8
US-09-840-459-106
; Sequence 106, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-09-840-459-106

Query Match      99.0%; Score 584; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLDS 61
   |||||
Db 2 VVMTQSPSLPVLTLGQPASISCKSSQSLDSDGKTFNLNWFQORFGQSPRRILIYLVSKLDS 61

QY 62 GVPDRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112
   |||||
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDGVIYVCWQGTFFPYTFGGQTRLEIK 112

RESULT 9
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US-10-766-773-106
; Sequence 106, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-10-766-773-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112

RESULT 10
US-10-766-610-106
; Sequence 106, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
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; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
US-10-766-610-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112

RESULT 11
US-10-733-563-106
; Sequence 106, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain
US-10-733-563-106

Query Match          99.0%; Score 584; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61
Db 2 VVMTQSPSLPVTILGQPASISCKSSQSLDSDGKTFLNWFQQRPGQSPRLIYLVSKLDS 61

Qy 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112
Db 62 GVPDRFSGSGGTDTLTLSIRVEADVGYYVCWQGTTHPPYTFGGQTRLEIK 112

RESULT 12
US-09-835-087-4
; Sequence 4, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
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Db 1 DVVMTQSPVSLPVTLGQPASISCKSSQSLDSDGKTFPLNWLQRFQSPRRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYWCQGTHFPYTFGQGTLEIK 112  
Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYWCQGTHFPYTFGQGTLEIK 112

Search completed: January 28, 2006, 10:11:21  
Job time : 47.7598 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 6.72673 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-12

Perfect score: 590

Sequence: 1 DVVMTQSPSLPVTIGQPAS.....CMQGTTHPPYFGQTRLRIK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New.\*

- 1: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	7	US-11-075-184A-3
2	577	97.8	112	7	US-11-075-184A-4
3	572	96.9	112	7	US-11-075-184A-7
4	570	96.6	112	7	US-11-075-184A-5
5	565	95.8	112	7	US-11-075-184A-6
6	542	91.9	132	6	US-10-789-273-11
7	536	90.8	112	7	US-11-075-184A-1
8	536	90.8	132	6	US-10-789-273-5
9	520	88.1	132	6	US-10-789-273-2
10	510	86.4	253	7	US-11-054-515-1964
11	507	85.9	112	6	US-10-477-950-4
12	491.5	83.3	244	7	US-11-054-515-1991
13	490.5	83.1	261	7	US-11-056-825-2
14	485.5	82.3	259	7	US-11-056-825-7
15	483	81.9	113	7	US-11-054-669-122
16	480	81.4	139	7	US-11-128-900-25
17	480	81.4	139	7	US-11-128-900-114
18	474	80.3	132	6	US-10-489-866-30
19	470	79.7	100	7	US-11-054-669-75
20	470	79.7	100	7	US-11-054-669-76
21	470	79.7	100	7	US-11-084-554-103
22	470	79.7	100	7	US-11-084-554-107
23	470	79.7	100	7	US-11-128-900-113
24	470	79.7	100	7	US-11-004-590-82
25	470	79.7	100	7	US-11-004-590-83

26	459	77.8	112	7	US-11-012-353-57
27	457	77.5	112	7	US-11-012-353-61
28	457	77.5	131	7	US-11-012-353-63
29	456	77.3	112	7	US-11-012-353-65
30	456	77.3	131	7	US-11-012-353-67
31	451	76.4	112	7	US-11-012-353-60
32	451	76.4	113	6	US-10-834-397-15
33	447	75.8	113	6	US-10-932-334-60
34	447	75.8	113	6	US-10-932-334-65
35	447	75.8	131	7	US-11-125-837-23
36	446	75.6	113	6	US-10-932-334-59
37	445	75.4	112	7	US-11-012-353-55
38	445	75.4	112	7	US-11-012-353-56
39	445	75.4	263	7	US-11-089-266-66
40	444	75.3	144	7	US-11-055-163-16
41	443	75.1	113	6	US-10-932-334-61
42	443	75.1	149	7	US-11-089-266-2
43	443	75.1	239	7	US-11-139-499-6
44	441	74.7	113	6	US-10-489-866-20
45	441	74.7	116	7	US-11-065-943-49

ALIGNMENTS

RESULT 1  
US-11-075-184A-3  
; Sequence 3, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; PRIOR FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKA  
US-11-075-184A-3

Query Match	100.0%	Score 590;	DB 7;	Length 112;
Best Local Similarity	100.0%	Pred. No. 1.2e-40;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DVVMTQSPSLPVTIGQPASISCKSSQSLSDGKTFILNWFQQRFGSPRLIYLVS	KLD 60	
Db	1	DVVMTQSPSLPVTIGQPASISCKSSQSLSDGKTFILNWFQQRFGSPRLIYLVS	KLD 60	
QY	61	SGVPRFSGSGSGTDTFLTKISRVEADGVVYCMQGTTHPPYFGQTRLRIK	112	
Db	61	SGVPRFSGSGSGTDTFLTKISRVEADGVVYCMQGTTHPPYFGQTRLRIK	112	

RESULT 2  
US-11-075-184A-4  
; Sequence 4, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669

; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKB  
US-11-075-184A-4

Query Match 97.8%; Score 577; DB 7; Length 112;  
Best Local Similarity 98.2%; Pred. No. 1.3e-39;  
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWFQRPQSPRRLIYLVSKLD 60  
Db 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWLLQRPQSPRRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112  
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112

## RESULT 3

US-11-075-184A-7  
; Sequence 7, Application US/11075184A  
; Publication No. US20050260139A1

; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-7

Query Match 96.9%; Score 572; DB 7; Length 112;  
Best Local Similarity 97.3%; Pred. No. 3.3e-39;  
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWFQRPQSPRRLIYLVSKLD 60  
Db 1 DVWMTQSLSLPVTLGHPASISCKSSQSLLSDSGKTFNLWLLQRPQSPRRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112  
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112

## RESULT 4

US-11-075-184A-5  
; Sequence 5, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel

; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKC  
US-11-075-184A-5

Query Match 96.6%; Score 570; DB 7; Length 112;  
Best Local Similarity 97.3%; Pred. No. 4.7e-39;  
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWFQRPQSPRRLIYLVSKLD 60  
Db 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWLLQRPQSPRRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112  
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112

## RESULT 5

US-11-075-184A-6  
; Sequence 6, Application US/11075184A  
; Publication No. US20050260139A1

; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelhiem International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKC  
US-11-075-184A-6

Query Match 95.8%; Score 565; DB 7; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-38;  
Matches 108; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 DVWMTQSLSLPVTLGQPASISCKSSQSLLSDSGKTFNLWFQRPQSPRRLIYLVSKLD 60  
Db 1 DVWMTQSLSLPVTLGHPASISCKSSQSLLSDSGKTFNLWLLQRPQSPRRLIYLVSKLD 60  
Qy 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112  
Db 61 SGVPDRFSGSGGTDTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK 112

## RESULT 6

US-10-789-273-11  
; Sequence 11, Application US/10789273  
; Publication No. US20050249725A1



GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
; OTHER INFORMATION: humanized 3D6 light chain variable region  
US-10-789-273-11

Query Match 91.9%; Score 542; DB 6; Length 132;  
Best Local Similarity 91.1%; Pred. No. 8.6e-37;  
Matches 102; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60  
DB 21 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTYLNWLLQKPGQSPQRILYLVSKLD 80  
QY 61 SGVDPDFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 112  
DB 81 SGVDPDFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 132

RESULT 7  
US-11-075-184A-1  
; Sequence 1, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Murine 1D9 antibody kappa light chain variable (VK) region;  
; OTHER INFORMATION: presumably Mus musculus  
US-11-075-184A-1

Query Match 90.8%; Score 536; DB 7; Length 112;  
Best Local Similarity 89.3%; Pred. No. 2.2e-36;  
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLD 60  
DB 1 DVVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPQRILYLVSKLD 60

QY 61 SGVDPDFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 112  
DB 61 SGVDPDFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 112  
RESULT 8  
US-10-789-273-5  
; Sequence 5, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(20)  
; OTHER INFORMATION: humanized 3D6 light chain variable region  
US-10-789-273-5

Query Match 90.8%; Score 536; DB 6; Length 132;  
Best Local Similarity 91.0%; Pred. No. 2.5e-36;  
Matches 101; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 VVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTFLNWFQRPQSPRRILYLVSKLDS 61  
DB 22 VVMTQSPSLPVTIGQPASISCKSSQSLDSDGKTYLNWLLQKPGQSPQRILYLVSKLDS 81  
QY 62 GVPDRFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 112  
DB 82 GVPDRFSGSGGTDTFLKISRVEADGVVYCWQGTTHPPTFGQGTREIK 132

RESULT 9  
US-10-789-273-2  
; Sequence 2, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 132  
; TYPE: PRT

```
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-789-273-2

Query Match      88.1%; Score 520; DB 6; Length 132;
Best Local Similarity 86.5%; Pred. No. 4.6e-35;
Matches 96; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 2 VVMTQSPSLPVTLGQPASISCKSSQSLSDGKTFLNWFQORPGQSPRLIYLVSKLDS 61
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 GVPDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGTGLEIK 112
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 82 GVPDRFSGSGGTDFTLKISRVEAEDGLXYCWQGTFFPYTFGGTGLEIK 132
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
US-11-054-515-1964
; Sequence 1964, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1964
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1964

Query Match      86.4%; Score 510; DB 7; Length 253;
Best Local Similarity 86.6%; Pred. No. 4.8e-34;
Matches 97; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DVVMTQSPSLPVTLGQPASISCKSSQSLSDGKTFLNWFQORPGQSPRLIYLVSKLD 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 141 DVVMTQSPSLPVTLGQPASISCKSSQSLVSDGNTYLNWFLQRPQSPRLIYKVSNRD 200
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 SGVDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGTGLEIK 112
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 201 SGVDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTATRPFTFGGTGKWEIK 252
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
US-10-477-950-4
; Sequence 4, Application US/10477950
```

```
; Publication No. US20050260207A1
; GENERAL INFORMATION:
; APPLICANT: Krka tovarna zdravlil, d.d., Novo mesto
; TITLE OF INVENTION: Monoclonal antibody neutralising Cathepsin B activity
; TITLE OF INVENTION: and uses thereof
; FILE REFERENCE: 28880
; CURRENT APPLICATION NUMBER: US/10/477,950
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: SI/P200100132
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mouse
US-10-477-950-4

Query Match      85.9%; Score 507; DB 6; Length 112;
Best Local Similarity 84.8%; Pred. No. 4.3e-34;
Matches 95; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DVVMTQSPSLPVTLGQPASISCKSSQSLSDGKTFLNWFQORPGQSPRLIYLVSKLD 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 SGVDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGTGLEIK 112
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 SGVDRFSGSGGTDFTLKISRVEAEDGVVYCWQGTFFPYTFGGTGLEIK 112
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
US-11-054-515-1991
; Sequence 1991, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1991

Query Match      83.3%; Score 491.5; DB 7; Length 244;
Best Local Similarity 87.5%; Pred. No. 1.3e-32;
Matches 98; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
```

Qy	1	DVWMTQSPLSPVTILGQPASISCKSSQSLDDSDGKTFLNWFQORPQSGPRRLIYLVSULD	60
		:           :           :	
Db	133	DVWMTQSPLSPVTILGQPASISCKSSQLVHSDGNTLYLNMFWQORPQSGPRRLIYKVSNRD	192
		:           :           :	
Qy	61	SGVPDRFSGSGGTFTLKISRVEAEDVGVYYCWQGTTHPPYTFGGQTRLEIK	112
		:           :           :	
Db	193	FGVPDRFSGSGGTFTLKISRVEAEDVGVYYCMQOTH-RIFGGQTRLEIK	243

```

RESULT 13
US-11-056-825-2
: Sequence 2, Application US/11056825
: Publication No. US20050255109A1
: GENERAL INFORMATION:
: APPLICANT: Felding-Habermann, Brunhilde
: APPLICANT: Janda, Kim D.
: APPLICANT: Saven, Alan
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
: FILE REFERENCE: SRCP-0042
: CURRENT APPLICATION NUMBER: US/11/056,825
: CURRENT FILING DATE: 2005-02-11
: PRIOR APPLICATION NUMBER: US 60/626,726
: PRIOR FILING DATE: 2004-11-10
: PRIOR APPLICATION NUMBER: US 60/544,807
: PRIOR FILING DATE: 2004-02-13
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: Patent version 3.3
: SEQ ID NO 2
: LENGTH: 261
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Synthetic Construct
US-11-056-825-2

```

```

Query Match      83.1%; Score 490.5; DB 7; Length 261;
Best Local Similarity 82.3%; Pred. No. 1.7e-32;
Matches 93; Conservative 12; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DVMTQSLPLSVTLGPASISCKSSQSLDSDGKTFLNWFOQRPQSGPRRLIYLVSKLD 60
      ::::::::::::::::::::::::::::
Db 134 EIVLTQSLPLSVTLGPASISCRSSQNLVYSDGNTVLSWFQQRPGQSPRRLIYKVSNRD 193
      ::::::::::::::::::::::::::::

Qy 61 SGVDDRSGSGSGTDFTLKISRVAEADGVGYICWQGTHP -PYTFQGQTRLEIK 112
      ::::::::::::::::::::::::::::
Db 194 SGVDDRSGSGSGTDFTLKISRVAEADGVYICWQGTHPRPFGQGTKEIK 246
      ::::::::::::::::::::::::::::

```

```

RESULT 14
US-11-056-825-7
; Sequence 7, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SSCP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-7

```

Query Match	82.3%	Score 485.5	DB 7	Length 259
Best Local Similarity	81.4%	Pred. No. 4.2e-32		
Matches	92	Conservative 12	Mismatches 8	Indels 1
Qy	1	DVWVTQSLPVLTLGPASISCKSSQSLDSDGKTFLNWFQQRPGSGPRRLIYLVSKLD	60	
	:	:	:	:
Db	134	EIVLTQSLPVLTLGPASISCKSSQSLDSDGKTFLNWFQQRPGSGPRRLIYLVSKNRD	193	
Qy	61	SGVPDRFSGSGGTDFTLKLSRVEAEADVGYVYCHQGTHP-PYTFGQGRLEIK	112	
	:	:	:	:
Db	194	SGVPDRFSGSGGTDFTLKLSRVEREDIGVYVYCHQGTHPPTTFGQGTQVKIK	246	

```

RESULT 15
US-11-054-669-122
; Sequence 122, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patencin version 3.3
; SEQ ID NO 122
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-122

```

[illegible]

Search completed: January 28, 2006, 10:12:13  
Job time : 6.72673 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 61.3108 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGLVKPGSRLR.....CTTFYGVGWGQGLTVTSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	620	100.0	117	4	Aae06954 Humanised
2	620	100.0	117	4	Aau09927 Humanised
3	620	100.0	117	5	Abg75536 Humanised
4	620	100.0	117	5	Aaol14980 Humanised
5	620	100.0	117	5	Adf98240 Humanised
6	620	100.0	117	8	Adq89239 Humanised
7	620	100.0	117	9	Aeb09512 Humanised
8	620	100.0	119	4	Aae07034 Humanised
9	620	100.0	119	8	Adq89326 Humanised
10	620	100.0	119	9	Aeb09599 Humanised
11	613	98.9	117	4	Aae06955 Humanised
12	613	98.9	117	5	Abg75537 Humanised
13	613	98.9	117	5	Aaol14981 Humanised
14	613	98.9	117	5	Adf98241 Humanised
15	613	98.9	117	8	Adq89240 Humanised
16	613	98.9	117	9	Aeb09513 Humanised
17	604	97.4	117	4	Aae06956 Humanised
18	604	97.4	117	4	Aau09929 Humanised
19	604	97.4	117	4	Aau09928 Humanised
20	604	97.4	117	5	Abg75538 Humanised
21	604	97.4	117	5	Aaol14982 Humanised
22	604	97.4	117	5	Adf98242 Humanised
23	604	97.4	117	8	Adq89241 Humanised
24	604	97.4	117	9	Aeb09514 Humanised

ALIGNMENTS

RESULT 1  
AAE06954  
ID AAE06954 standard; protein; 117 AA.

XX AC AAE06954;

XX DT 11-SEP-2003 (revised)

DT 16-OCT-2001 (first entry)

XX DE Humanised murine 1D9 antibody heavy chain variable region, 1D9RHA.

XX KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; KW neuroprotective; immunosuppressive; human immunodeficiency virus; KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; KW multiple sclerosis; atherosclerosis; arteriosclerosis; stenosis; asthma; KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; KW inflammatory glomerulopathy; vascular intervention; 1D9 antibody; KW neonatal hyperplasia; VH; heavy chain variable region; 1D9RHA.

XX OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX Key Location/Qualifiers

XX Region 27..35 /label= CDR1

XX Region 50..68 /note= "Complementarity determining region 1"

XX Region /label= CDR2

XX Region 101..106 /note= "Complementarity determining region 2"

XX Region /label= CDR3

XX Region /note= "Complementarity determining region 3"

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX WPI; 2001-489889/53.

DR Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated

XX disorder in a patient, comprises a binding specificity for CCR2, and a

PT non-human antigen binding region and human immunoglobulin.

PT Claim 62; Fig 12; 183pp; English.

XX

CC The patent discloses a humanised antibody or its antigen-binding

CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),

CC comprising an antigen binding region of non-human origin and at least a

CC portion of an immunoglobulin of human origin. The humanised antibodies

CC are useful for inhibiting the interaction of a cell expressing CCR2. They

CC are useful for inhibiting or treating HIV infection. The proteins of the

CC invention are useful for inhibiting leukocyte trafficking, for treating

CC CCR2-mediated disorders such as inflammatory disorder, autoimmune

CC disorders such as rheumatoid arthritis and multiple sclerosis,

CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They

CC are useful in therapy or diagnosis, and in the manufacture of a

CC medicament for treating CCR-2 mediated disease. They are also useful for

CC treating allergy, anaphylaxis, malignancy, chronic and acute

CC inflammation, histamine and IGE-mediated allergic reaction, shock,

CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory

CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis

CC associated with vascular intervention, including angioplasty and/or stent

CC placement in a mammal. Humanised antibodies are also useful for

CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting

CC neointimal hyperplasia of a vessel in a mammal, preferably associated

CC with vascular intervention. The present sequence is humanised murine 1D9

CC antibody heavy chain variable (VH) region, 1D9RHA. (Updated on 11-SEP-

CC 2003 to standardise OS field)

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 620; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 8.1e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNTAT 60

Db 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNTAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

RESULT 2

ID AAU09927 standard; protein; 117 AA.

XX

AC AAU09927;

XX

XX 18-JUN-2002 (first entry)

XX

DE Humanised 1D9 heavy chain variable region, 1D9RHA protein sequence.

XX

KW Human; mouse; 4B4'CL heavy chain variable region; vasotropic;

KW antiinflammatory; collagen disease; immunosuppressive; antiaesthetic;

KW insulin-dependent diabetes mellitus; inflammatory bowel disease;

KW ulcerative colitis; 1D9RHA; graft rejection; allergic disease;

KW antiperititic; antiarthritic; nephrotropic; antithyroid; restenosis;

KW dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury;

KW autoimmune disease; immunoglobulin; complementarity determining region;

XX CDR; CD18; CCR2; atherosclerosis; mutant; mutein.

XX

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

OS Chimeric.

XX

PH Key Location/Qualifiers

PT Region 27. .30 /note= "Part of H1 structure loop"

FT Region 31. .35 /note= "Complementarity determining region 1 (CDR1),

FT grafted from mouse mAb 1D9 heavy chain sequence

FT (AAU09919)"

FT Region 50. .68 /note= "Complementarity determining region 2 (CDR2),

FT grafted from mouse mAb 1D9 heavy chain sequence

FT (AAU09919)"

FT Region 101. .108 /note= "Complementarity determining region 3 (CDR3),

FT grafted from mouse mAb 1D9 heavy chain sequence

FT (AAU09919)"

XX WO200170266-A2.

XX 27-SEP-2001.

XX 15-MAR-2001; 2001WO-US008266.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Rao PE;

XX WPI; 2001-607511/69.

XX Inhibiting stenosis or restenosis of a blood vessel following vascular

XX injury or angioplasty in a subject by administering agent which inhibits

XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.

PS Claim 32; Fig 18; 108pp; English.

XX

CC The present invention relates to a new method of inhibiting stenosis or

CC restenosis of a blood vessel following vascular injury in a subject. The

CC new method comprises administering to the subject agents which inhibit

CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a

CC site of vascular injury by binding CD18 or CCR2. The method of the

CC invention inhibits stenosis or restenosis of a blood vessel following

CC vascular injury arising from a vascular intervention procedure such as

CC vascular by-pass or transplantation surgery. The method is also useful

CC for treating a subject having an inflammatory disease or condition

CC mediated by neutrophil and mononuclear cell activity e.g. asthma and

CC graft versus host disease. Chronic inflammatory diseases of the lung,

CC collagen diseases, and insulin-dependent diabetes mellitus can also be

CC treated. The method is further useful for treating inflammatory bowel

CC diseases, such as ulcerative colitis. Additional diseases or conditions

CC include inflammatory or allergic diseases and conditions, including

CC systemic anaphylaxis of hypersensitivity responses, drug allergies,

CC psoriasis and inflammatory dermatoses, autoimmune diseases such as

CC arthritis, graft rejection and other diseases including atherosclerosis.

CC This sequence represents the variable region of one of several humanised

CC 1D9 heavy chains (AAU09927-AAU09930). These heavy chains were used in the

CC invention for the production of anti-CCR2 antibody or antigen-binding

CC fragment

XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 620; DB 4; Length 117;

Best Local Similarity 100.0%; Pred. No. 8.1e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNTAT 60

Db 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNTAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

RESULT 3  
 ABG75536  
 ID ABG75536 standard; protein; 117 AA.  
 AC  
 AC ABG75536;  
 DT  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHAVH.  
 XX  
 KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
 KW endovascular stenting; prosthetic valve; transplantation;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
 KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHAVH;  
 KW heavy chain variable region; VH; complementarity determining region; CDR;  
 KW mutant; mutein.  
 XX  
 XX Mus sp.  
 OS  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /note="Mouse complementarity determining region 1  
 FT (CDR1)"  
 FT Region 50..68  
 FT /note="Mouse complementarity determining region 2  
 FT (CDR2)"  
 FT Region 101..106  
 FT /note="Mouse complementarity determining region 3  
 FT (CDR3)"  
 XX  
 XX US2002106369-A1.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 15-MAR-2001; 2001US-00809739.  
 XX  
 XX 17-MAR-2000; 2000US-00528267.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Horvath CJ, Rao PE;  
 XX  
 XX WPI; 2002-697861/75.  
 XX  
 XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 PT administering first and second agents that inhibit adhesion and/or  
 PT recruitment of neutrophils and mononuclear cells, respectively to site of  
 PT vascular injury.  
 XX  
 XX Claim 32; Fig 18; 59pp; English.  
 XX  
 CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty

CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC asthma and graft-versus-host disease, cholecystitis, chronic bronchitis,  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
 CC chain variable region (VH), 1D9RHAVH, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human 4B4 CL  
 CC mAb VH regions  
 XX  
 SQ Sequence 117 AA;  
 Query Match 100.0%; Score 620; DB 5; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYANMVVRQAQPGKLEWVGRIKNNYAT 60  
 DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYANMVVRQAQPGKLEWVGRIKNNYAT 60  
 QY 61 YYADSVKDRPTISRDDSKNTLYLQWNSLKTEDTAVYCTTFFGNGWGOGTLVTVSS 117  
 DB 61 YYADSVKDRPTISRDDSKNTLYLQWNSLKTEDTAVYCTTFFGNGWGOGTLVTVSS 117  
 RESULT 4  
 AA014980  
 ID AA014980 standard; protein; 117 AA.  
 AC  
 AC AA014980;  
 DT  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Humanised murine heavy chain variable region (1D9RHa Vh).  
 KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody heavy chain variable region; 1D9RHa Vh.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 XX US2002042370-A1.  
 XX  
 XX 11-APR-2002.  
 XX  
 XX 13-APR-2001; 2001US-00835087.  
 XX  
 XX 14-APR-2000; 2000US-00549448.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Hancock WJ;  
 XX  
 XX WPI; 2002-351265/38.  
 XX  
 XX Inhibiting graft rejection, graft versus host disease or chronic

PT rejection of a transplanted graft, involves administering a CCR2  
PT antagonist.

XX Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
CC versus host disease or chronic rejection of a transplanted graft. The  
CC method involves administering an antagonist of CC chemokine receptor 2  
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
CC complementarity determining regions from various non-human origins). CCR2  
CC is known to be involved in the rejection of transplanted grafts. The  
CC method of the invention is useful for inhibiting graft rejection -  
CC particularly allografts such as kidney, liver, lung, heart-lung,  
CC pancreas, bowel and heart. The method of the invention is also useful for  
CC inhibiting graft versus host disease and for inhibiting chronic rejection  
CC of a transplanted graft. The present amino acid sequence represents a  
CC humanised murine antibody heavy chain variable region (1D9Rha Vh)

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

RESULT 5

ADF98240  
ID ADF98240 standard; protein; 117 AA.

XX ADF98240;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 heavy chain variable region, 1D9RHA VH, SEQ ID 10.

XX Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft versus host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.

XX Synthetic.

OS Mus musculus.

OS Homo sapiens.

XX WO200178653-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012139.

XX 14-APR-2000; 2000US-00549448.

PA (MILL-) MILLENNIUM PHARM INC.

XX Hancock WW;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
PT involves use of CC chemokine receptor 2 inhibitor.

XX Claim 26; Fig 2; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection  
CC or graft versus host diseases. The method comprises administration of a

CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
CC recipient of a transplanted graft. The CCR2 function antagonist is an  
CC anti-CCR2 antibody or its antigen-binding fragment (ADF98233-ADF98237,  
CC ADF98240-ADF98249). The method is useful for inhibiting rejection,  
CC particularly chronic rejection of a graft, particularly an allograft of  
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
CC inhibiting graft versus host disease for a bone marrow graft.

XX Sequence 117 AA;

Query Match 100.0%; Score 620; DB 5; Length 117;  
Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLVTVSS 117

RESULT 6

ADQ89239  
ID ADQ89239 standard; protein; 117 AA.

XX ADQ89239;

XX 21-OCT-2004 (first entry)

XX Humanised immunoglobulin protein #5.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.

XX Synthetic.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

XX 26-JUN-2002; 2002US-0392364P.

XX 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

PA (PONA/) PONAETH P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.

XX Claim 1; SEQ ID NO 17; 129pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised



immunoglobulin protein of the invention.

Sequence 117 AA;

Query Match 100.0%; Score 620; DB 8; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60  
 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60

61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGWGQGLTVTVSS 117  
 61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGWGQGLTVTVSS 117

RESULT 7  
 AEB09512  
 ID AEB09512 standard; protein; 117 AA.  
 AC AEB09512;  
 DT 08-SEP-2005 (first entry)  
 DE Humanized 1D9 heavy chain variable region SEQ ID NO 17.  
 KW antinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain variable region.  
 OS Synthetic.  
 PN WO2005060368-A2.  
 XX 07-JUL-2005.  
 XX 10-DEC-2003; 2003WO-US039599.  
 XX 10-DEC-2003; 2003WO-US039599.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PI Okeefe T, Ponath P;  
 XX WPI; 2005-488561/49.  
 XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.  
 XX Claim 1; SEQ ID NO 17; 192pp; English.

The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (1); a  
 CC construct comprising nucleic acid molecule encoding (1); and host cell  
 CC comprising the nucleic acid molecule. (1) Is useful as a therapeutic

agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g. in  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of a humanized 109  
 CC heavy chain variable region used in the creation of a humanized anti-CCR2  
 CC -antibody.

Sequence 117 AA;

Query Match 100.0%; Score 620; DB 9; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60  
 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIITKNNYAT 60

61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGWGQGLTVTVSS 117  
 61 YYADSVKDRPTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGWGQGLTVTVSS 117

RESULT 8  
 AAE07034  
 ID AAE07034 standard; protein; 119 AA.  
 XX AAE07034;  
 XX 11-SEP-2003 (revised)  
 DT 16-OCT-2001 (first entry)  
 DE Humanised murine antibody heavy chain 1D9RHA protein.  
 KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention; ID9RHA.  
 XX neointimal hyperplasia; antibody 1D9 heavy chain; ID9RHA.

Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX WO200157226-A1.  
 XX 09-AUG-2001.  
 XX 02-FEB-2001; 2001WO-US003537.  
 XX 03-FEB-2000; 2000US-00497625.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
 XX WPI; 2001-488888/53.  
 XX N-PSDB; AAD13179.  
 XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
 PT disorder in a patient, comprises a binding specificity for CCR2, and a  
 PT non-human antigen binding region and human immunoglobulin.  
 XX Disclosure; Fig 23; 183pp; English.

CC The patent discloses a humanised antibody or its antigen-binding  
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
 CC comprising an antigen binding region of non-human origin and at least a  
 CC portion of an immunoglobulin of human origin. The humanised antibodies  
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
 CC are useful for inhibiting or treating HIV infection. The proteins of the  
 CC invention are useful for inhibiting leukocyte trafficking, for treating  
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
 CC disorders such as rheumatoid arthritis and multiple sclerosis,  
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
 CC are useful in therapy or diagnosis, and in the manufacture of a  
 CC medicament for treating CCR-2 mediated disease. They are also useful for  
 CC treating allergy, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,  
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
 CC associated with vascular intervention, including angioplasty and/or stent  
 CC placement in a mammal. Humanised antibodies are also useful for  
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
 CC with vascular intervention. The present sequence is humanised murine  
 CC antibody heavy chain region, 1D9RHA. 1D9RHA sequence consist of the  
 CC complementarity determining regions (CDRs) of the murine 1D9 antibody  
 CC heavy chain variable (VH) region genetically inserted into the framework  
 CC regions (FRs) of the human 4B4'CL antibody VH region. (Updated on 11-SEP-  
 CC 2003 to standardise OS field)

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 620; DB 4; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
 Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 9

ID AQ89326 standard; protein; 119 AA.

XX AC AQ89326;

XX DT 21-OCT-2004 (first entry)

XX DE Humanised immunoglobulin protein #9.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 KW inflammatory disease; autoimmune disorder; graft rejection;  
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 KW anti-HIV; virucide; antiarteriosclerotic.

XX OS Synthetic.

XX FN US2004151721-A1.

XX PD 05-AUG-2004.

XX PF 10-DEC-2003; 2003US-00733563.

XX PR 19-OCT-2001; 2001US-0350166P.

XX PR 26-JUN-2002; 2002US-0392364P.

XX PR 17-OCT-2002; 2002US-00272899.

XX XX (O'KEEFE/) O'KEEFE T.

XX FA (PONA/) PONA P.

XX O'Keefe T, Ponath P;

XX WPI; 2004-580175/56.  
 DR N-PSDB; AQ89319.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
 PT useful for diagnosing and/or treating inflammatory or autoimmune  
 PT diseases, and HIV infection.

XX Disclosure; SEQ ID NO 104; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
 CC infection and atherosclerosis. This sequence represents a humanised  
 CC immunoglobulin protein of the invention.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 620; DB 8; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-48;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIITKNNYAT 60  
 Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
 Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10

ID AEB09599 standard; protein; 119 AA.

XX AC AEB09599;

XX DT 08-SEP-2005 (first entry)

XX DE Humanized heavy chain 1D9RHA.

XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain variable region.

XX OS Synthetic.

XX FN WO2005060368-A2.

XX PD 07-JUL-2005.

XX PF 10-DEC-2003; 2003WO-US039599.

XX PR 10-DEC-2003; 2003WO-US039599.

XX FA (MILL-) MILLENNIUM PHARM INC.

XX PI O'Keefe T, Ponath P;

XX WPI; 2005-488561/49.

DR N-PSDB; AEB09592.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune

PT diseases.

PS Disclosure; SEQ ID NO 104; 192pp; English.

XX

CC The invention describes a humanized immunoglobulin (I) or its antigen binding portion having binding specificity for CC-chemokine receptor 2 (CCR2) and having a heavy chain and a light chain, where the heavy chain comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110) sequence, given in specification or its portion, and the light chain comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given in specification. Also described are: a humanized immunoglobulin heavy chain, or its antigen binding fragment, having binding specificity for CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the amino acid of (SEQ ID NO: 110), or its portion; and a humanized immunoglobulin light chain, or its antigen binding fragment, having binding specificity for CCR2 and comprising the amino acid (SEQ ID NO: 12) sequence, given in specification. The following are disclosed: isolated nucleic acid molecules comprising nucleic acid sequence encoding (I); a construct comprising nucleic acid molecule encoding (I); and host cell comprising the nucleic acid molecule. (I) Is useful as a therapeutic agent for controlling lymphocyte homing the mucosal lymphoid tissue thus reducing inflammatory response for use in the treatment of diseases associated with leukocyte infiltration of tissue, e.g. in the treatment of inflammatory diseases, autoimmune diseases, graft rejection, HIV infection and monocyte-mediated disorders such as atherosclerosis. (I) Is useful for detecting and/or measuring the level of CCR2 in a sample (e.g. tissues or body fluids such as inflammatory exudates, blood, serum, bowel fluid), and for modulating binding function and/or leukocyte trafficking modulated by CCR2. This is the amino acid sequence of humanized heavy chain 1D9RHA.

XX

XX Sequence 119 AA;

Query Match 100.0%; Score 620; DB 9; Length 119;

Best Local Similarity 100.0%; Pred. No. 8.3e-48;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60

DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFFYGNVGWGQGLTLVTSS 117

DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFFYGNVGWGQGLTLVTSS 117

RESULT 11

AAE06955

ID AAE06955 standard; protein; 117 AA.

AC AAE06955;

XX

XX 11-SEP-2003 (revised)

DT 16-OCT-2001 (first entry)

XX

XX Humanised murine 1D9 antibody heavy chain variable region, 1D9RHB.

DE

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neonatal hyperplasia; VH; heavy chain variable region; 1D9RHB.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

XX Key Location/Qualifiers

PH

FT Region 27..35

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT 50..68

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT 101..106

FT /label= CDR3

FT /note= "Complementarity determining region 3"

XX

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

XX Claim 62; Fig 12; 183pp; English.

CC The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and Ige-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neonatal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is humanised murine 1D9 antibody heavy chain variable (VH) region, 1D9RHB. (Updated on 11-SEP-2003 to standardise OS field)

XX

XX Sequence 117 AA;

Query Match 98.9%; Score 613; DB 4; Length 117;

Best Local Similarity 98.3%; Pred. No. 3.4e-47;

Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60

DB 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMWVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFFYGNVGWGQGLTLVTSS 117

DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFFYGNVGWGQGLTLVTSS 117

RESULT 12

ABG75537

ID ABG75537 standard; protein; 117 AA.

XX

AC ABG75537;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHBVH.  
 XX  
 KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
 KW endovascular stenting; prosthetic valve; transplantation;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
 KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RHBVH;  
 KW heavy chain variable region; VH; complementarity determining region; CDR;  
 KW mutant; mutein.  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 28 /note= "Thr derived from the mouse 1D9 mAb sequence"  
 FT FT  
 FT Misc-difference 30 /note= "Ser derived from the mouse 1D9 mAb sequence"  
 FT 31..35  
 FT /note= "Mouse complementarity determining region 1  
 (CDR1)"  
 FT Region 50..68  
 FT /note= "Mouse complementarity determining region 2  
 (CDR2)"  
 FT Region 101..106  
 FT /note= "Mouse complementarity determining region 3  
 (CDR3)"  
 FT FT  
 FN US2002106369-A1.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 15-MAR-2001; 2001US-00809739.  
 XX  
 PR 17-MAR-2000; 2000US-00528267.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Horvath CJ, Rao PE;  
 XX WPI; 2002-697861/75.  
 XX  
 FT Inhibiting (re)stenosis of blood vessel following vascular injury, by  
 FT administering first and second agents that inhibit adhesion and/or  
 FT recruitment of neutrophils and mononuclear cells, respectively to site of  
 FT vascular injury.  
 XX  
 PS Claim 32; Fig 18; 59pp; English.  
 XX  
 CC The invention discloses a method for inhibiting stenosis or restenosis of  
 CC a blood vessel following vascular injury in a subject. The method  
 CC involves administering to the subject a first therapeutic agent, which  
 CC comprises an antibody or its antigen binding fragment which binds a  
 CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
 CC of neutrophils to a site of vascular injury and a second therapeutic  
 CC agent, which comprises an antagonist of CCR2 function, that inhibits  
 CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
 CC injury. The vascular injury arises from a vascular intervention procedure  
 CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty

CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
 CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
 CC stenting, insertion of a prosthetic valve and transplantation of organs,  
 CC tissues or cells. The method is also useful for treating inflammatory  
 CC diseases or conditions mediated by early neutrophil activity and later  
 CC mononuclear cell activity. Preferably, the method is useful for treating  
 CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
 CC asthma and graft-versus-host disease, chronic inflammatory disease of  
 CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
 CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
 CC mellitus. The method is also useful for treating inflammatory bowel  
 CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
 CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
 CC chain variable region (VH), 1D9RHBVH, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human 4B4'CL  
 CC mAb VH regions with a mouse derived Thr at position 28 and Ser at  
 CC position 30  
 XX  
 SQ Sequence 117 AA;  
 Query Match 98.9%; Score 613; DB 5; Length 117;  
 Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
 Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRIITKNNYAT 60  
 Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRIITKNNYAT 60  
 Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGVNGVGGGLTVTVSS 117  
 Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYCTTFYGVNGVGGGLTVTVSS 117  
 RESULT 13  
 AA014981  
 ID AA014981 standard; protein; 117 AA.  
 XX  
 AC AA014981;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Humanised murine heavy chain variable region (1D9RHB VH).  
 XX  
 KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody heavy chain variable region; 1D9RHB VH.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 FN US2002042370-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 13-APR-2001; 2001US-00835087.  
 XX  
 PR 14-APR-2000; 2000US-00549448.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 FI Hancock WW;  
 DR WPI; 2002-351265/38.  
 XX

PT Inhibiting graft rejection, graft versus host disease or chronic  
 PT rejection of a transplanted graft, involves administering a CCR2  
 antagonist.

PS Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody heavy chain variable region (1D9RHB VH)

XX Sequence 117 AA;

Query Match 98.9%; Score 613; DB 5; Length 117;  
 Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
 Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGSRLRLSCAAGFTPSAYAMNVRQAPGKGLEWGRIRTKNNYAT 60  
 DB 1 EVQLVESGGGLVKPGSRLRLSCAAGFTPSAYAMNVRQAPGKGLEWGRIRTKNNYAT 60  
 QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGGTLVTYSS 117  
 DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGGTLVTYSS 117

RESULT 14

ADP98241  
 ID ADP98241 standard; protein; 117 AA.

XX ADP98241;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 heavy chain variable region, 1D9RHB VH, SEQ ID 11.

XX Immunosuppressive; CCR2 function inhibitor; graft rejection;

XX graft versus host disease; CC chemokine receptor 2; CCR2;

XX anti-CCR2 antibody.

XX Synthetic.

XX Mus musculus.

XX Homo sapiens.

XX WO200178653-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US012139.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WM;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft versus host disease  
 PT involves use of CC chemokine receptor 2 inhibitor.  
 XX Claim 26; Fig 2; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection

CC or graft versus host diseases. The method comprises administration of a  
 CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
 CC recipient of a transplanted graft. The CCR2 function antagonist is an  
 CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADP98237,  
 CC ADP98240-ADP98249). The method is useful for inhibiting rejection,  
 CC particularly chronic rejection of a graft, particularly an allograft of  
 CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
 CC inhibiting graft versus host disease for a bone marrow graft.

XX Sequence 117 AA;

Query Match 98.9%; Score 613; DB 5; Length 117;  
 Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
 Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGSRLRLSCAAGFTPSAYAMNVRQAPGKGLEWGRIRTKNNYAT 60  
 DB 1 EVQLVESGGGLVKPGSRLRLSCAAGFTPSAYAMNVRQAPGKGLEWGRIRTKNNYAT 60  
 QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGGTLVTYSS 117  
 DB 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGNVGWGGTLVTYSS 117

RESULT 15

ADQ89240

ID ADQ89240 standard; protein; 117 AA.

XX ADQ89240;

XX 21-OCT-2004 (first entry)

XX Humanised immunoglobulin protein #6.

XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;

XX inflammatory disease; autoimmune disorder; graft rejection;

XX HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;

XX anti-HIV; virucide; antiarteriosclerotic.

XX Synthetic.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

XX 26-JUN-2002; 2002US-0392364P.

XX 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

XX (PONA/) PONATH P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,

XX useful for diagnosing and/or treating inflammatory or autoimmune

XX diseases, and HIV infection.

XX Example 2; SEQ ID NO 18; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains  
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
 CC immunoglobulin or its antigen binding fragment comprising the chains. The  
 CC humanised immunoglobulin or its antigen binding fragment preferably  
 CC comprises two heavy chains and two light chains. The humanised  
 CC immunoglobulin and its heavy and light chains are useful for the  
 CC diagnosis, prevention and/or treatment of diseases or conditions  
 CC associated with aberrant expression or activity of the CCR2 polypeptide,  
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV

CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.

XX  
SQ Sequence 117 AA;

Query Match 98.9%; Score 613; DB 8; Length 117;  
Best Local Similarity 98.3%; Pred. No. 3.4e-47;  
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRAQPGKGLEWVGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRAQPGKGLEWVGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNQVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNQVWGQGLTVTVSS 117

Search completed: January 28, 2006, 09:38:13  
Job time : 62.3108 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 11.9459 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-17  
Perfect score: 620  
Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGMGGTLVTVSS 117  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	492.5	79.4	137	2	S42467	Ig heavy chain V r
2	490	79.0	121	2	S31106	Ig heavy chain - h
3	485	78.2	127	2	S58213	Ig heavy chain V r
4	483	77.9	121	2	H36005	Ig heavy chain V r
5	482	77.7	117	2	S31109	Ig heavy chain V r
6	480	77.4	121	2	A41940	Ig heavy chain V r
7	479.5	77.3	141	2	I32513	Ig heavy chain pre
8	478	77.1	123	2	A36006	Ig heavy chain V r
9	477	76.9	138	2	A30561	Ig heavy chain pre
10	474	76.5	139	2	S31678	Ig heavy chain V r
11	472.5	76.2	126	2	S44107	Ig heavy chain V-D
12	467	75.3	160	2	S05271	Ig heavy chain pre
13	463.5	74.8	122	2	S30533	Ig heavy chain V r
14	463.5	74.8	147	2	I37780	Ig variable region
15	463	74.7	123	2	S26794	Ig heavy chain V r
16	463	74.7	140	2	S31588	Ig heavy chain V r
17	461	74.4	119	2	C36005	Ig heavy chain V r
18	460	74.2	115	1	AVMS06	Ig heavy chain V r
19	460	74.2	119	2	S31107	Ig heavy chain V-I
20	459.5	74.1	120	2	B49590	Ig heavy chain - h
21	458	73.9	138	2	S31666	Ig heavy chain V r
22	457.5	73.8	120	2	S48798	Ig heavy chain V r
23	456	73.5	119	2	S31108	Ig heavy chain V r
24	456	73.5	143	2	S23624	Ig heavy chain - h
25	454.5	73.3	122	2	E36005	Ig heavy chain V r
26	454.5	73.3	124	2	S20775	Ig heavy chain V r
27	454.5	73.3	124	2	S20782	Ig heavy chain V r
28	454	73.2	119	2	D36005	Ig heavy chain V r
29	454	73.2	123	2	S34009	Ig heavy chain V r

30	454	73.2	140	2	S31686	Ig heavy chain V r
31	453.5	73.1	114	2	S46390	Ig heavy chain V r
32	453	73.1	134	2	S31699	Ig heavy chain V r
33	452	72.9	133	2	S34010	Ig heavy chain V r
34	450	72.6	113	1	AVMSAB	Ig heavy chain V-I
35	450	72.6	113	1	AVMSB7	Ig heavy chain V-I
36	450	72.6	115	1	AVMS82	Ig heavy chain V-I
37	450	72.6	123	2	S31114	Ig heavy chain - h
38	448.5	72.3	140	2	S70442	Ig heavy chain pre
39	448	72.3	125	2	S30531	Ig heavy chain V r
40	448	72.3	135	2	S31598	Ig heavy chain V r
41	447.5	72.2	118	2	S31116	Ig heavy chain - h
42	447	72.1	134	2	S31679	Ig heavy chain V r
43	446.5	72.0	122	2	S20772	Ig heavy chain V r
44	446	71.9	121	2	S31113	Ig heavy chain - h
45	445.5	71.9	114	2	S46391	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S42467  
Ig heavy chain V region precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S42467  
R:Shiyanov, P.A.; Bepalov, I.A.; Terletskaya, H.N.; Deyev, S.M.  
submitted to the EMBL Data Library, March 1994  
A:Reference number: S42466  
A:Accession: S42467  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <SH1>  
A:Cross-references: UNIPARC:UPI00001161DB; EMBL:X78107; NID:G460798; PIDN:CAAS4997.1; PII  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match	79.4%	Score	492.5	DB	2	Length	137
Best Local Similarity	79.2%	Pred. No.	3.9e-37				
Matches	95	Conservative	11	Mismatches	9	Indels	5
						Gaps	2
QY	1	EVQLVESGGGLVPGGSLRLSCAASGTFPSYAAMNWVRQAPGKLEWYGRITKNNYAT	60				
DB	20	EVQLVESGGGLVPGKSLKLSAASGTFITFYAMNWVRQAPGKLEWVARISKSNNYAT	79				
QY	61	YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYCTTFYGN--GVGQGTILTVSS	117				
DB	80	YYGNSVKDRFTISRDDSQSMLYLQWNLKTEDTAMYCYV--YGNFPGPAYWGQTLTVTSA	137				

RESULT 2

S31106  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31106  
R:Kaaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Bur. J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31106  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-121 <RAA>  
A:Cross-references: UNIPARC:UPI0000176C8E; EMBL:X62954  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 490; DB 2; Length 121;



```
Best Local Similarity 81.0%; Pred. No. 5.8e-37;
Matches 98; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSANWMSVVRQAPGKGLEWVGRIKSKTDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNVGWQGLTVTVS 116
Db 61 DYAAPVKGRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTIDYYGYMDVWGQGLTVTVS 120
Qy 117 S 117
Db 121 S 121

RESULT 3
S58213
Ig heavy chain V region (anti-F(ab')2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C;Accession: S58213; S58212
R;Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region
A;Reference number: S58206
A;Accession: S58213
A;Molecule type: mRNA
A;Residues: 1-127 <WEL>
A;Cross-references: UNIPARC:UPI000003PEA8; EMBL:X89055; NID:G929638; PIDN:CAA61442.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 485; DB 2; Length 127;
Best Local Similarity 75.6%; Pred. No. 1.7e-36;
Matches 96; Conservative 7; Mismatches 14; Indels 10; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSSTHWRQASGKGLEWVGRIIRKNSVAT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNVGWQGL 110
Db 61 AYASVKGKFTISRDDSENTAYLQMSLKIEDTAVYYCTTGRSSWVRGVNGYGMVDWGQGL 120
Qy 111 TLTVSS 117
Db 121 TTVTVSS 127

RESULT 4
H36005
Ig heavy chain V region (M85) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: H36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: H36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPARC:UPI0000176C28; GB:M34032
C;Genetics:
A;Gene: GDB:IGH@; IGHY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
```

```
Query Match 77.9%; Score 483; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 2.4e-36;
Matches 98; Conservative 3; Mismatches 16; Indels 4; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSANWMSVVRQAPGKGLEWVGRIKSKTDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTTFYGNNG-----VWQGGTLTVTS 116
Db 61 DYAAPVKGRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTDRGGSSQGDYWGQGLTVTVS 120
Qy 117 S 117
Db 121 S 121

RESULT 5
S31109
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31109
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31109
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <RAA>
A;Cross-references: UNIPARC:UPI0000176DCA; EMBL:X62960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
```

```
Query Match 77.7%; Score 482; DB 2; Length 117;
Best Local Similarity 82.1%; Pred. No. 2.9e-36;
Matches 96; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSQAASGFTFSANWMSVVRQAPGKGLEWVGRIKSKTDGGTT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTTFYGNVGWQGLTVTVSS 117
Db 61 DYAAPVKGRFTISRDDSKNTLYLQMSLKTEDTAVYYCTATYYFDYWGQGLTVTVSS 117

RESULT 6
A41940
Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)
A;Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C;Accession: A41940; PL0201
R;Herzon, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss J.;
Proteins 11, 159-175, 1991
A;Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional str
A;Reference number: A41940; MUID:92086633; PMID:1749770
A;Accession: A41940
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-121 <HER>
A;Cross-references: UNIPARC:UPI0000176D34
A;Note: sequence extracted from NCBI backbone (NCBIP:70715)
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from NZ
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0201
```



A:Reference number: A36005; MUID:90349571; PMID:21172723  
A:Accession: A36006  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <SCH>  
A:Cross-references: UNIPARC:UPI000003FEED; GB:M34023  
C:Genetics:  
A:Gene: GDB:IGH6, IGHY1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14Q32.33-14Q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
F:15-100/Domain: immunoglobulin homology <IMW>

Query Match 77.1%; Score 478; DB 2; Lenth  
Best Local Similarity 78.9%; Pred. No. 6.9e-36;  
Matches 97; Conservative 4; Mismatches 16;

QY 1 EVQLVESGGGLVPGGSLRLSCASGFTFSAYAMNWVRQAP  
DB 1 EVQLVESGGGLVPGGSLRLSCASGFTFSANMWSVRQAP  
QY 61 YYADSVKDRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTT-  
DB 61 DYAAPVKGRFTISRDSDSKNTLYLQMSLKTEDTAVYYCTTS  
QY 115 VSS 117  
DB 121 VSS 123

RESULT 9  
A30561  
Ig heavy chain precursor V-III region (4B4) - human (fr  
N;Alternate names: Ig heavy chain V region (DP-38)  
C:Species: Homo sapiens (man)  
C:Date: 23-Mar-1989 #sequence revision 23-Mar-1989 #tex  
C:Accession: A30561; S26931; S34008  
F:Sanz, I.; Dang, H.; Takei, M.; Talal, N.; Capra, J.D.  
J. Immunol. 142, 883-887, 1989  
A:Title: V-H sequence of a human anti-Sm autoantibody. I  
A:Reference number: A30561; MUID:89110065; PMID:2492331  
A:Accession: A30561  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <SAN>  
A:Cross-references: UNIPARC:UPI0000176C80  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences  
A:Reference number: S26985; MUID:93021117; PMID:1404388  
A:Accession: S26931  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 20-119 <TOM>  
A:Cross-references: UNIPARC:UPI000011640B; EMBL:Z123338;  
E:Marlette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A:Title: Nucleotide sequence analysis of the variable  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34008  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 20-119 <MAR>  
A:Cross-references: UNIPARC:UPI000011640B  
C:Superfamily: immunoglobulin V region; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMW>

Query Match 76.9%; Score 477; DB 2; Lenth  
Best Local Similarity 81.5%; Pred. No. 9.5e-36;  
Matches 97; Conservative 5; Mismatches 15;

```
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLEWVGRIRTKNNYAT 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSANMSWVRQAPGKGLEWVGRIRKSTDGGTT 79
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT--FYGNGVWGQGLVTVSS 117
Db 80 DYAAPVKGRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTDSLPHRVWGQGLVTVSS 138

RESULT 10
S31678
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31678
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31678
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CUI>
A:Cross-references: UNIPARC:UPI0000116456; EMBL:Z14169; NID:G31003; PIDN:CAA78538.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:31-116/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 474; DB 2; Length 139;
Best Local Similarity 77.2%; Pred. No. 1.8e-35;
Matches 95; Conservative 6; Mismatches 16; Indels 6; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLEWVGRIRTKNNYAT 60
Db 17 EVQLVESGGGLVPGGSLRLSCAASGFTFSANMSWVRQAPGKGLEWVARIKSTDGGTT 76
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYNG-----VWGQGLTVT 114
Db 77 DYAAPVKGRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTDSIQGNLLAFDIWGQGTMT 136
Qy 115 VSS 117
Db 137 VSS 139

RESULT 11
S44107
Ig heavy chain V-D-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44107
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A:Reference number: S44105
A:Accession: S44107
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <HAW>
A:Cross-references: UNIPARC:UPI0000116634; EMBL:Z31394; NID:9472961; PIDN:CAA83269.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-100/Domain: immunoglobulin homology <IMM>

Query Match 76.2%; Score 472.5; DB 2; Length 126;
Best Local Similarity 74.6%; Pred. No. 2.2e-35;
Matches 94; Conservative 6; Mismatches 13; Indels 13; Gaps 1;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLEWVGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSANMSWVRQASGKGLEWVGRIRSKANSYAT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT-----FYGNGV 107
```

```
Db 61 AYAAASVKGRTISRDDSKNTLYLQNSLKTEDTAVYYCTTRHVNDWFSGYPTLYYIGMDVW 120
Qy 108 GQGTLV 113
Db 121 GQGPTV 126

RESULT 12
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of e
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 467; DB 2; Length 160;
Best Local Similarity 73.2%; Pred. No. 8.7e-35;
Matches 93; Conservative 8; Mismatches 14; Indels 12; Gaps 2;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANMWVRQAPGKGLEWVGRIRTKNNYAT 60
Db 20 EVQLVESGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSAL--SGSGST 77
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTT-----FYGNGVWGQ 110
Db 78 YYADSVKGRFTISRDDSKNTLYLQNSLRAEDTAVYYCAKAVVRGVISYYYIGMDVWGQ 137
Qy 111 TLTVSS 117
Db 138 TTVTVSS 144

RESULT 13
S30533
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S30533
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30533
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MAR>
A:Cross-references: UNIPROT:Q9UL88; UNIPARC:UPI0000176C2E; EMBL:Z18319
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 463.5; DB 2; Length 122;
Best Local Similarity 77.9%; Pred. No. 1.4e-34;
Matches 95; Conservative 7; Mismatches 15; Indels 5; Gaps 2;
```

```
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EQVNVESGGLVQPGGSLRLSCAASRFTPTNAWMSVVRQAPGKLEWGRIRKSDGGTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-FYNG-----VNGQGLVTV 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DYAAPVKGRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFTFSADGDYVRYNGQGLVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 SS 117
   ||
Db 121 SS 122
   ||

RESULT 14
I37780
IG variable region (VDJ) (clone T20-11) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C:Accession: I37780; S25474
R:Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A38876; MUID:94119917; PMID:8290556
A:Accession: I37780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <RES>
A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 463.5; DB 2; Length 147;
Best Local Similarity 73.8%; Pred. No. 1.5e-34;
Matches 93; Conservative 7; Mismatches 15; Indels 11; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 EVQLVESGGLVQPGGSLRLSCAASGFTFSYMSVVRQAPGKLEWVANI--KQDGSEK 71
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----FYNGVWGQGT 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 YYADSVKGRFTISRDNKNTLYLQWNSLRDEDTAVYYCAKGEGWGLYYYGYGMDVWGQGT 131
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 112 LTVSS 117
   ||||
Db 132 TVTVSS 137
   ||||

RESULT 15
S26794
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C:Accession: S26794
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26794
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MOR>
A:Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 463; DB 2; Length 123;
Best Local Similarity 72.8%; Pred. No. 1.5e-34;
Matches 91; Conservative 11; Mismatches 13; Indels 10; Gaps 2;

QY 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIRTKNNYAT 60
```

```
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFSYMSVVRQAPGKLEWVSYISSSS--TI 58
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YYADSVKORFTISRDDSKNTLYLQWNSLKTEDTAVYYCTT-----TPYNGVWGQGT 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLRDEDTAVYYCARSIKYYDENTYYGMDVWGQGT 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 VTVSS 117
   ||||
Db 119 VTVSS 123
   ||||
```

Search completed: January 28, 2006, 09:45:38  
Job time : 11.9459 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 62.0135 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	477.5	77.0	471	2	Q66K04_MOUSE	Q66K04 mus musculus
2	463	74.7	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
3	460	74.2	115	1	HV32_MOUSE	P01801 mus musculus
4	453	73.1	113	2	Q9ULJ0_HUMAN	Q9ulj0 homo sapien
5	453	73.1	131	2	Q9UL88_HUMAN	Q9ul88 homo sapien
6	452	72.9	240	2	Q6SZC9_HUMAN	Q6szc9 homo sapien
7	450	72.6	113	1	HV27_MOUSE	P01796 mus musculus
8	450	72.6	113	1	HV30_MOUSE	P01799 mus musculus
9	450	72.6	115	1	HV33_MOUSE	P01802 mus musculus
10	447	72.1	597	2	Q9GBB9_HUMAN	Q9gbb9 homo sapien
11	446.5	72.0	494	2	Q9K668_HUMAN	Q9k668 homo sapien
12	446.5	72.0	613	2	Q8WUK3_HUMAN	Q8wuk1 homo sapien
13	446	71.9	121	1	HV28_MOUSE	Q9ul71 homo sapien
14	444	71.6	113	1	HV28_MOUSE	Q802i7 mus musculus
15	444	71.6	487	2	Q9UL93_HUMAN	Q9ul93 homo sapien
16	443	71.5	116	2	Q9UL93_HUMAN	Q802i7 mus musculus
17	442.5	71.4	606	2	Q6GMV2_HUMAN	Q6gmv2 homo sapien
18	442	71.3	113	1	HV31_MOUSE	P01800 mus musculus
19	440.5	71.0	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
20	440	71.0	113	1	HV29_MOUSE	P01798 mus musculus
21	439	70.8	468	2	Q569B4_RAT	Q569b4 rattus norv
22	437	70.5	458	2	Q65ZQ1_HUMAN	Q65zq1 homo sapien
23	436.5	70.4	469	2	Q569P4_HUMAN	Q569f4 homo sapien
24	436	70.3	472	2	Q6N089_HUMAN	Q6n089 homo sapien
25	434	70.0	478	2	H6P181_HUMAN	Q6p181 homo sapien
26	432.5	69.8	122	1	HV3G_HUMAN	P01768 homo sapien
27	432.5	69.8	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
28	431	69.5	470	2	Q6RJA4_HUMAN	Q6pia4 homo sapien
29	429	69.2	142	1	HV01_RAT	P01805 rattus norv
30	429	69.2	464	2	Q6PIF8_MOUSE	Q6pif8 mus musculus
31	429	69.2	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien

32	426.5	68.8	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
33	426	68.7	120	1	HV3E_HUMAN	P01766 homo sapien
34	424.5	68.5	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
35	424	68.4	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
36	423	68.2	113	1	HV34_MOUSE	P01803 mus musculus
37	422.5	68.1	119	2	Q5F2I8_MOUSE	Q5f2i8 mus musculus
38	422.5	68.1	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
39	418	67.4	119	2	Q920E7_MOUSE	Q920e7 mus musculus
40	417.5	67.3	122	1	HV21_MOUSE	P01790 mus musculus
41	416.5	67.2	465	2	Q5IOJ0_RAT	Q5ioj0 rattus norv
42	416.5	67.2	475	2	Q6GMW7_HUMAN	Q6gmw7 homo sapien
43	415.5	67.0	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
44	415.5	67.0	114	1	HV3B_HUMAN	P01763 homo sapien
45	415.5	67.0	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv

ALIGNMENTS

RESULT 1  
Q66K04\_MOUSE PRELIMINARY; PRT; 471 AA.  
AC Q66K04\_...  
DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DE Hypothetical protein.  
GN Name=Igh-la;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC080671; AAH80671.1; -; mRNA.  
DR SMR; Q66K04; 20-467.  
DR MGI; MGI:96443; Igh-la.  
DR GO; GO:0003823; F:antigen binding; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG\_v.

```
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 52259 MW; 81BB7C322E315AC2 CRC64;

Query Match 77.0%; Score 477.5; DB 2; Length 471;
Best Local Similarity 75.4%; Pred. No. 7.4e-42;
Matches 92; Conservative 12; Mismatches 13; Indels 5; Gaps 1;

Qy 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIIRTKNNYAT 60
Db 20 EVQLVETGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPGKGLWVGRIIRTKNNYAT 79
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----YGNVGWGQGLTVTV 115
Db 80 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----YGNVGWGQGLTVTV 139
Qy 116 SS 117
Db 140 SS 141

RESULT 2
Q6MZU6_HUMAN
ID Q6MZU6_HUMAN PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFPZP686C15213.
GN Name=DKFPZP686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Rectum tumor;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -; mRNA.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C65E8A0ABC CRC64;

Query Match 74.7%; Score 463; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 2.5e-40;
Matches 90; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

Qy 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIIRTKNNYAT 60
Db 20 EVQLVETGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPGKGLWVGRIIRTKNNYAT 78
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNVGWGQGLTVTVSS 117
Db 116 SS 117
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```
Db 79 YYADSVKGRFTISRDNKSNLYLQMSLRANTAVYYCARDLGHFGLDYGQGLTVTVSS 138

RESULT 3
HV32_MOUSE
ID HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=8209361; PubMed=6798111;
RA Johnson N., Sliankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; C92811; AVMS06.
DR HSP; P01852; INFD.
DR Ensembl; ENSMUSG0000045097; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114 Ig-like
FT DISULFID 22 98 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 74.2%; Score 460; DB 1; Length 115;
Best Local Similarity 73.5%; Pred. No. 1e-40;
Matches 86; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLWVGRIIRTKNNYAT 60
Db 1 EVKLEESGGGLVQPGGSLRLSCVSGFTFSYAMNVRQSPKGLWVAEIRLSNNYAT 60
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFTFYGNVGWGQGLTVTVSS 117
Db 61 HYAESVKGRTISRDDSKSVYLQMNLRADTDGIYCTT--GFAYWGQGLTVTVSA 115

RESULT 4
Q9UL90_HUMAN
ID Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
```

```
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Rasphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RL immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07P CRC64;

Query Match 73.1%; Score 453; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 5.5e-40;
Matches 91; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

Qy 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKLEWVGRIKTKNNYAT 60
Db 1 EVQLVESGGVVPQGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIRYDGSN--K 58

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLR AEDTAVYYCAK--DLN YWGQGLTVTVSS 113

RESULT 5
Q9UL88 HUMAN
ID Q9UL88 HUMAN PRELIMINARY; PRT; 131 AA.
AC Q9UL88
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Clq/7;
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;

Query Match 72.9%; Score 452; DB 2; Length 240;
Best Local Similarity 74.8%; Pred. No. 1.7e-39;
Matches 89; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

Qy 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKLEWVGRIKTKNNYAT 60
Db 1 QVQLVQSGGVLVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSN--K 58

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV--WGQGLTVTVSS 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLR AEDTAVYYCARDWGSDSLDPWGKGLTVTVSS 117
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DR PIR; S21205; S21205.
DR PIR; S30533; S30533.
DR HSSP; P01852; 1NFD.
DR SMR; Q9UL88; 1-131.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 73.1%; Score 453; DB 2; Length 131;
Best Local Similarity 69.6%; Pred. No. 6.5e-40;
Matches 94; Conservative 6; Mismatches 13; Indels 22; Gaps 2;

Qy 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKLEWVGRIKTKNNYAT 60
Db 1 EVQLVESGGGVLPQGGSLRLSCAASGFTFSKAWMSVVRQAPGKLEWVGRIKSKTDGGTT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV----- 106
Db 61 DYAPVKGRFTISRDNKNTLYLQWNSLKTEDTAVYYCTT-----GITMIIVITSSKRT 116

Qy 107 ----WGQGLTVTVSS 117
Db 117 SFYWGQGLTVTVSS 131
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RESULT 6
Q65ZC9 HUMAN
ID Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Clq/7;
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;
```

```
Query Match 72.9%; Score 452; DB 2; Length 240;
Best Local Similarity 74.8%; Pred. No. 1.7e-39;
Matches 89; Conservative 12; Mismatches 14; Indels 4; Gaps 2;

Qy 1 EVQLVESGGLVKPGGSLRLSCAASGFTFSAYAMNWVRQAPGKLEWVGRIKTKNNYAT 60
Db 1 QVQLVQSGGVLVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSN--K 58

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGV--WGQGLTVTVSS 117
Db 59 YYADSVKGRFTISRDNKNTLYLQWNSLR AEDTAVYYCARDWGSDSLDPWGKGLTVTVSS 117
```

```
RESULT 7
HV27 HV27 MOUSE STANDARD; PRT; 113 AA.
AC P01796;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region A4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

PROTEIN SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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removed.
CC
CC PIR; A93818; AVMSAB.
DR HSSP; P01783; IIGC.
DR SMR; P01796; 1-113.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 >113 Ig-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWVGRIRTRKNNYAT 60
Db 1 EVKLEESGGGLVQPGGSKLSCLVASGFTFSNWNWVRQSPKGLVWVAEIRLASHNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTGIYCTT--GFAIYWGQGLTVTV 113

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWVGRIRTRKNNYAT 60
Db 1 EVKLEESGGGLVQPGGSKLSCLVASGFTFSNWNWVRQSPKGLVWVAEIRLASHNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTGIYCTT--GFAIYWGQGLTVTV 113

RESULT 8
HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region ABB-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

PROTEIN SEQUENCE.
RX MEDLINE=82099361; PubMed=679811;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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use as long as its content is in no way modified and this statement is not
removed.
CC
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PROTEIN SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
protein.";
RL Biochemistry 16:1170-1175(1977).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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removed.
CC
CC PIR; A90400; AVMSB7.
DR HSSP; P01810; 2PBJ.
DR SMR; P01799; 1-113.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 >113 Ig-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 72.6%; Score 450; DB 1; Length 113;
Best Local Similarity 73.0%; Pred. No. 1.1e-39;
Matches 84; Conservative 16; Mismatches 13; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLVWVGRIRTRKNNYAT 60
Db 1 EVKLEESGGGLVQPGGSKLSCLVASGFTFSNWNWVRQSPKGLVWVAEIRLASHNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTV 115
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRAEDTGIYCTT--GFAIYWGQGLTVTV 113

RESULT 9
HV33 MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

PROTEIN SEQUENCE.
RX MEDLINE=82099361; PubMed=679811;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
binds inulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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removed.
CC
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CC -----
DR PIR; D92811; AVMS82.
DR HSSP; P01852; INF.
DR SMR; P01802; 1-115.
DR Ensembl; ENSMUSG00000045097; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 114 Ig-like.
FT DISULPID 22 98 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 72.6%; Score 450; DB 1; Length 115;
Best Local Similarity 71.8%; Pred. NO. 1.2e-39;
Matches 84; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLGWGRIPTKNNYAT 60
D 1 EVKLESGGGLVQPGGSKLSVSGFTFSNTMWNVRQSPKGLWVAEIRLKSNNYAT 60

QY 61 YYADSVKDRFTISRDRSKNTLYLQWNSLKTEDTAVYCTTFYGVNGVWGQGLTLVTSS 117
D 61 HYAESVKGRFTISRDRSKSSVYLRMNLRPEDTGIYCTT--GFAYWGQGLTLVTSSA 115

RESULT 10
Q96BB9 HUMAN
ID Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells."
RL Nucleic Acids Res. 17:4385-0 (1989).
DR EMBL; BC015760; AAH15760.1; -; mRNA.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 72.1%; Score 447; DB 2; Length 597;
Best Local Similarity 70.1%; Pred. NO. 1.7e-38;
Matches 89; Conservative 11; Mismatches 15; Indels 12; Gaps 2;

QY 1 EVLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLGWGRIPTKNNYAT 60
D 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMNVRQAPGKGLWWSAI--SGSGGT 77

QY 61 YYADSVKDRFTISRDRSKNTLYLQWNSLKTEDTAVYCTT-----TFYGVNGVWGQ 110
D 78 YYADSVKGRFTISRDRSKNTLYLQWNSLKTEDTAVYCTT-----TFYGVNGVWGQ 137

QY 111 TLVTSS 117
D 138 TLVTSS 144

RESULT 11
Q96K68 HUMAN
ID Q96K68 HUMAN PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Mammary gland;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

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RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikemori Y., Okamoto S.,  
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Maemura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togeishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
RN [2]  
RX PubMed=1555592;  
RP PROTEIN SEQUENCE.  
RA Makiya R., Stigbrand T.;  
RT "Placental alkaline phosphatase has a binding site for the human  
immunoglobulin-G Fc portion.";  
RL Eur. J. Biochem. 205:341-345(1992).  
DR EMBL; AK027379; BAB55072.1; -; mRNA.  
DR PIR; S21205; S21205.  
DR HSSP; P01876; 10W0.  
DR SMR; Q96K68; 264-472.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AE5BAEAC0E CRC64;

Query Match 72.0%; Score 446.5; DB 2; Length 494;  
Best Local Similarity 71.8%; Pred. NO. 1.5e-38;  
Matches 89; Conservative 10; Mismatches 16; Indels 9; Gaps 2;

Qy 1 EVQLVESGGGLVPGGSLRLSQAASGTPFSAYAMNVRQAPKGLEWVGRIITKNNYAT 60  
Db 20 EVQLVESGGGLVPGGSLRLSQAASGLSFSTAYAMNVRQAPKGLEWVSSISRSDD--YI 77  
Qy 61 YYADSVKDRPTISRDSKNTLYLQNSLKTEDTAVYYC-----TFYFGNGVWGQGTFLV 113  
Db 78 YYRDSVKGRPTISRDNAKNSLYLQNSLRVDDTAVYYCARDSCNGAICYGFSPWGQGTFLV 137  
Qy 114 TVSS 117  
Db 138 TVSS 141

RESULT 12  
Q8WUK1\_HUMAN  
ID Q8WUK1\_HUMAN PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Iqbalulano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX Schroeder H.W. Jr, Wang J.Y.;  
RT "Preferential utilization of conserved immunoglobulin heavy chain  
variable gene segments during human fetal life.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;  
RA Cuisinier A.M., Fumoux F., Fougereau M., Tonnelie C.;  
RT "IGM kappa/lambda EBV human B cell clone: an early step of  
differentiation of fetal B cells or a distinct B lineage?";  
RL Mol. Immunol. 29:1363-1373(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
complementarity-determining regions (CDR3) in human fetal B lymphocyte  
immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1904154;  
RA Neale G.A., Kitchingman G.R.;  
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
chain enhancer region contain a non-translatable exon and are  
extremely heterogeneous at the 5' end.";  
RL Nucleic Acids Res. 19:2427-2433(1991).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;  
RA Bird J., Galili N., Link M., Stites D., Sklar J.;  
RT "Continuing rearrangement but absence of somatic hypermutation in  
immunoglobulin genes of human B cell precursor leukemia.";  
RL J. Exp. Med. 168:229-245(1988).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;  
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;  
RT "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal  
B cell lines. Preferential utilization of the most JH-proximal D  
segment (DQ52) and two unusual VH-related rearrangements.";  
RL J. Exp. Med. 169:1391-1403(1989).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;



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Matches 83; Conservative 15; Mismatches 15; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60
Db 1 EVKLEESGGGLVQPGGSMKLSAAAGFTFSNYMNNVVRQSPKGLVWVAEIRLSHNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGN-----GVWGOGTLVT 114
Db 61 HYAESVKGRTISRDDSKSSVYLQNNLRADDTGIYYCTT--GFAYWGOGTLVPV 113

RESULT 15
Q802I7_MOUSE
ID Q802I7_MOUSE PRELIMINARY; PRT; 487 AA.
AC Q802I7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049143; AAH49143.1; -, mRNA.
DR HSP; P01789; IMCP.
DR SMR; Q802I7; 20-242.
DR MGI; MGI:96486; Igh-VJ558.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 71.6%; Score 444; DB 2; Length 487;
Best Local Similarity 69.1%; Pred. No. 2.8e-38;
Matches 85; Conservative 17; Mismatches 15; Indels 6; Gaps 2;
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QY 1 EVQLVESGGGLVQPGGSLRLSAAAGFTFSAYAMNVRQAPGKGLVWVGRIRTKNNYAT 60
Db 20 EVKLEESGGGLVQPGGSMKLSAAAGFTFSNYMNNVVRQSPKGLVWVAEIRLSHNYAT 79
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGN-----GVWGOGTLVT 114
Db 80 HYAESVKGRTISRDDSKSSVYLQNNLRADDTGIYYCTTRRGYGDPNWYFDWGAGTTVT 139
QY 115 VSS 117
Db 140 VSS 142
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Search completed: January 28, 2006, 09:44:18  
Job time : 62.0135 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 17.2162 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVKPGGSLRL.....CTTFYGVGNGWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	620	100.0	117	2	US-09-840-459-17
3	620	100.0	117	2	US-09-497-625A-17
4	620	100.0	119	2	US-09-840-459-104
5	620	100.0	119	2	US-09-497-625A-104
6	613	98.9	117	2	US-09-809-739-21
7	613	98.9	117	2	US-09-840-459-18
8	613	98.9	117	2	US-09-497-625A-18
9	604	97.4	117	2	US-09-809-739-22
10	604	97.4	117	2	US-09-840-459-19
11	604	97.4	117	2	US-09-497-625A-19
12	599	96.6	117	2	US-09-809-739-23
13	599	96.6	117	2	US-09-840-459-20
14	599	96.6	117	2	US-09-497-625A-20
15	548	88.4	117	2	US-09-809-739-12
16	548	88.4	117	2	US-09-840-459-10
17	548	88.4	117	2	US-09-497-625A-10
18	548	88.4	148	2	US-09-840-459-100
19	548	88.4	148	2	US-09-497-625A-100
20	486.5	78.8	116	1	US-08-428-197-10
21	486.5	78.8	116	4	PCT-US93-10555-10
22	487	78.5	123	2	US-09-097-055B-87
23	487	78.5	123	1	US-09-893-615-87
24	485	78.2	125	1	US-08-428-197-9
25	485	78.2	125	4	PCT-US93-10555-9
26	485	78.2	127	2	US-09-840-459-71
27	485	78.2	127	2	US-09-497-625A-71

28	483.5	78.0	126	2	US-09-840-459-74	Sequence 74, Appl
29	483.5	78.0	126	2	US-09-497-625A-74	Sequence 74, Appl
30	482	77.7	115	2	US-08-767-128-36	Sequence 36, Appl
31	482	77.7	117	2	US-09-840-459-83	Sequence 83, Appl
32	482	77.7	117	2	US-09-497-625A-83	Sequence 83, Appl
33	480.5	77.5	126	2	US-09-840-459-73	Sequence 73, Appl
34	480.5	77.5	126	2	US-09-497-625A-73	Sequence 73, Appl
35	480.5	77.5	130	1	US-08-478-039-70	Sequence 70, Appl
36	480.5	77.5	130	1	US-08-478-039-93	Sequence 93, Appl
37	480.5	77.5	130	1	US-08-476-349A-70	Sequence 70, Appl
38	480.5	77.5	130	1	US-08-476-349A-93	Sequence 93, Appl
39	480	77.1	332	2	US-09-133-121B-7	Sequence 7, Appl
40	478	77.1	123	2	US-09-840-459-94	Sequence 94, Appl
41	478	77.1	123	2	US-09-497-625A-94	Sequence 94, Appl
42	477	76.9	119	1	US-08-428-197-11	Sequence 11, Appl
43	477	76.9	119	2	US-09-809-739-19	Sequence 19, Appl
44	477	76.9	119	2	US-09-840-459-16	Sequence 16, Appl
45	477	76.9	119	2	US-09-840-459-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1

US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-20

Query Match 100.0%; Score 620; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.1e-54;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNWVQAPKGLGWGRTTKNNYAT 60

Db 1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSAYAMNWVQAPKGLGWGRTTKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVGNGWGQGLTVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVGNGWGQGLTVTVSS 117

RESULT 2

US-09-840-459-17  
; Sequence 17, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; METHODS OF USE THEREFOR

```

; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-17

Query Match      100.0%; Score 620; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117

RESULT 3
US-09-497-625A-17
; Sequence 17, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-17

Query Match      100.0%; Score 620; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
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; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
US-09-840-459-104

Query Match      100.0%; Score 620; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLGWGRIIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117

RESULT 5
US-09-497-625A-104
; Sequence 104, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
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/ SEQ ID NO 104
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized heavy chain
US-09-497-625A-104

Query Match      100.0%; Score 620; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 6
US-09-809-739-21
/ Sequence 21, Application US/09809739
/ Patent No. 6663863
/ GENERAL INFORMATION:
/ APPLICANT: Horvath, Christopher J.
/ APPLICANT: Rao, Patricia E.
/ TITLE OF INVENTION: Method of Inhibiting Stenosis and
/ TITLE OF INVENTION: Restenosis
/ FILE REFERENCE: 1855.1069-003
/ CURRENT APPLICATION NUMBER: US/09/809,739
/ PRIOR FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: US 09/528,267
/ PRIOR FILING DATE: 2000-03-17
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 5.5e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 7
US-09-840-459-18
/ Sequence 18, Application US/09840459
/ Patent No. 6696550
/ GENERAL INFORMATION:
/ APPLICANT: LaRosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ TITLE OF INVENTION: METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-012
/ CURRENT APPLICATION NUMBER: US/09/840,459

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 5.5e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117

RESULT 8
US-09-497-625A-18
/ Sequence 18, Application US/09497625A
/ Patent No. 6727349
/ GENERAL INFORMATION:
/ APPLICANT: LaRosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ TITLE OF INVENTION: METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-004
/ CURRENT APPLICATION NUMBER: US/09/497,625A
/ CURRENT FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 18
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized sequence
US-09-497-625A-18

Query Match      98.9%; Score 613; DB 2; Length 117;
Best Local Similarity 98.3%; Pred. No. 5.5e-54;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVNGVWGQGLTLVTSS 117
```



```
RESULT 9
US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 10
US-09-840-459-19
; Sequence 19, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
```

```
Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Query Match          97.4%; Score 604; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 4.4e-53;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLVWGRIRTKNNYAT 60

Qy 61 YYADSVKDRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTISSRDDSKNTLYLQMNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
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; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 14
US-09-497-625A-20
; Sequence 20, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
```

```
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-20

Query Match          96.6%; Score 599; DB 2; Length 117;
Best Local Similarity 95.7%; Pred. No. 1.4e-52;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWVGRIIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117
Db 61 YYADSVKDRYTIISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGVGVWGQGLVTVSS 117

RESULT 15
US-09-809-739-12
; Sequence 12, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12
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Query Match 88.4%; Score 548; DB 2; Length 117;  
Best Local Similarity 86.3%; Fred.No. 1.7e-47;  
Matches 101; Conservative 10; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNWVRQAPGKGLEWYGRIRTKNNYAT 60  
Db 1 EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMNWVRQAPGKGLEWYGRIRTKNNYAT 60  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGNQVWGQGLVTVSS 117  
Db 61 YYADSVKDRYTI SRDDSESLFLQWNLKTEDTAMYYCVTFYGNQVWGQGLVTVSS 117

Search completed: January 28, 2006, 09:47:28  
Job time : 17.2162 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 49.8919 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVNGVWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

1: /cgn2\_6/protdata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/protdata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/protdata/1/pubpaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/protdata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/protdata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/protdata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	3	US-09-835-087-10
2	620	100.0	117	3	US-09-809-739-20
3	620	100.0	117	3	US-09-840-459-17
4	620	100.0	117	4	US-10-766-773-17
5	620	100.0	117	4	US-10-766-610-17
6	620	100.0	117	4	US-10-733-563-17
7	620	100.0	117	5	US-10-662-061-20
8	620	100.0	119	3	US-09-840-459-104
9	620	100.0	119	4	US-10-766-773-104
10	620	100.0	119	4	US-10-766-610-104
11	620	100.0	119	4	US-10-733-563-104
12	613	98.9	117	3	US-09-835-087-11
13	613	98.9	117	3	US-09-809-739-21
14	613	98.9	117	3	US-09-840-459-18
15	613	98.9	117	4	US-10-766-773-18
16	613	98.9	117	4	US-10-766-610-18
17	613	98.9	117	4	US-10-733-563-18
18	613	98.9	117	5	US-10-662-061-21
19	604	97.4	117	3	US-09-835-087-12
20	604	97.4	117	3	US-09-809-739-22
21	604	97.4	117	3	US-09-840-459-19
22	604	97.4	117	4	US-10-766-773-19
23	604	97.4	117	4	US-10-766-610-19
24	604	97.4	117	4	US-10-733-563-19
25	604	97.4	117	5	US-10-662-061-22
26	599	96.6	117	3	US-09-835-087-13
27	599	96.6	117	3	US-09-809-739-23

28	599	96.6	117	3	US-09-840-459-20	Sequence 20, Appl
29	599	96.6	117	4	US-10-766-773-20	Sequence 20, Appl
30	599	96.6	117	4	US-10-766-610-20	Sequence 20, Appl
31	599	96.6	117	4	US-10-733-563-20	Sequence 20, Appl
32	599	96.6	117	5	US-10-662-061-23	Sequence 23, Appl
33	548	88.4	117	3	US-09-835-087-8	Sequence 8, Appl
34	548	88.4	117	3	US-09-809-739-12	Sequence 12, Appl
35	548	88.4	117	3	US-09-840-459-10	Sequence 10, Appl
36	548	88.4	117	4	US-10-766-773-10	Sequence 10, Appl
37	548	88.4	117	4	US-10-766-610-10	Sequence 10, Appl
38	548	88.4	117	4	US-10-733-563-10	Sequence 10, Appl
39	548	88.4	117	5	US-10-662-061-12	Sequence 12, Appl
40	548	88.4	125	4	US-10-272-899A-84	Sequence 84, Appl
41	548	88.4	148	3	US-09-840-459-100	Sequence 100, App
42	548	88.4	148	4	US-10-766-773-100	Sequence 100, App
43	548	88.4	148	4	US-10-766-610-100	Sequence 100, App
44	548	88.4	148	4	US-10-733-563-100	Sequence 100, App
45	499.5	80.6	120	5	US-10-920-899-1779	Sequence 1779, Ap

ALIGNMENTS

RESULT 1

US-09-835-087-10  
; Sequence 10, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-10

Query Match	100.0%	Score 620;	DB 3;	Length 117;
Best Local Similarity	100.0%;	Pred. No. 1.7e-49;		
Matches 117;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60		
Db	1	EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKNNYAT 60		
Qy	61	YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGVNGVWGQGLTVTVSS 117		
Db	61	YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYCTTFYGVNGVWGQGLTVTVSS 117		

RESULT 2

US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17

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; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-20

Query Match          100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
    |||||

RESULT 3
US-09-840-459-17
; Sequence 17, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-17

Query Match          100.0%; Score 620; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
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RESULT 4
US-10-766-773-17
; Sequence 17, Application US/10766773
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; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-17

Query Match          100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKGLEWVGRIIRTKNNYAT 60
    |||||

Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
    |||||
Db 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYYCTTFYGNVGWGQGLVTVSS 117
    |||||

RESULT 5
US-10-766-610-17
; Sequence 17, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
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/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized sequence
US-10-766-610-17

Query Match      100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 6
US-10-733-563-17
/ Sequence 17, Application US/107333563
/ Publication No. US20040151721A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Keefe, Theresa
/ APPLICANT: Ponath, Paul
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ FILE OF INVENTION: METHODS OF USE THEREOF
/ CURRENT APPLICATION NUMBER: US/10/733,563
/ CURRENT FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: US 10/272,899
/ PRIOR FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: US 60/392,364
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: US 60/350,166
/ PRIOR FILING DATE: 2001-10-19
/ NUMBER OF SEQ ID NOS: 122
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: humanized sequence
US-10-733-563-17

Query Match      100.0%; Score 620; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 7
US-10-662-061-20
/ Sequence 20, Application US/10662061
/ Publication No. US20050214299A1
/ GENERAL INFORMATION:
/ APPLICANT: Horvath, Christopher J.
/ APPLICANT: Rao, Patricia E.
/ TITLE OF INVENTION: Method of Inhibiting Stenosis and
/ FILE OF INVENTION: Restenosis
/ FILE REFERENCE: 1855.1069-003
/ CURRENT APPLICATION NUMBER: US/10/662,061
/ CURRENT FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: US/09/809,739
/ PRIOR FILING DATE: 2001-03-15
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/ PRIOR APPLICATION NUMBER: US 09/528,267
/ PRIOR FILING DATE: 2000-03-17
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized sequence
US-10-662-061-20

Query Match      100.0%; Score 620; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 8
US-09-840-459-104
/ Sequence 104, Application US/09840459
/ Patent No. US20020150576A1
/ GENERAL INFORMATION:
/ APPLICANT: Larosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ FILE OF INVENTION: METHODS OF USE THEREOF
/ FILE REFERENCE: 1855.1052-012
/ CURRENT APPLICATION NUMBER: US/09/840,459
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: PCT/US01/03537
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/497,625
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 104
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized heavy chain
US-09-840-459-104

Query Match      100.0%; Score 620; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWVGRIITKNNYAT 60

QY 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117
DB 61 YYADSVKORFTISRDDSKNTLYQMNSLKTEDTAVYCTTFYGNVGWGQGLTLVTSS 117

RESULT 9
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US-10-766-773-104  
; Sequence 104, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-773-104

Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 10  
US-10-766-610-104  
; Sequence 104, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104

; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-610-104  
  
Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 11  
US-10-733-563-104  
; Sequence 104, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Ponath, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 10448-213001  
; CURRENT APPLICATION NUMBER: US/10/733,563  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US 10/272,899  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized heavy chain  
US-10-733-563-104

Query Match 100.0%; Score 620; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 1.7e-49;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANNVRAQAPGKGLEWVGRIIRTKNNYAT 60  
  
Qy 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117  
Db 61 YYADSVKDRFTISRDDSKNTLYLQMSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 12  
US-09-835-087-11  
; Sequence 11, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448

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; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-11

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||

RESULT 13
US-09-809-739-21
; Sequence 21, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||

RESULT 14
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
```

```
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18

Query Match      98.9%; Score 613; DB 3; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||

RESULT 15
US-10-766-773-18
; Sequence 18, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-18

Query Match      98.9%; Score 613; DB 4; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||

RESULT 16
US-10-766-773-18
; Sequence 18, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-18

Query Match      98.9%; Score 613; DB 4; Length 117;
Best Local Similarity 98.3%; Pred. No. 7.4e-49;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIKTKNNYAT 60
      |||

QY      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
DB      61 YYADSVKDRFTISRDDSKNTLYQMNSLKTEDTAVYYCTTFYGNVGWGQGLTVTVSS 117
      |||
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Db	1	EVQLVESGGGLV	KPGSLRLSCAASG	PSFNA	YAMNWVRQ	APGKGL	EWGRI	RTKNN	YAT	60
Qy	61	YYADSVKDRFT	ISRDDSKNTLY	LQNSL	KTEDTAV	YCYCTTF	YGN	GWGQ	TLVT	SS 117
Db	61	YYADSVKDRFT	ISRDDSKNTLY	LQNSL	KTEDTAV	YCYCTTF	YGN	GWGQ	TLVT	SS 117

Search completed: January 28, 2006, 10:11:22  
Job time : 50.8919 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 7.02703 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-17

Perfect score: 620

Sequence: 1 EVQLVESGGGLVPGGSLRL.....CTTFYGVNGVWGQGLTVTVSS 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: . 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New.\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*

2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*

3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*

4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*

5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pap.\*

6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*

7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*

8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	100.0	117	7	US-11-075-184A-8
2	613	98.9	117	7	US-11-075-184A-9
3	604	97.4	117	7	US-11-075-184A-10
4	599	96.6	117	7	US-11-075-184A-11
5	548	88.4	117	7	US-11-075-184A-2
6	487	78.5	123	7	US-11-193-440-87
7	478.5	77.2	251	7	US-11-054-515-997
8	478.5	77.2	251	7	US-11-054-515-1346
9	476.5	76.9	139	7	US-11-125-837-24
10	475	76.6	257	7	US-11-054-515-958
11	474	76.5	244	7	US-11-054-515-1991
12	473.5	76.4	258	7	US-11-054-515-1841
13	471.5	76.0	120	6	US-10-834-397-38
14	471.5	76.0	120	6	US-10-834-397-63
15	471.5	76.0	256	7	US-11-054-515-1209
16	471.5	76.0	281	6	US-10-834-397-178
17	471	76.0	250	7	US-11-054-515-1179
18	470	75.8	253	7	US-11-054-515-1650
19	469.5	75.7	256	7	US-11-054-515-843
20	468	75.5	115	7	US-11-127-903-33
21	468	75.5	470	7	US-11-144-248-46
22	468	75.5	470	7	US-11-144-222-46
23	467.5	75.4	116	6	US-10-925-366A-1
24	467.5	75.4	240	6	US-10-925-366A-219
25	467	75.3	117	7	US-11-127-903-32

ALIGNMENTS

RESULT 1

US-11-075-184A-8

; Sequence 8, Application US/11075184A

; Publication No. US20050260139A1

; GENERAL INFORMATION:

; APPLICANT: Boehringer Ingelheim International GmbH

; APPLICANT: PAIRET, Michel

; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2

; TITLE OF INVENTION: Receptor Antagonists

; FILE REFERENCE: 1/1669

; CURRENT APPLICATION NUMBER: US/11/075,184A

; CURRENT FILING DATE: 2005-03-08

; PRIOR APPLICATION NUMBER: EP 04 007 635.8

; PRIOR FILING DATE: 2004-03-30

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 8

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,

; OTHER INFORMATION: 1D9RKE

US-11-075-184A-8

Query Match

Best Local Similarity 100.0%; Score 620; DB 7; Length 117;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRITKNNYAT 60

Db 1 EVQLVESGGGLVPGGSLRLSCAASGFTFSAYANWVRQAPGKLEWVGRITKNNYAT 60

QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

Db 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYGVNGVWGQGLTVTVSS 117

RESULT 2

US-11-075-184A-9

; Sequence 9, Application US/11075184A

; Publication No. US20050260139A1

; GENERAL INFORMATION:

; APPLICANT: Boehringer Ingelheim International GmbH

; APPLICANT: PAIRET, Michel

; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2

; TITLE OF INVENTION: Receptor Antagonists

; FILE REFERENCE: 1/1669

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; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region, 1D9RHE
US-11-075-184A-9

Query Match      98.9%; Score 613; DB 7; Length 117;
Best Local Similarity 98.3%; Pred. No. 1.9e-46;
Matches 115; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117

RESULT 3
US-11-075-184A-10
; Sequence 10, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region, 1D9RHE
US-11-075-184A-10

Query Match      97.4%; Score 604; DB 7; Length 117;
Best Local Similarity 96.6%; Pred. No. 1.1e-45;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117

RESULT 4
US-11-075-184A-11
; Sequence 11, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; FILE REFERENCE: 1/1669
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; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody heavy chain variable region, 1D9RHE
US-11-075-184A-11

Query Match      96.6%; Score 599; DB 7; Length 117;
Best Local Similarity 95.7%; Pred. No. 2.9e-45;
Matches 112; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117

RESULT 5
US-11-075-184A-2
; Sequence 2, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelhiem International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Murine antibody 1D9 heavy chain variable region; presumably Mus
US-11-075-184A-2

Query Match      88.4%; Score 548; DB 7; Length 117;
Best Local Similarity 86.3%; Pred. No. 6.8e-41;
Matches 101; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKGLVWGRIRTKNNYAT 60
QY 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117
DB 61 YYADSVKDRFTISRDDSKNTLYLQWNSLKTEDTAVYYCTTFYNGVWGQGLVTVSS 117

RESULT 6
US-11-193-440-87
; Sequence 87, Application US/11193440
; Publication No. US20060002939A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; APPLICANT: Schuman, Richard F.
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RESULT 7
US-11-054-515-997
; Sequence 997, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418

```

```

RESULT 8
US-11-054-515-1346
, Sequence 1346, Application US/11054515
, Publication No. US2005025532A1
, GENERAL INFORMATION:
, APPLICANT: Ruben et al.
, TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
, FILE REFERENCE: PFS523P3
, CURRENT APPLICATION NUMBER: US/11/054,515
, CURRENT FILING DATE: 2005-02-10
, PRIOR APPLICATION NUMBER: 60/543,296
, PRIOR FILING DATE: 2004-02-11
, PRIOR APPLICATION NUMBER: 60/580,347
, PRIOR FILING DATE: 2004-06-18
, PRIOR APPLICATION NUMBER: 10/293,418
, PRIOR FILING DATE: 2002-11-14
, PRIOR APPLICATION NUMBER: 60/331,469
, PRIOR FILING DATE: 2001-11-16
, PRIOR APPLICATION NUMBER: 60/340,817
, PRIOR FILING DATE: 2001-12-19
, PRIOR APPLICATION NUMBER: 09/880,748
, PRIOR FILING DATE: 2001-06-15
, PRIOR APPLICATION NUMBER: 60/293,499
, PRIOR FILING DATE: 2001-05-25
, PRIOR APPLICATION NUMBER: 60/277,379
, PRIOR FILING DATE: 2001-03-21
, PRIOR APPLICATION NUMBER: 60/276,248
, PRIOR FILING DATE: 2001-03-16
, PRIOR APPLICATION NUMBER: 60/240,816
, PRIOR FILING DATE: 2000-10-17
, Remaining Prior Application data removed - See File wrapper or PR
, NUMBER OF SEQ ID NOS: 3247
, SEQ ID NO 1346

```

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; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1346

Query Match      77.2%; Score 478.5; DB 7; Length 251;
Best Local Similarity 73.4%; Pred. No. 1.2e-34;
Matches 94; Conservative 10; Mismatches 13; Indels 11; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLWVGRIIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYHMDWVRQAPGKGLWVGRIIRKANSYTI 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYIC-----TFYGNVGWQ 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EYAASVGRFTISRDDSKNSLFQNSLKTEDTAVYICARAPYDILTGYSDYGMVNR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 110 GTLVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GTLVTVSS 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match      76.9%; Score 476.5; DB 7; Length 139;
Best Local Similarity 75.0%; Pred. No. 1.1e-34;
Matches 90; Conservative 15; Mismatches 12; Indels 3; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLWVGRIIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVQLVETGGGLVQPGKSLKLSCAASGFTFNTAMNWRQAPGKGLWVGRIIRSKNNYAT 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYICT---TFYGNVGWGGTLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 YYADSVKDRFTISRDDTQSMYLFQNSLKTEDTGMTCYVGRGSYFDVWVGAGITTVTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-11-054-515-958
; Sequence 958, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
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; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 958
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-958

Query Match      76.6%; Score 475; DB 7; Length 257;
Best Local Similarity 73.3%; Pred. No. 2.5e-34;
Matches 96; Conservative 7; Mismatches 14; Indels 14; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNWRQAPGKGLWVGRIIRTKNNYAT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSNANMSWRQAPGKGLWVGRIKSKTDGTT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 YYADSVKDRFTISRDDSKNTLYLQNSLKTEDTAVYICTT-----FYGNV 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 DYAAPVGRFTISRDDSKNTLYLQNSLKTEDTAVYICTTQAHYDILTGYLWSYGMVDV 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 107 WGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 WGRGLTVTVSS 131
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-11-054-515-1991
; Sequence 1991, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
```



```
;
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-834-397-63
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Query Match          76.0%; Score 471.5; DB 6; Length 120;
Best Local Similarity 77.0%; Pred. No. 2.5e-34;
Matches 94; Conservative 9; Mismatches 12; Indels 7; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVSAL--SGSGGST 58

Qy 61 YYADSVKDRPTISRDDSKNTLYLQMSLKTEDTAVYYCTTNG-----VQGQGLTVTV 115
Db 59 YYADSVKGRFTISRDNKNTLYLQMSLKRAEDTAVYYCARWGGDGFYAMDYWGQGLTVV 118

Qy 116 SS 117
Db 119 SS 120
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```
RESULT 15
US-11-054-515-1209
; Sequence 1209, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
```

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;
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1209
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1209

Query Match          76.0%; Score 471.5; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 5e-34;
Matches 91; Conservative 11; Mismatches 15; Indels 13; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYAMNVRQAPGKLEWVGRIIRTKNNYAT 60
Db 1 EVQLVETGGGLVQPGGSLRLSCAASGFTFSYGSNNWVRLAPGKLEWVASIRSRGGTYI 60

Qy 61 YYADSVKDRPTISRDDSKNTLYLQMSLKTEDTAVYYCTT-----FYGNQVW 107
Db 61 YYADSVKGRFTISRDNKNTLYLQMSLKRAEDTAVYYCARDPGNYDILTGYYYYGMDVW 120

Qy 108 GQGTLTVTVSS 117
Db 121 GQGTWTVTVSS 130

Search completed: January 28, 2006, 10:12:14
Job time : 8.02703 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using franklin's n2p model

Run on: January 28, 2006, 08:12:21 ; Search time 54.8108 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 9gggtgaattggttgagtc.....ccctggtcaccgcagctca 351

Scoring table: BLOSUM62  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-O=/cpn2\_1/USPTO\_spool\_p/US10733563/runat\_27012006\_180005\_4773/app\_query.fasta\_1.2716  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CN 1 1 624 @runat\_27012006\_180005\_4773 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 21:\*  
1: Geneseq1980s:\*  
2: Geneseq1980s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003ba:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	4	Aae06954 Humanised
2	620	98.3	117	4	Aau09927 Humanised
3	620	98.3	117	5	Abg75536 Humanised
4	620	98.3	117	5	Aao14980 Humanised
5	620	98.3	117	5	Adf98240 Humanised
6	620	98.3	117	8	Adq99239 Humanised
7	620	98.3	117	9	Aeb09512 Humanised
8	620	98.3	119	4	Aae07034 Humanised
9	620	98.3	119	8	Adq89326 Humanised

10	620	98.3	119	9	AEB09599	Aeb09599 Humanised
11	613	97.1	117	4	AAE06954	Aae06955 Humanised
12	613	97.1	117	5	ABG75537	Abg75537 Humanised
13	613	97.1	117	5	AAO14981	Aao14981 Humanised
14	613	97.1	117	5	ADF98241	Adf98241 Humanised
15	613	97.1	117	8	ADQ89240	Adq89240 Humanised
16	613	97.1	117	9	AEB09513	Aeb09513 Humanised
17	604	95.7	117	4	AAE06956	Aae06956 Humanised
18	604	95.7	117	4	AAU09929	Aau09929 Humanised
19	604	95.7	117	4	AAU09928	Aau09928 Humanised
20	604	95.7	117	5	ABG75538	Abg75538 Humanised
21	604	95.7	117	5	AAO14982	Aao14982 Humanised
22	604	95.7	117	5	ADF98242	Adf98242 Humanised
23	604	95.7	117	8	ADQ89241	Adq89241 Humanised
24	604	95.7	117	9	AEB09514	Aeb09514 Humanised
25	599	94.9	117	4	AAE06957	Aae06957 Humanised
26	599	94.9	117	4	AAU09930	Aau09930 Humanised
27	599	94.9	117	5	ABG75539	Abg75539 Humanised
28	599	94.9	117	5	ADF98243	Adf98243 Humanised
29	599	94.9	117	8	ADQ89242	Adq89242 Humanised
30	599	94.9	117	9	AEB09515	Aeb09515 Humanised
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32	548	86.8	117	4	AAE06947	Aae06947 Murine 1D
33	548	86.8	117	4	AAU09919	Aau09919 Murine MA
34	548	86.8	117	5	ABG75528	Abg75528 Mouse mAb
35	548	86.8	117	5	ADF98238	Adf98238 Murine mAb
36	548	86.8	117	8	ADQ89232	Adq89232 Mouse imm
37	548	86.8	117	9	AEB09505	Aeb09505 Murine 1D
38	548	86.8	125	8	ADJ95988	Adj95988 Immunoglo
39	548	86.8	148	8	AAU07033	Aau07033 Murine an
40	548	86.8	148	8	ADQ89322	Adq89322 Mouse imm
41	548	86.8	148	9	AEB09595	Aeb09595 Murine 1D
42	539	85.4	117	5	AAO14978	Aao14978 Mouse hea
43	505.5	80.1	452	9	ADX01863	Adx01863 SARS coro
44	505	80.0	120	9	ADV86726	Adv86726 Anti-FLJ3
45	502	79.6	120	9	ADV86731	Adv86731 Anti-FLJ3

ALIGNMENTS

RESULT 1  
AAE06954  
ID AAE06954 standard; protein; 117 AA.

XX	AAE06954;				
AC					
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DT	11-SEP-2003	(revised)			
DT	16-OCT-2001	(first entry)			
XX					
DE	Humanised murine 1D9 antibody heavy chain variable region, 1D9RHA.				
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KW	Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; allograft rejection; anaphylaxis; malignancy; inflammation; acquired immune deficiency syndrome; AIDS; fibrotic disease; angioplasty; vascular intervention; 1D9 antibody; inflammatory glomerulopathy; VH; heavy chain variable region; 1D9RHA.				
KW					
OS	Mus sp.				
OS	Homo sapiens.				
OS	Chimeric.				
XX					
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FT		/label= CDR1			
FT		/note= "Complementarity determining region 1"			
FT	Region	50..68			
FT		/label= CDR2			
FT		/note= "Complementarity determining region 2"			
FT	Region	101..106			

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FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US003537.
XX 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-48888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
FT non-human antigen binding region and human immunoglobulin.
XX Claim 62; Fig 12; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE-mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is humanised murine 1D9
CC antibody heavy chain variable (VH) region, 1D9RHA. (Updated on 11-SEP-
CC 2003 to standardise OS field)
XX SQ Sequence 117 AA;

Alignment Scores:
Pred. No.: 1.75e-59 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x AA06954 (1-117)
QY 1 GAGGTGCAATGGTGGTGGAGTGGTGGAGAGTGGTGGAGCTGGGGGTGATTGAGATC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCGAGCTCTGGATTCACTTTCAGTGGCTACGCGCATGAGTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGAAAGGTTTGGATTGGTTCGGCCGATAGCAACTAAATAATTAATATGTCACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCGGATTCAGTAAAGACAGATTCACCATCTCCAGNAGTATCAAAAACAG 240
DB: |||

61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80
241 CTCTATCTGCAATGCAACAGCTTCAAACTGAGACACAGCCGTGTATTACTGTACCAACC 300
81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGTCA 351
101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 2
AAU09927
ID AAU09927 standard; protein; 117 AA.
XX
AC AAU09927;
XX
DT 18-JUN-2002 (first entry)
XX
DE Humanised 1D9 heavy chain variable region, 1D9RHA protein sequence.
XX
KW Human; mouse; 4B4'CL heavy chain variable region; vasotropic;
KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
KW insulin-dependent diabetes mellitus; inflammatory bowel disease;
KW ulcerative colitis; 1D9RHA; graft rejection; allergic disease;
KW antipsoriatic; antiarthritic; nephrotropic; antithyroid; restenosis;
KW dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury;
KW autoimmune disease; immunoglobulin; complementarity determining region;
XX CDR; CD18; CCR2; atherosclerosis; mutant; mutein.
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 27..30
FT /note= "Part of H1 structure loop"
FT Region 31..35
FT /note= "Complementarity determining region 1 (CDR1),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
FT Region 50..68
FT /note= "Complementarity determining region 2 (CDR2),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
FT Region 101..108
FT /note= "Complementarity determining region 3 (CDR3),
FT grafted from mouse mAb 1D9 heavy chain sequence
FT (AAU09919)"
XX WO200170266-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008266.
XX 17-MAR-2000; 2000US-00528267.
XX (MILL-) MILLENNIUM PHARM INC.
XX Horvath CJ, Rao PE;
XX WPI; 2001-607511/69.
XX Inhibiting stenosis or restenosis of a blood vessel following vascular
PT injury or angioplasty in a subject by administering agent which inhibits
PT recruitment or adhesion of neutrophils, mononuclear cells to injury site.
XX Claim 32; Fig 18; 108pp; English.
XX The present invention relates to a new method of inhibiting stenosis or
CC restenosis of a blood vessel following vascular injury in a subject. The
CC new method comprises administering to the subject agents which inhibit
```



CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
CC site of vascular injury by binding CD18 or CCR2. The method of the  
CC invention inhibits stenosis or restenosis of a blood vessel following  
CC vascular injury arising from a vascular intervention procedure such as  
CC vascular by-pass or transplantation surgery. The method is also useful  
CC for treating a subject having an inflammatory disease or condition  
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
CC graft versus host disease. Chronic inflammatory diseases of the lung,  
CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
CC treated. The method is further useful for treating inflammatory bowel  
CC diseases, such as ulcerative colitis. Additional diseases or conditions  
CC include inflammatory or allergic diseases and conditions, including  
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,  
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
CC arthritis, graft rejection and other diseases including atherosclerosis.  
CC This sequence represents the variable region of one of several humanised  
CC ID9 heavy chains (AAU09927-AAU09930). These heavy chains were used in the  
CC invention for the production of anti-CCR2 antibody or antigen-binding  
CC fragment

XX SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1,75e-59 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x AAU09927 (1-117)

QY 1 GAGGTGCAATTGTTGAGTCTGAGGAGGATTGGTGAAGCTGGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlySerLeuArgLeu 20  
QY 61 TCATGTGACCTCTGGATTCACTTTTCAGTGCTACGCCATGAACTGGCTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTTGAAGGGTTGGCCGTCATAGAACTAAAATATATTATGCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCAACATCTCCAGAGATGATTCACAAAACAGC 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGAACACAGCTTGAACACTGAGGACACACAGCCGTGTATTACTGTACCAC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTCTCTGGGCGCAGGGGACCTCGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 3

ABG75536

ID ABG75536 standard; protein; 117 AA.

XX AC ABG75536;

XX AC ABG75536;

XX 16-APR-2003 (first entry)

XX Humanised mouse mAb 1D9 heavy chain variable region, 1D9RHAVH.

XX Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
KW antigen binding fragment; cellular adhesion molecule; adhesion;  
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
KW endovascular stenting; prosthetic valve; transplantation;  
KW inflammatory disease; mastitis; vaginitis; cholecystitis;

KW chronic bronchitis; asthma; graft-versus-host disease;  
KW chronic inflammatory disease; hypersensitivity pneumonitis;  
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
KW graft rejection; atherosclerosis; myositis; therapy; ID9; 1D9RHAVH;  
KW heavy chain variable region; VH; complementarity determining region; CDR;  
mutant; mutein.

XX Mus sp.  
OS Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers

FT Region 31..35 /note="Mouse complementarity determining region 1

FT (CDR1)"

FT 50..68 /note="Mouse complementarity determining region 2

FT (CDR2)"

FT 101..106 /note="Mouse complementarity determining region 3

FT (CDR3)"

FT US2002106369-A1.

XX 08-AUG-2002.

XX 15-MAR-2001; 2001US-00809739.

XX 17-MAR-2000; 2000US-00528267.

XX (MILL-) MILLENNIUM PHARM INC.

XX Horvath CJ, Rao PE;

XX WPI; 2002-697861/75.

XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
XX administering first and second agents that inhibit adhesion and/or  
XX recruitment of neutrophils and mononuclear cells, respectively to site of  
XX vascular injury.

XX Claim 32; Fig 18; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of  
XX a blood vessel following vascular injury in a subject. The method  
XX involves administering to the subject a first therapeutic agent, which  
XX comprises an antibody or its antigen binding fragment which binds a  
XX cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
XX of neutrophils to a site of vascular injury and a second therapeutic  
XX agent, which comprises an antagonist of CCR2 function, that inhibits  
XX adhesion and/or recruitment of mononuclear cells to a site of vascular  
XX injury. The vascular injury arises from a vascular intervention procedure  
XX such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
XX (PTCA) or angioplasty including placement of a stent), vascular by-pass  
XX surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
XX stenting, insertion of a prosthetic valve and transplantation of organs,  
XX tissues or cells. The method is also useful for treating inflammatory  
XX diseases or conditions mediated by early neutrophil activity and later  
XX mononuclear cell activity. Preferably, the method is useful for treating  
XX asthma and graft-versus-host disease, chronic inflammatory disease of  
XX lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
XX other idiopathic conditions, pancreatitis and insulin dependent diabetes  
XX mellitus. The method is also useful for treating inflammatory bowel  
XX disease, Crohn's disease, inflammatory or allergic diseases (such as  
XX psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
XX (such as arthritis and multiple sclerosis), graft rejection,  
XX atherosclerosis and myositis. The method enables simultaneous inhibition  
XX of neutrophil and mononuclear cell participation in response to vascular  
XX injury or inhibition of neutrophil participation followed by inhibition

CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
CC chain variable region (VH), 1D9RHA VH, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human 4B4/CL  
CC MAB VH regions  
XX

SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.75e-59 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x ABG75536 (1-117)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGGAGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATCAAGTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaLeuSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCGCATPAAGAACTAAATAATTAATTCACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATTCAGTGAAGACAGTTCGAACTGAGGACACAGCGGTATTAATCTGACACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 4

AA014980  
ID AA014980 standard; protein; 117 AA.

AC AA014980;

XX 05-SEP-2002 (first entry)

XX Humanised murine heavy chain variable region (1D9RHa VH).

DE Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
KW bowel transplant; heart transplant; graft versus host disease;  
KW chronic graft rejection; antibody heavy chain variable region; 1D9RHa VH.  
XX

OS Mus musculus.

OS Synthetic.

XX US2002042370-A1.

XX 11-APR-2002.

XX 13-APR-2001; 2001US-00835087.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WH;

PI

XX WPI; 2002-351265/38.

XX Inhibiting graft rejection, graft versus host disease or chronic  
PT rejection of a transplanted graft, involves administering a CCR2  
PT antagonist.

XX Claim 26; Fig 2; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
CC versus host disease or chronic rejection of a transplanted graft. The  
CC method involves administering an antagonist of CC chemokine receptor 2  
CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
CC complementarity determining regions from various non-human origins). CCR2  
CC is known to be involved in the rejection of transplanted grafts. The  
CC method of the invention is useful for inhibiting graft rejection -  
CC particularly allografts such as kidney, liver, lung, heart-lung,  
CC pancreas, bowel and heart. The method of the invention is also useful for  
CC inhibiting graft versus host disease and for inhibiting chronic rejection  
CC of a transplanted graft. The present amino acid sequence represents a  
CC humanised murine antibody heavy chain variable region (1D9RHa VH)

XX Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1.75e-59 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-108 (1-351) x AA014980 (1-117)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGGAGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATCAAGTGGTCCGCCAGGCT 120  
DB 21 SerCysAlaLeuSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGATTGGTTCGGCGCATPAAGAACTAAATAATTAATTCACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCATCTGCAATTCAGTGAAGACAGTTCGAACTGAGGACACAGCGGTATTAATCTGACACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 5

ADF98240

ID ADF98240 standard; protein; 117 AA.

XX ADF98240;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 heavy chain variable region, 1D9RHa VH, SEQ ID 10.  
DE Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft versus host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.

XX



Db 61 TyrTyrAlaAspSerValysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
 QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACACACC 300  
 Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
 QY 301 TTTTACGGTACGGTGTCTGGGGCCAGGGGACCCTGGTCACCGTCAGCTCA 351  
 Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 7

AE09512  
 ID AE09512 standard; protein; 117 AA.

AC AE09512;

XX 08-SEP-2005 (first entry)

XX Humanized ID9 heavy chain variable region SEQ ID NO 17.

DE antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW heavy chain variable region.

XX Synthetic.

XX WO2005060368-A2.

XX 07-JUL-2005.

XX 10-DEC-2003; 2003WO-US039599.

XX 10-DEC-2003; 2003WO-US039599.

XX (MILL-) MILLENNIUM PHARM INC.

PA Okeefe T, Ponath P;

XX WPI, 2005-488561/49.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX Claim 1; SEQ ID NO 17; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion, and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell  
 CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.

CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of a humanized ID9  
 CC heavy chain variable region used in the creation of a humanized anti-CCR2  
 CC -antibody.

SQ Sequence 117 AA;

## Alignment Scores:

Pred. No.: 1.75e-59 Length: 117  
 Score: 620.00 Matches: 117  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.26% Indels: 0  
 DB: 9 Gaps: 0

US-10-733-563-108 (1-351) x AE09512 (1-117)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGTCAATTGAGATC 60

Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTCACTTTCAGTCCCTACGCCATGAACCTGGTCCGCCAGGCT 120

Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGGAAAGGTTTGGGAATGGTGGCGCATAGAACTAAATAATAATATATGCAACA 180

Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTCAAGTGAAGACAGATTCAACATCTCCAGAGATGATTTCAAAAACACG 240

Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACACACC 300

Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGGTAAACGGTGTCTGGGGCCAGGGGACCCTGGTCACCGTCAGCTCA 351

Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 8

AAE07034

ID AAE07034 standard; protein; 119 AA.

XX AC AAE07034;

XX 11-SEP-2003 (revised)

DT 16-OCT-2001 (first entry)

XX Humanised murine antibody heavy chain ID9RHA protein.

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention;  
 KW neointimal hyperplasia; antibody ID9 heavy chain; ID9RHA.

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

PN WO200157226-A1.

PD 09-AUG-2001.

PF 02-FEB-2001; 2001WO-US003537.

XX

PR 03-FEB-2000; 2000US-00497625.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
XX WPI; 2001-488888/53.  
DR N-PSDB; AAD13179.  
XX  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
PT disorder in a patient, comprises a binding specificity for CCR2, and a  
PT non-human antigen binding region and human immunoglobulin.  
XX  
XX Disclosure; Fig 23; 183pp; English.  
XX  
XX The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
CC comprising an antigen binding region of non-human origin and at least a  
CC portion of an immunoglobulin of human origin. The humanised antibodies  
CC are useful for inhibiting the interaction of a cell expressing CCR2. They  
CC are useful for inhibiting or treating HIV infection. The proteins of the  
CC invention are useful for inhibiting leukocyte trafficking, for treating  
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune  
CC disorders such as rheumatoid arthritis and multiple sclerosis,  
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They  
CC are useful in therapy or diagnosis, and in the manufacture of a  
CC medicament for treating CCR-2 mediated disease. They are also useful for  
CC treating allergy, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and IgE- mediated allergic reaction, shock,  
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
CC associated with vascular intervention, including angioplasty and/or stent  
CC placement in a mammal. Humanised antibodies are also useful for  
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
CC neointimal hyperplasia of a vessel in a mammal, preferably associated  
CC with vascular intervention. The present sequence is humanised murine  
CC antibody heavy chain region, ID9RHA. ID9RHA sequence consist of the  
CC complementarity determining regions (CDRs) of the murine ID9 antibody  
CC heavy chain variable (VH) region genetically inserted into the framework  
CC regions (FRs) of the human 4B4'CL antibody VH region. (Updated on 11-SEP-  
CC 2003 to standardise OS field)  
XX  
XX Sequence 119 AA;

Alignment Scores:  
Pred. No.: Length: 1,76e-59 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 4 Gaps: 0  
US-10-733-563-108 (1-351) x AAE07034 (1-119)  
QY 1 GAGTGCATTTGGTTCGAGGAGGATTGGTGAAGCCCTGGGGGTTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGACCTCTGGATTCTTCACTTCAGTGCCTAGCCATCACTGGTCCGCCAGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTTGAATGGGTTCGCCGATAGAACTTAAATAATTAATTCACACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTrpAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAAACAG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCATATCTCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117  
RESULT 9  
ADQ89326  
ID ADQ89326 standard; protein; 119 AA.  
XX AC ADQ89326;  
XX 21-OCT-2004 (first entry)  
XX Humanised immunoglobulin protein #9.  
XX Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX Synthetic.  
OS US2004151721-A1.  
PN 05-AUG-2004.  
PD 10-DEC-2003; 2003US-00733563.  
PF 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
PR 17-OCT-2002; 2002US-00272899.  
XX (OKEE/) O'KEEFE T.  
PA (PONA/) PONA P.  
XX O'keefe T, Ponath P;  
PI WPI; 2004-580175/56.  
XX N-PSDB; ADQ89319.  
DR New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX Disclosure; SEQ ID NO 104; 128pp; English.  
XX The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX  
XX Sequence 119 AA;  
Alignment Scores:  
Pred. No.: Length: 1,76e-59 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 8 Gaps: 0  
US-10-733-563-108 (1-351) x ADQ89326 (1-119)  
QY 1 GAGTGCATTTGGTTCGAGGAGGATTGGTGAAGCCCTGGGGGTTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTCACTGCTCCTAGCGCATGACTGGTCCGCCAGGCT 120  
Db |||||||  
21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGTTTGGATGGTGGCCGATAGACTAAAGCTAAAAATAATATTCACACA 180  
Db |||||||  
41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCGGATTCACTGAAAGACAGATTCCACATCTCCAGAGATGATTCAAAAAACAG 240  
Db |||||||  
61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCAACC 300  
Db |||||||  
81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTACGGTAAACGGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351  
Db |||||||  
101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 10

AEB09599

ID AEB09599 standard; protein; 119 AA.

XX AC AEB09599;  
XXXX 08-SEP-2005 (first entry)  
XXXX Humanized heavy chain 1D9RHA.  
XX

KW antinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
KW antibody engineering; therapeutic; diagnosis; inflammation;  
KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
KW heavy chain variable region.

XX Synthetic.

XX WO2005060368-A2.  
XXXX 07-JUL-2005.  
XXXX 10-DEC-2003; 2003WO-US039599.  
XXXX 10-DEC-2003; 2003WO-US039599.  
XXXX (MILL-) MILLENNIUM PHARM INC.  
XXXX Okeefe T, Ponath P;  
PIXX WPI, 2005-488561/49.  
XXXX N-PSDB; AEB09592.  
XX

XX New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.

XX Disclosure; SEQ ID NO 104; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen  
XX binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
CC immunoglobulin light chain, or its antigen binding fragment, having  
CC binding specificity for CCR2 and comprising the amino acid sequence of

CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
CC sequence, given in specification. The following are disclosed: isolated  
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
CC construct comprising nucleic acid molecule encoding (I); and host cell  
CC comprising the nucleic acid molecule. (I) is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response, for use in the treatment of disease  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocyte-mediated disorders such as atherosclerosis. (I) is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of humanized heavy  
CC chain 1D9RHA.

SQ Sequence 119 AA;

## Alignment Scores:

Pred. No.:	1.76e-59	Length:	119
Score:	620.00	Matches:	117
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.26%	Indels:	0
DB:	9	Gaps:	0

US-10-733-563-108 (1-351) x AEB09599 (1-119)

QY 1 GAGGTGCATTTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGCTCATTTGAGACTC 60

Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTCACTGCTCCTAGCGCATGACTGGTCCGCCAGGCT 120

Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGGAAAGGTTTGGATGGTGGCGGCATAGAAGCTAAAAATAATATTCACACA 180

Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCGGATTCACTGAAAGACAGATTCCACATCTCCAGAGATGATTCAAAAAACAG 240

Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCAACC 300

Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100

QY 301 TTTACGGTAAACGGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351

Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 11

AAB06955

ID AAB06955 standard; protein; 117 AA.

XX AC AAB06955;  
XXXX 11-SEP-2003 (revised)  
XXXX 16-OCT-2001 (first entry)  
XX

XX Humanised murine 1D9 antibody heavy chain variable region, 1D9RHB.

XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
XX neuroprotective; immunosuppressive; human immunodeficiency virus;  
XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
XX multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
XX fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
XX inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
XX neonatal hyperplasia; VH; heavy chain variable region; 1D9RHB.





XX 17-MAR-2000; 2000US-00528267.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Horvath CJ, Rao PE;  
XX WPI; 2002-697861/75.  
XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
PT administering first and second agents that inhibit adhesion and/or  
PT recruitment of neutrophils and mononuclear cells, respectively to site of  
PT vascular injury.  
XX  
PS Claim 32; Fig 18; 59pp; English.  
XX  
CC The invention discloses a method for inhibiting stenosis or restenosis of  
CC a blood vessel following vascular injury in a subject. The method  
CC involves administering to the subject a first therapeutic agent, which  
CC comprises an antibody or its antigen binding fragment which binds a  
CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
CC of neutrophils to a site of vascular injury and a second therapeutic  
CC agent, which comprises an antagonist of CCR2 function, that inhibits  
CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
CC injury. The vascular injury arises from a vascular intervention procedure  
CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
CC stenting, insertion of a prosthetic valve and transplantation of organs,  
CC tissues or cells. The method is also useful for treating inflammatory  
CC diseases or conditions mediated by early neutrophil activity and later  
CC mononuclear cell activity. Preferably, the method is useful for treating  
CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
CC asthma and graft-versus-host disease, chronic inflammatory disease of  
CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
CC mellitus. The method is also useful for treating inflammatory bowel  
CC disease, Crohn's disease, inflammatory or allergic diseases (such as  
CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
CC (such as arthritis and multiple sclerosis), graft rejection,  
CC atherosclerosis and myositis. The method enables simultaneous inhibition  
CC of neutrophil and mononuclear cell participation in response to vascular  
CC injury or inhibition of neutrophil participation followed by inhibition  
CC of mononuclear cell participation, and thus provides superior therapy for  
CC inhibiting stenosis or restenosis following vascular injury. The sequence  
CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, heavy  
CC chain variable region (VH), 1D9RHBVH, which is comprised of the mouse 1D9  
CC mAb complementarity determining regions (CDR's) linked by human 4B4'CL  
CC MAB VH regions with a mouse derived Thr at position 28 and Ser at  
CC position 30  
XX  
SQ Sequence 117 AA;  
Alignment Scores:  
Pred. No.: 1,04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 5 Gaps: 0  
US-10-733-563-108 (1-351) x ABG75537 (1-117)  
QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATGGTGGAAGCCCTGGGGGTCTATTGAGATC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCATCTTTCAGTGCCTACGCCATGAACCTGGGTCCGCGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTGGATGGTTCGGCGCATGAAGAACTAAATAAATAATATATCAACA 180

Db 41 ProGlyIysGlyLeuGluTrpValGlyArgIleArgThrIysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTTCAAAAAACAG 240  
DB 61 TyrTyrAlaAspSerValIysAspArgPheThrIleSerArgAspAspSerIysAsnThr 80  
QY 241 CTCATATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuIysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTCTCTGCGGCGGACCCCTGGTCCAGCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117  
RESULT 13  
AAO14981  
ID AAO14981 standard; protein; 117 AA.  
XX  
AC AAO14981;  
XX  
DT 05-SEP-2002 (first entry)  
XX  
DE Humanised murine heavy chain variable region (1D9RHB VH).  
XX  
KW Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
KW bowel transplant; heart transplant; graft versus host disease;  
KW chronic graft rejection; antibody heavy chain variable region; 1D9RHB VH.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
XX US2002042370-A1.  
XX  
PD 11-APR-2002.  
XX  
PF 13-APR-2001; 2001US-00835087.  
XX  
XX 14-APR-2000; 2000US-00549448.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Hancock WW;  
XX  
XX WPI; 2002-351265/38.  
XX  
XX Inhibiting graft rejection, graft versus host disease or chronic  
XX rejection of a transplanted graft, involves administering a CCR2  
XX antagonist.  
XX  
XX Claim 26; Fig 2; 16pp; English.  
XX  
XX The invention comprises a method of inhibiting graft rejection, graft  
XX versus host disease or chronic rejection of a transplanted graft. The  
XX method involves administering an antagonist of CC chemokine receptor 2  
XX (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
XX be an anti-CCR2 antibody (i.e. containing light and heavy chain  
XX complementarity determining regions from various non-human origins). CCR2  
XX is known to be involved in the rejection of transplanted grafts. The  
XX method of the invention is useful for inhibiting graft rejection -  
XX particularly allografts such as kidney, liver, lung, heart-lung,  
XX pancreas, bowel and heart. The method of the invention is also useful for  
XX inhibiting graft versus host disease and for inhibiting chronic rejection  
XX of a transplanted graft. The present amino acid sequence represents a  
XX humanised murine antibody heavy chain variable region (1D9RHB VH)  
SQ Sequence 117 AA;  
Alignment Scores:  
Pred. No.: 1,04e-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2



Best Local Similarity:	98.29%	Mismatches:	0
Query Match:	97.15%	Indels:	0
DB:	5	Gaps:	0

US-10-733-563-108 (1-351) x AAO14981 (1-117)

Qy	1	GAGGTGCAATTTGGTTGAGTCTCGAGAGAGATTGGTGAAGCCCTGGGGGGTCAATTGAGACTC	60
Db	1	GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu	20
Qy	61	TCATGTGCAGCCTCTGGATTCACTTTCAGTGTGCTACGCCATGAATCGGTCTCGCCAGGCT	120
Db	21	SerCysAlaAsnSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla	40
Qy	121	CCAGGAAAGGGTTTCGAATGGGTGGCCGCAATAAGAACTAAAAATAATAATTATTCGAACA	180
Db	41	ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr	60
Qy	181	TATTATGCCGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAAACAG	240
Db	61	TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr	80
Qy	241	CTCTATCTGCAATGAACAGCTTGAAAACTAGGACACAGCCGTGTATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr	100
Qy	301	TTTTACGTTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA	351
Db	101	PheTyrGlyAsnGlyValTropGlyGlnGlyThrLeuValThrValSerSer	117

## RESULT 14

ADF98241  
ID ADF98241 standard; protein: 117 AA.

XX ADF98241;

DT 26-FEB-2004 (first entry)

Humanised 1D9 heavy chain variable region, 1D9RHB VH, SEQ ID 11.  
XX  
KW Immunosuppressive; CCR2 function inhibitor; graft rejection;  
KW graft versus host disease; CC chemokine receptor 2; CCR2;  
KW anti-CCR2 antibody.

OS Synthetic.  
OS Mus musculus.  
OS Homo sapiens.

XX  
PN WO200178653-A2.

PD 25-OCT-2001.

13-APR-2001: 2001WO-US012139-

14-APR-2000: 2000UIS-00549448

XX PA (MILV.-) MILLENNIUM PHARM INC

XX DI Hancock, Mass.

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XX Inhibition of rejection of graft e.g. heart or graft verses host disease  
PT involves use of CC chemokine receptor 2 inhibitor.

PS Claim 26; Fig 2; 44pp; English.

CC The present invention relates to a method for inhibiting graft rejection  
CC or graft verses host diseases. The method comprises administration of a  
CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
CC recipient of a transplanted graft. The CCR2 function antagonist is an  
CC anti-CCR2 antibody or its antigen-binding fragment (ADFP98233-ADFP98237,  
CC ADFP98240-ADFP98249). The method is useful for inhibiting rejection,

CC particularly chronic rejection of a graft, particularly an allograft of  
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
CC inhibiting graft versus host disease for a bone marrow graft.

**SQ Sequence 117 AA;**

Alignment Scores:	
Pred. No.:	1,046-58
Score:	613.00
Percent Similarity:	100.00%
Best Local Similarity:	98.29%
Query Match:	97.15%
DB:	5
Length:	117
Matches:	115
Conservative:	2
Mismatches:	0
Indels:	0
Gaps:	0

US-10-733-563-108 (1-351) x ADF98241 (1-117)

Qy	1	GAGGTGCAATGTGGTTCGAGCTCGAGGAGGATTTGGTGAAGCCTCGGGGGTCATTGAGACTC	60
Db	1	GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuLeuArgLeu	20
Qy	61	TCATGTGAGCCTCTGGAATTCATTTTCAGTCGCTACGCCATGAACCTGGGTCCGCCAGGCT	120
Db	21	SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla	40
Qy	121	CCAGGAAGGGTTTCGAATGGTGGCCGCATAGAACATAAAATAATATATTATGCAACA	180
Db	41	ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr	60
Qy	181	TATTATGCCGATTTCAGTCTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACG	240
Db	61	TyrTyrAlaaspSerValLysaspArgPheThrIleSerArgaspSerLysAsnThr	80
Qy	241	CTCTATCTGCAATGAACAGCTTCAAAACTCAGGACACAGCCGTGTATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuLysThrGluaspThrAlaValTyrTyrCysThrThr	100
Qy	301	TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGTGTACCGTCAGCTCA	351
Db	101	PheTyrGlyAspGlnValTrrGlyGlnGlyThrLeuValThrValSerSer	117

**RESULT 15**

ADQ89240  
ID ADQ89240 standard; protein; 117 AA.

AC ADQ89240:

DT 21-OCT-2004 (first entry)

Humanised immunoglobulin protein #6

xx Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
 kw inflammatory disease; autoimmune disorder; graft rejection;  
 kw HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
 kw anti-HIV; virucide; antiarteriosclerotic.

OS Synthetic.

AA  
PN  
US2004151721-A1XX  
PD  
05-AUG-2004XX  
10-DEC-2003. 2003118-00733563[illegible]

PR 26-JUN-2002; 2002US-0392364P.

XX

PA (PONA/) PONATH P.

**PI O'keefe T, Ponat**

DR WPI; 2004-580175/56.

100

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
PS Example 2; SEQ ID NO 18; 128pp; English.  
XX  
CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a humanised  
CC immunoglobulin protein of the invention.  
XX  
SQ Sequence 117 AA;

Alignment Scores:  
Pred. No.: 1,048-58 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-108 (1-351) x ADQ89240 (1-117)

QY	1	GAGGTGCAATTGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC	60
Db	1	GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu	20
QY	61	TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTACGCCATGAACCTGGTCCGCCAGGCT	120
Db	21	SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla	40
QY	121	CCAGGAAAGGGTTTGGATTGGTTCGCCGATAGAACTAAAAATAATATTATCAACA	180
Db	41	ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnIleArgAlaThr	60
QY	181	TATTATGCCGATTCACTGAAAGACAGATTCAACATCTCCAGAGATGATTCAAAAAACACG	240
Db	61	TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr	80
QY	241	CTCTATCTGCRAATGACAGCTTGAAACTGAGGACACAGCCGCTGTATTACTGTACCACC	300
Db	81	LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr	100
QY	301	TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA	351
Db	101	PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer	117

Search completed: January 28, 2006, 08:33:31  
Job time : 57.8108 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: January 28, 2006, 08:20:11 ; Search time 9.57432 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gaggtgcaattgggttgagtc.....ccttggtcaccgtcagctca 351

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delext 7.0  
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO spool\_p/US10733563/runat\_27012006\_180006\_4797/app\_query.fasta\_1.2716  
-DB=PIR\_QMPT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CNC 1.1.83 @runat\_27012006\_180006\_4797 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492.5	78.1	137	2 S42467	Ig heavy chain V r
2	490	77.7	121	2 S31106	Ig heavy chain - h
3	485	76.9	127	2 S58213	Ig heavy chain V r
4	483	76.5	121	2 H36005	Ig heavy chain V r
5	482	76.4	117	2 S31109	Ig heavy chain - h
6	480	76.1	121	2 A41940	Ig heavy chain V r
7	479.5	76.0	141	2 I32513	Ig heavy chain pre
8	478	75.8	123	2 A36006	Ig heavy chain V r
9	477	75.6	138	2 A30561	Ig heavy chain pre
10	474	75.1	139	2 S31678	Ig heavy chain V r
11	472.5	74.9	126	2 S4107	Ig heavy chain V-D
12	467	74.0	160	2 S05271	Ig heavy chain pre
13	463.5	73.5	122	2 S30533	Ig heavy chain V r
14	463.5	73.5	147	2 I37780	Ig variable region

15	463	73.4	123	2 S26794	Ig heavy chain V r
16	463	73.4	140	2 S31588	Ig heavy chain V r
17	461	73.1	119	2 S36005	Ig heavy chain V r
18	460	72.9	115	1 AVMS06	Ig heavy chain V-I
19	460	72.9	119	2 S31107	Ig heavy chain - h
20	459.5	72.8	120	2 E49590	Ig heavy chain V r
21	458	72.6	138	2 S31666	Ig heavy chain V r
22	457.5	72.5	120	2 S48798	Ig heavy chain V r
23	456	72.3	119	2 S31108	Ig heavy chain - h
24	456	72.3	143	2 S21624	Ig heavy chain V r
25	454.5	72.0	122	2 E36005	Ig heavy chain V r
26	454.5	72.0	124	2 S20775	Ig heavy chain V r
27	454.5	72.0	124	2 S20782	Ig heavy chain V r
28	454	71.9	123	2 D36005	Ig heavy chain V r
29	454	71.9	123	2 S34009	Ig heavy chain V r
30	454	71.9	140	2 S31686	Ig heavy chain V r
31	453.5	71.9	114	2 S46390	Ig heavy chain V r
32	453	71.8	134	2 S31699	Ig heavy chain V r
33	452	71.6	133	2 S34010	Ig heavy chain V r
34	450	71.3	113	1 AVMSAB	Ig heavy chain V-I
35	450	71.3	113	1 AVMSB7	Ig heavy chain V-I
36	450	71.3	115	1 AVMS82	Ig heavy chain V-I
37	450	71.3	123	2 S31114	Ig heavy chain - h
38	448.5	71.1	140	2 S70442	Ig heavy chain pre
39	448	71.0	125	2 S30531	Ig heavy chain V r
40	448	71.0	135	2 S31598	Ig heavy chain V r
41	447.5	70.9	118	2 S31116	Ig heavy chain - h
42	447	70.8	134	2 S31679	Ig heavy chain V r
43	446.5	70.8	122	2 S20772	Ig heavy chain V r
44	446	70.7	121	2 S31113	Ig heavy chain - h
45	445.5	70.6	114	2 S46391	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S42467  
Ig heavy chain V region precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S42467  
R:Shiyanov, P.A.; Bessalov, I.A.; Terletskaya, H.N.; Deyev, S.M.  
submitted to the EMBL Data Library, March 1994  
A:Reference number: S42466  
A:Accession: S42467  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <SH1>  
A:Cross-references: UNIPARC:UPI00001161DB; EMBL:X78107; NID:G460798; PIDN:CAA54997.1; P:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.2e-40 Length: 137  
Score: 492.50 Matches: 95  
Percent Similarity: 88.33% Conservative: 11  
Best Local Similarity: 79.17% Mismatches: 9  
Query Match: 78.05% Indels: 5  
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x S42467 (1-137)

Qy	1	GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTTCATTGAGACTC	60
Db	20	GluValGlnLeuValGlnSerGlyGlyGluLeuValGlnProLysGlySerLeuLysLeu	39
Qy	61	TCATGTGCAGCCTCTGGATTCTTTCAGTGCCTACGCCATCACTGGGTTCGCCAGGCT	120
Db	40	SerCysAlaAlaSerGlyPheThrPheAlaMetAsnTrpValArgGlnAla	59
Qy	121	CCAGGAAGGGTTTGGAAATGGGTTGGCCGCATAGAAGCTAAATAATTAATTATGCAACA	180

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Db 60 ProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAlaThr 79
Qy 181 TATTATGCGCATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 80 TyrTyrGlyAenSerValLysAspArgPheThrIleSerArgAspSerGlnSerMet 99
Qy 241 CTCATCTCGCAATGAACAGCTTGAAACTGAGGACACAGCCGCGTATATTACTGTACACACC 300
Db 100 LeuTyrLeuGlnMetAsnLeuLysThrGluAspThrAlaMetTyrTyrCysVal--- 118
Qy 301 TTTTACGGTAAC-----GGTCTCTGGGGCCAGGGGACCTCGTCACCGTCAGCTCA 351
Db 119 ---TyrGlyAsnPheGlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 137

RESULT 2
S31106
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31106
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31106
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: UNIPARC:UPI0000176C8E; EMBL:X62954
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2,156-40 Length: 121
Score: 490.00 Matches: 98
Percent Similarity: 85.12% Conservative: 5
Best Local Similarity: 80.99% Mismatches: 14
Query Match: 77.65% Indels: 4
Gaps: 2

US-10-733-563-108 (1-351) x S31106 (1-121)

Qy 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
Qy 61 TCATGTGACGCTCTGGATTCACTTTGAGTCGCTACGCCATGAACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCGCATAGAAGCTTAAATAATATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyThrThr 60
Qy 181 TATTATGCGCATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 21 SerCysAlaIaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCGCATAGAAGCTTAAATAATATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleLysSerLysThrAspGlyThrThr 60
Qy 181 TATTATGCGCATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 80
Qy 241 CTCATCTCGCAATGAACAGCTTGAAACTGAGGACACAGCCGCGTATATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
Qy 301 -----TTTTACGGTAACCGTGTCTGGGGCCAGGGGACCTCGTCACCGCTCAGC 348
Db 101 ValIleAspTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrThrValThrValSer 120

349 TCA 351
Db 121 Ser 121

RESULT 3
```

```
S58213
Ig heavy chain V region (anti-F(ab')2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C:Accession: S58213; S58212
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling,
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206
A:Accession: S58213
A:Molecule type: mRNA
A:Residues: 1-127 <WEI>
A:Cross-references: UNIPARC:UPI000003FEA8; EMBL:X89055; NID:G929638; PIDN:CAA61442.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 6,66e-40 Length: 127
Score: 485.00 Matches: 96
Percent Similarity: 81.10% Conservative: 7
Best Local Similarity: 75.59% Mismatches: 14
Query Match: 76.86% Indels: 10
Gaps: 1

US-10-733-563-108 (1-351) x S58213 (1-127)

Qy 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuLysLeu 20
Qy 61 TCATGTGCGAGCTCTGGATTCACTTTGAGTCGCTACGCCATGAACTGGGTCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerGlySerThrMetHisTrpValArgGlnAla 40
Qy 121 CCAGAAAGGGTTTGGAAATGGTGGCCGCGCATAGAAGCTTAAATAATATTATGCAACA 180
Db 41 SerGlyLysGlyLeuGluTrpValGlyArgIleArgAsnLysAspAsnSerTyrAlaThr 60
Qy 181 TATTATGCGCATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCACAAAACACG 240
Db 61 AlaTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspSerGlnAsnThr 80
Qy 241 CTCATCTCGCAATGAACAGCTTGAAACTGAGGACACAGCCGCGTATATTACTGTACACACC 300
Db 81 AlaTyrLeuGlnMetAsnSerLeuLysIleGluAspThrAlaValTyrTyrCysThrArg 100
Qy 301 -----TTTTACGGTAACCGTGTCTGGGGCCAGGGGACCTCGTCACCGCTCAGC 330
Db 101 GlySerSerMetValArgGlyValAsnGlyTyrTyrGlyMetAspValTrpGlyGlnGly 120
Qy 331 ACCCTGGTCACCGCTCAGCTCA 351
Db 121 ThrThrValThrValSerSer 127

RESULT 4
H36005
Ig heavy chain V region (W85) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: H36005
R:Schröder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: H36005
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPARC:UPI0000176C28; GB:M34032
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
```

A:Map position: 14q32.33-14q32.33  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1,05e-39 Length: 121  
 Score: 483.00 Matches: 98  
 Percent Similarity: 83.47% Conservative: 3  
 Best Local Similarity: 80.99% Mismatches: 16  
 Query Match: 76.55% Indels: 4  
 DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x H36005 (1-121)

```

QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTGGTCAAGCGCTGGGGGGTCATTGAGACTC 60
   |||||
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTCGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
   |||||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetAsnTrpValArgGlnAla 40

QY 121 CCAGGAAGCGTTTGAATGGTTGGCCGCATGAAGAACTAAATAATTAATTATGCAACA 180
   |||||
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGileLysSerLysThrAspGlyGlyThrThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCANAAAAACACG 240
   |||||
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCTATCTCAATGAACAGCTTGAACACTGAGGACACAGCCGTGTATTACTGTACACC 300
   |||||
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100

QY 301 TTTTACGGTAACGGT-----GTCGTGGGCGCAGGGACCCCTGTCACCGTCACG 348
   |||||
Db 101 AspArgGlyGlySerSerGlnGlyAspTyrTrpGlyGlnGlyThrLeuValThrValSer 120

QY 349 TCA 351
   |||||
Db 121 Ser 121

```

RESULT 5  
 Ig heavy chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C:Accession: S31109  
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
 A:Reference number: S31104; MUID:92111633; PMID:1730252  
 A:Accession: S31109  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <RAA>

A:Cross-references: UNIPARC:UPI0000176DCA; EMBL:X62960  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
 Pred. No.: 1,33e-39 Length: 117  
 Score: 482.00 Matches: 96  
 Percent Similarity: 85.47% Conservative: 4  
 Best Local Similarity: 82.05% Mismatches: 17  
 Query Match: 76.39% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x S31109 (1-117)

```

QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTGGTGAAGCGCTGGGGGGTCATTGAGACTC 60
   |||||
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValValProGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTCGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
   |||||
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40

QY 121 CCAGGAAGCGTTTGAATGGTTGGCCGCATGAAGAACTAAATAATTAATTATGCAACA 180
   |||||
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgGileLysSerLysThrAspGlyGlyThrThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCANAAAAACACG 240
   |||||
Db 61 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCTATCTCAATGAACAGCTTGAACACTGAGGACACAGCCGTGTATTACTGTACACC 300
   |||||
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrAla 100

QY 301 TTTTACGGTAACGGTCTCTCGGGCGCAGGGACCCCTGTCACCGTCAGCTCA 351
   |||||
Db 101 ThrTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 117

```

# RESULT 6

A41940  
 Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment)  
 N:Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-May-1999  
 C:Accession: A41940; PL0201  
 R:Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss  
 Proteins 11, 159-175, 1991  
 A:Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional st  
 A:Reference number: A41940; MUID:92086633; PMID:1749770  
 A:Accession: A41940  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-121 <HER>

A:Cross-references: UNIPARC:UPI0000176D34  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70715)  
 R:Smith, R.G.; Voss Jr., E.W.  
 Mol. Immunol. 27, 463-470, 1990  
 A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from:

A:Reference number: PL0198; MUID:90309768; PMID:2114528

A:Accession: PL0201  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <SMI>  
 A:Cross-references: UNIPARC:UPI0000176D35  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-100/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:50-68/Region: complementarity-determining 2  
 F:101-110/Region: complementarity-determining 3  
 F:101-106/Region: D region  
 F:107-115/Region: JH region

Alignment Scores:  
 Pred. No.: 2,08e-39 Length: 121  
 Score: 480.00 Matches: 93  
 Percent Similarity: 86.18% Conservative: 13  
 Best Local Similarity: 75.61% Mismatches: 9  
 Query Match: 76.07% Indels: 8  
 DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x A41940 (1-121)

```

QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTGGTGAAGCGCTGGGGGGTCATTGAGACTC 60
   |||||
Db 1 GluValGlnProValGluThrGlyGlyLeuValProLysGlySerLeuValLeu 20

QY 61 TCATGTGCAGCCTCTGGATTCTTCTAGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120

```



C:Accession: A30561; S26931; S34008  
R:Sanz, I.; Dang, H.; Takei, M.; Talal, N.; Capra, J.D.  
J. Immunol. 142, 883-887, 1989  
A:Title: V-H sequence of a human anti-Sm autoantibody. Evidence that autoantibodies can  
A:Reference number: A30561; MUID:89110065; PMID:2492331  
A:Accession: A30561  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <SAN>  
A:CROSS-references: UNIPARC:UPI0000176C80  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A:Reference number: S26985; MUID:93021117; PMID:1404388  
A:Accession: S26931  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 20-119 <TOM>  
A:CROSS-references: UNIPARC:UPI000011640B; EMBL:Z12338; NID:G32896; PIDN:CAA78208.1; PIDN:  
R:Marlette, X.; Tsapis, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
A:Reference number: S34001; MUID:93209281; PMID:7681398  
A:Accession: S34008  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 20-119 <MAR>  
A:CROSS-references: UNIPARC:UPI000011640B  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 4,07e-39 Length: 138  
Score: 477.00 Matches: 97  
Percent Similarity: 85.71% Conservative: 15  
Best Local Similarity: 81.51% Mismatches: 5  
Query Match: 75.59% Indels: 2  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x A30561 (1-138)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
|||||  
Db 20 GluValGlnLeuValGluSerGlyGlyLeuValValysProGlyGlySerLeuArgLeu 39  
|||||  
QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGTCTAGCCATGACCTGGGTCCGCCAGGCT 120  
|||||  
Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 59  
|||||  
QY 121 CCAGGAAAGGGTTTGAATGGGTTGGCCGCATAGAAGCTAAATAATAATTATGCAACA 180  
|||||  
Db 60 ProGlyLysGlyLeuGluTrpValGlyArgLleLysSerLysThrAspGlyThrThr 79  
|||||  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCATCCATCTCCAGAGATGATTCAAAAACACG 240  
|||||  
Db 80 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 99  
|||||  
QY 241 CTCTATCTGCAATGACGCTTGAACCTGAGGACACAGCCGTGTATTACTGTACCACC 300  
|||||  
Db 100 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 119  
|||||  
QY 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGACCTGGTCAACCGTCAGCTCA 351  
|||||  
Db 120 AspSerLeuProHisArgValTrpGlyGlnGlyThrLeuValThrValSerSer 138  
|||||

RESULT 10

S31678  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31678  
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31678  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <CUI>  
A:CROSS-references: UNIPARC:UPI0000116456; EMBL:Z14169; NID:G31003; PIDN:CAA78538.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 8,04e-39 Length: 139  
Score: 474.00 Matches: 95  
Percent Similarity: 82.11% Conservative: 6  
Best Local Similarity: 77.24% Mismatches: 16  
Query Match: 75.12% Indels: 6  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S31678 (1-139)

QY 1 GAGGTGCAATGTTGAGTCTGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
|||||  
Db 17 GluValGlnLeuValGluSerGlyGlyLeuValValysProGlyGlySerLeuArgLeu 36  
|||||  
QY 61 TCATGTGCAGCTCTGGATTCACTTTCAGTGTCTAGCCATGACCTGGGTCCGCCAGGCT 120  
|||||  
Db 37 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 56  
|||||  
QY 121 CCAGGAAAGGGTTTGAATGGGTTGGCCGCATAGAAGCTAAATAATAATTATGCAACA 180  
|||||  
Db 57 ProGlyLysGlyLeuGluTrpValAlaArgLleLysSerLysThrAspGlyThrThr 76  
|||||  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCATCTCCAGAGATGATTCAAAAACACG 240  
|||||  
Db 77 AspTyrAlaAlaProValLysGlyArgPheThrIleSerArgAspSerLysAsnThr 96  
|||||  
QY 241 CTCTATCTGCAATGACGCTTGAACCTGAGGACACAGCCGTGTATTACTGTACCACC 300  
|||||  
Db 97 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 116  
|||||  
QY 301 TTTTACGGTAACCGT -----GTCTGGGGCCAGGGACCTGGTGGTCAACC 342  
|||||  
Db 117 AspLleSerGlnGlyAsnLeuLeuAlaPheAspLleTrpGlyGlnGlyThrMetValThr 136  
|||||  
QY 343 GTCAGCTCA 351  
|||||  
Db 137 ValSerSer 139  
|||||

RESULT 11

S44107

Ig heavy chain V-D-J region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001

C:Accession: S44107

R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, P.K.

submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable

A:Reference number: S44105

A:Accession: S44107

A:Molecule type: DNA

A:Residues: 1-126 <HAW>

A:CROSS-references: UNIPARC:UPI0000116634; EMBL:Z31394; NID:G472961; PIDN:CAA83269.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1.14e-38 Length: 126  
Score: 472.50 Matches: 94  
Percent Similarity: 79.37% Conservative: 6



```
Best Local Similarity: 74.60% Mismatches: 13
Query Match: 74.88% Indels: 13
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S44107 (1-126)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuLeuVal 20

QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATCGCAATCGGCTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerGlySerAlaMetHisTrpValArgGlnAla 40

QY 121 CCAGAAAGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATATATGCAACA 180
Db 60 ProGlyIysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThr 77

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACAG 240
Db 78 TyrTyrAlaAspSerValIysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97

QY 241 CTCATCTGCAAAATGAACAGCTTGAAGAACTCAGGACACAGCCGCTGATTTACTGTACCACC 300
Db 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117

QY 301 -----TTTACGGTAACGGTGTCTGGGGCCAGGG 330
Db 118 AlaValValArgGlyValIleSerTyrTyrTyrGlyMetAspValTrpGlyGlnGly 137

QY 331 ACCCTGGTCAACCGTCAGCTCA 351
Db 138 ThrThrValThrValSerSer 144

RESULT 13
S30533
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S30533
R:Marlette, X.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MAR>
A:Cross-references: UNIPROT:Q9UL88; UNIPARC:UPI0000176C2E; EMBL:Z18319
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 8.84e-38 Length: 122
Score: 463.50 Matches: 95
Percent Similarity: 83.61% Conservative: 7
Best Local Similarity: 77.87% Mismatches: 15
Query Match: 73.45% Indels: 5
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x S30533 (1-122)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnValGluSerGlyGlyLeuValIysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATCGCAATCGGCTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerArgPheThrPheThrAsnAlaTrpMetSerTrpValArgGlnAla 40

QY 121 CCAGAAAGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATATATGCAACA 180
Db 41 ProGlyIysGlyLeuGluTrpValGlyArgIleIysSerLysThrAspGlyGlyThrThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACAG 240
Db 61 AspTyrAlaAlaProValIysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCATCTGCAAAATGAACAGCTTGAAGAACTCAGGACACAGCCGCTGATTTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrThr 100

Best Local Similarity: 74.60% Mismatches: 13
Query Match: 74.88% Indels: 13
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x S44107 (1-126)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuLeuVal 20

QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATCGCAATCGGCTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerGlySerAlaMetHisTrpValArgGlnAla 40

QY 121 CCAGAAAGGTTTGGAAATGGTGGCCGCAATAAGAACTAAATAATAATATATGCAACA 180
Db 41 SerGlyIysGlyLeuGluTrpValGlyArgIleArgSerLysAlaAsnSerTyrAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAACACAG 240
Db 61 AlaTyrAlaAlaSerValIysGlyArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCATCTGCAAAATGAACAGCTTGAAGAACTCAGGACACAGCCGCTGATTTACTGTACCACC 300
Db 81 AlaTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysThrArg 100

QY 301 -----TTTACGGTAACGGTGTCTGG 321
Db 101 HisValAsnAspPheTrpSerGlyTyrProThrLeuTyrTyrTyrGlyMetAspValTrp 120

QY 322 GGCCAGGGGACCGTGC 339
Db 121 GlyGlnGlyProThrVal 126

RESULT 12
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
Submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
F:20-160/Product: Ig heavy chain (fragment) #status predicted <SIG>
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.9e-38 Length: 160
Score: 467.00 Matches: 93
Percent Similarity: 79.53% Conservative: 8
Best Local Similarity: 73.23% Mismatches: 14
Query Match: 74.01% Indels: 12
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x S05271 (1-160)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
```



QY 301 ----TTTTACGGTAACGGT-----GTCGTGGGGCCAGGGACCTGCTGTCACCGTC 345  
Db 101 GluPheSerAlaAspGlyAspTyrValArgTyrTrpGlyGlnGlyThrLeuValThrVal 120  
QY 346 AGCTCA 351  
Db 121 SerSer 122  
RESULT 14  
I37780  
Ig variable region (VDJ) (clone T20-11) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #8sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999  
C:Accession: I37780; S25474  
R:Demaison, C.; Chaetagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B  
A:Reference number: A36876; MUID:94119917; PMID:8290556  
A:Accession: I37780  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <RES>  
A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:28-111/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 8,7e-38 Length: 147  
Score: 463.50 Matches: 93  
Percent Similarity: 79.37% Conservative: 7  
Best Local Similarity: 73.81% Mismatches: 15  
Query Match: 73.45% Indels: 11  
DB: 2 Gaps: 2  
US-10-733-563-108 (1-351) x I37780 (1-147)  
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
Db 14 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 33  
QY 61 TCATGTGACGCTCTGGATTCACTTTCAGTGTGCTACGCGCATGAACCTGGGTCCGCCAGGCT 120  
Db 34 SerCysAlaAlaSerGlyPheThrPheSerSerTyrTrpMetSerTrpValArgGlnAla 53  
QY 121 CCAGGAAAGGGTTTGAATGGTTGGCCGATGAAGAACTAAATAATAATTATGCAACA 180  
Db 54 ProGlyLysGlyLeuGluTrpValAlaAenlle-----LysGlnAspGlySerGluLys 71  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCAACCATCTCCAGAGATGATTCAAAAAACAGC 240  
Db 72 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAenThr 91  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCAACC 300  
Db 92 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 111  
QY 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGACCTG 333  
Db 112 AspGlyGluGlyTrpGlyLeuTyrTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThr 131  
QY 334 CTGGTCACCGTCAGCTCA 351  
Db 132 ThrValThrValSerSer 137  
RESULT 15  
S26794  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #8sequence\_revision 13-Jan-1995 #text\_change 17-Mar-1999  
C:Accession: S26794  
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992

A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam  
A:Reference number: S26786; MUID:92111632; PMID:1730251  
A:Accession: S26794  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <MOR>  
A:Cross-references: UNIPARC:UPI0000176C2B; EMBL:X61011  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 9,9e-38 Length: 123  
Score: 463.00 Matches: 91  
Percent Similarity: 81.60% Conservative: 11  
Best Local Similarity: 72.80% Mismatches: 13  
Query Match: 73.38% Indels: 10  
DB: 2 Gaps: 2  
US-10-733-563-108 (1-351) x S26794 (1-123)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGACGCTCTGGATTCACTTTCAGTGTGCTACGCGCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrSerMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGAATGGTTGGCCGATGAAGAACTAAATAATAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValSerTyrIleSerSerSerSer-----ThrIle 58  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCAACCATCTCCAGAGATGATTCAAAAAACAGC 240  
Db 59 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAenSer 78  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCC--- 297  
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAspGluAspThrAlaValTyrTyrCysAlaArg 98  
QY 298 -----ACCTTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTG 336  
Db 99 SerIleLysTyrTyrAspGluAenTyrTyrGlyMetAspValTrpGlyGlnGlyThrThr 118  
QY 337 CTCACCGTCAGCTCA 351  
Db 119 ValThrValSerSer 123

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Job time : 11.5743 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 / Search time 53.8446 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-108

Perfect score: 631

Sequence: 1 gagggtgaattgggtgagtc.....ccctgggtcacgcagtcac 351

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool.p/US10733563/runat.27012006.180005.4782/app.query.fasta\_1.2716  
-DB=UniProt -QFMT=fastn -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1.1.632 @runat.27012006.180005.4782 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	477.5	75.7	471	2 Q66K04 MOUSE
2	463	73.4	464	2 Q6MZU6 HUMAN
3	460	72.9	115	1 HV32 MOUSE
4	453	71.8	113	2 Q9UL90 HUMAN
5	453	71.8	131	2 Q9UL88 HUMAN
6	452	71.6	240	2 Q65ZC9 HUMAN
7	450	71.3	113	1 HV27 MOUSE
8	450	71.3	113	1 HV30 MOUSE
9	450	71.3	115	1 HV33 MOUSE
10	447	70.8	597	2 Q96BB9 HUMAN
11	446.5	70.8	494	2 Q96K68 HUMAN
12	446.5	70.8	613	2 Q8WUK1 HUMAN
13	446	70.7	121	2 Q9UL71 HUMAN
14	444	70.4	113	1 HV28 MOUSE
15	444	70.4	487	2 Q80Z17 MOUSE
16	443	70.2	116	2 Q9UL93 HUMAN

17	442.5	70.1	606	2 Q6GMY2 HUMAN	Q6gmy2 homo sapien
18	442	70.0	113	1 HV31 MOUSE	P01800 mus musculus
19	440.5	69.8	118	2 Q9UL91 HUMAN	Q9ul91 homo sapien
20	440	69.7	113	1 HV29 MOUSE	P01798 mus musculus
21	439	69.6	468	2 Q569B4 RAT	Q569b4 rattus norv
22	437	69.3	458	2 Q65ZQ1 HUMAN	Q65zq1 homo sapien
23	436.5	69.2	469	2 Q569F4 HUMAN	Q569f4 homo sapien
24	436	69.1	472	2 Q6N089 HUMAN	Q6n089 homo sapien
25	434	68.8	478	2 Q6PI81 HUMAN	Q6pi81 homo sapien
26	432.5	68.5	122	1 HV3G HUMAN	P01768 homo sapien
27	432.5	68.5	573	2 Q8WU38 HUMAN	Q8wu38 homo sapien
28	431	68.3	470	2 Q6FUA4 HUMAN	Q6fua4 homo sapien
29	429	68.0	142	1 HV01 RAT	P01805 rattus norv
30	429	68.0	464	2 Q6PIF8 MOUSE	Q6pif8 mus musculus
31	429	68.0	493	2 Q6GMY2 HUMAN	Q6gmy2 homo sapien
32	426.5	67.6	465	2 Q6P6C4 HUMAN	Q6p6c4 homo sapien
33	426	67.5	120	1 HV3E HUMAN	P01766 homo sapien
34	424.5	67.3	473	2 Q6MZV7 HUMAN	Q6mzv7 homo sapien
35	424	67.2	466	2 Q6IN78 HUMAN	Q6in78 homo sapien
36	423	67.0	113	1 HV34 MOUSE	P01803 mus musculus
37	422.5	67.0	119	2 Q5P2I8 MOUSE	Q5f2i8 mus musculus
38	422.5	67.0	475	2 Q6MZQ6 HUMAN	Q6mzq6 homo sapien
39	418	66.2	119	2 Q920E7 MOUSE	Q920e7 mus musculus
40	417.5	66.2	122	1 HV21 MOUSE	P01790 mus musculus
41	416.5	66.0	465	2 Q5IOJ0 RAT	Q5ioj0 rattus norv
42	416.5	66.0	475	2 Q6GMW7 HUMAN	Q6gmw7 homo sapien
43	415.5	65.8	112	2 Q9HCC1 HUMAN	Q9hcc1 homo sapien
44	415.5	65.8	114	1 HV3B HUMAN	P01763 homo sapien
45	415.5	65.8	467	2 Q4VBH1 RAT	Q4vbn1 rattus norv

#### ALIGNMENTS

RESULT 1  
Q66K04 MOUSE  
ID Q66K04 MOUSE PRELIMINARY; PRT; 471 AA.  
AC Q66K04;  
DT 25-OCT-2004 (Tremblrel. 28, Created)  
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Hypothetical protein.  
GN Name=Igh-1a;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH II;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.P., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CZECH 11;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
EMBL: BC080671, AH80671.1; -, mRNA.  
DR SMR; Q66K04; 20-467.  
DR MGI; 96443; Igh-1a.  
DR GO; GO:0003823; F-antigen binding; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00407; IGV; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 471 AA; 52259 MW; 81BB7C322B315AC2 CRC64;

Alignment Scores:  
Pred. No.: 2,41e-45 Length: 471  
Score: 477.50 Matches: 92  
Percent Similarity: 85.25% Conservative: 12  
Best Local Similarity: 75.41% Mismatches: 13  
Query Match: 75.67% Indels: 5  
DB: 2 Gaps: 1

US-10-733-563-108 (1-351) x Q66K04\_MOUSE (1-471)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGCTCATTTGAGACTC 60  
DB 20 GluValGlnLeuValGluThrGlyGlyLeuValGlnProLysGlySerLeuLysLeu 39  
QY 61 TCATGTGACGCTCTCGATTCACTTTTCAGTGCCTACGCCATCAACTGGGTCCGCCAGGCT 120  
DB 40 SerCysAlaAlaSerGlyPheSerPheAsnThrAsnAlaMetAsnTrpValArgGlnAla 59  
QY 121 CAGGAAAGGGTTTGGAAATGGTGGTCCCATCAAGAACTTAAATAATTAATTCACACA 180  
DB 60 ProGlyLysGlyLeuGluTrpValAlaAlaGlyIleArgSerLysSerAsnAsnTrpAlaThr 79  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACAG 240  
DB 80 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnSerMet 99  
QY 241 CTCTATCTGCAATGAACAGCTTGAACACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 100 LeuTyrLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValLys 119  
QY 301 TTT-----TACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCAACCGTC 345  
DB 120 GluGlyGlnLeuGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrThrIleThrVal 139  
QY 346 AGCTCA 351  
DB 140 SerSer 141

RESULT 2  
Q6MZU6 HUMAN  
ID Q6MZU6\_HUMAN PRELIMINARY; PRT; 464 AA.  
AC Q6MZU6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686C15213.  
GN Name=DKFZp686C15213.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC NCBI\_TaxID=9606;

OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Rectum tumor;  
RG The German CDNA Consortium;  
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
EMBL: BX640874; CAB45931.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IGV; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66B8A0ABC CRC64;

Alignment Scores:  
Pred. No.: 1.09e-43 Length: 464  
Score: 463.00 Matches: 90  
Percent Similarity: 85.00% Conservative: 12  
Best Local Similarity: 75.00% Mismatches: 14  
Query Match: 73.38% Indels: 4  
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q6MZU6\_HUMAN (1-464)

QY 1 GAGTGCATTTGGTTGAGTCTGGAGGAGGATTGGTGAAGCTGGGGGCTCATTTGAGACTC 60  
DB 20 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 39  
QY 61 TCATGTGACGCTCTCGATTCACTTTTCAGTGCCTACGCCATCAACTGGGTCCGCCAGGCT 120  
DB 40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrSerMetAsnTrpValArgGlnAla 59  
QY 121 CAGGAAAGGGTTTGGAAATGGTGGTCCCATCAAGAACTTAAATAATTAATTCACACA 180  
DB 60 ProGlyLysGlyLeuGluTrpValSerSerPheSerSerArgGlySerTyr---Glu 78  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACAG 240  
DB 79 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 98  
QY 241 CTCTATCTGCAATGAACAGCTTGAACACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 99 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAsnThrAlaValTyrTyrCysAlaArg 118  
QY 301 -----TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCAACCGTCAGCTCA 351  
DB 119 AspLeuGlyTrpPheGlyLeuAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 138

RESULT 3  
HV32\_MOUSE  
ID HV32\_MOUSE STANDARD; PRT; 115 AA.  
AC P01801;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-II region J606.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP PROTEIN SEQUENCE.  
RX MEDLINE=82099361; PubMed=6798111;  
RA Johnson N., Slankard J., Paul L., Hood L.;  
RT "The complete V domain amino acid sequences of two myeloma inulin-  
binding proteins.";  
RL J. Immunol. 128:302-307(1982).  
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
CC binds inulin.  
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC PIR; C92811; AVMS06.  
DR HSP; P01852; 1NFD.  
DR Ensembl; ENSMUSG00000045097; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00406; IG\_V.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DOMAIN 1 114 Ig-like.  
FT DISULFID 22 98 By similarity.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Alignment Scores:  
Pred. No.: 1.95e-43 Length: 115  
Score: 460.00 Matches: 86  
Percent Similarity: 86.32% Conservative: 15  
Best Local Similarity: 73.50% Mismatches: 14  
Query Match: 72.90% Indels: 2  
DB: 1 Gaps: 1

US-10-733-563-108 (1-351) x HV32\_MOUSE (1-115)

QY 1 GAGGTGCAATGCTGGTTCGAGCTCGAGGAGGATGGTGAAGCCCTGGGGGTCATTGAGACTC 60  
DB 1 GluValLeuGluSerGlyGlyGlyValGlnProGlySerMetLysLeu 20  
QY 61 TCATGTGACGCTCTGGATTCTTCACTTTCAGTGGCTGCGCATCACTCGGTCGCGCAGGCT 120  
DB 21 SerCysValAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValargGlnSer 40  
QY 121 CAGGAAGGGTTGGATGGTGGCCGCATCAAGAACTTAAATAATTAATTAATGCAACA 180  
DB 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLysSerAsnAsnTyrAlaThr 60  
QY 181 TATTATCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACAGC 240  
DB 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspAspSerLysSerSer 80  
QY 241 CTCATCTCCAATGAACCTTGAATGGTGGCCGCATCAAGAACTTAAATAATTAATTAATGCAACA 300  
DB 81 ValTyrLeuGlnMetAsnAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 115

RESULT 4

Q9UL90\_HUMAN  
ID Q9UL90\_HUMAN PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
(Fragment).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Raaphorst F.M.; Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RT immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
DR EMBL; AF035024; AAD56260.1; -; mRNA.  
DR FIR; S78486; S78486.  
DR HSP; P01772; 2FB4.  
DR SMR; Q9UL90; 1-113.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IG\_V; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
FT NON\_TER 1 113  
FT NON\_TER 1 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07P CRC64;

Alignment Scores:  
Pred. No.: 1.23e-42 Length: 113  
Score: 453.00 Matches: 91  
Percent Similarity: 83.76% Conservative: 7  
Best Local Similarity: 77.78% Mismatches: 15  
Query Match: 71.79% Indels: 4  
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q9UL90\_HUMAN (1-113)

QY 1 GAGGTGCAATGCTGGTTCGAGCTCGAGGAGGATGGTGAAGCCCTGGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlySerLysLeuArgLeu 20  
QY 61 TCATGTGACGCTCTGGATTCTTCACTTTCAGTGGCTGCGCATCAAGAACTTAAATAATTAATTAATGCAACA 180  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValargGlnAla 40  
QY 121 CAGGAAGGGTTGGATGGTGGCCGCATCAAGAACTTAAATAATTAATTAATTAATGCAACA 240  
DB 41 ProGlyLysGlyLeuGluTrpValAlaPheIleArgTyrAspGlySerAsn-----Lys 58  
QY 181 TATTATCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACAGC 300  
DB 59 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 78  
QY 241 CTCATCTCCAATGAACCTTGAATGGTGGCCGCATCAAGAACTTAAATAATTAATTAATGCAACA 351  
DB 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 99 -----AspLeuAsnTyrTrpGlyGlnGlyThrLeuValThrValSerSer 113

RESULT 5

Q9UL88\_HUMAN  
ID Q9UL88\_HUMAN PRELIMINARY; PRT; 131 AA.  
AC Q9UL88;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP PROTEIN SEQUENCE.  
RX PubMed=1555592;  
RA Makiya R., Stigbrand T.;  
RT "Placental alkaline phosphatase has a binding site for the human  
RT immunoglobulin-G Fc portion.";  
RL Eur. J. Biochem. 205:341-345(1992).  
DR EMBL; AF035026; AAD56262.1; -; mRNA.  
DR PIR; S21205; S21205.  
DR PIR; S30533; S30533.  
DR HSP; P01852; INFED.  
DR SMR; Q9UL88; 1-131.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 131  
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.26e-42 Length: 131  
Score: 453.00 Matches: 94  
Percent Similarity: 74.0% Conservative: 6  
Best Local Similarity: 69.6% Mismatches: 13  
Query Match: 71.7% Indels: 22  
DB: 2 Gaps: 2  
  
US-10-733-563-108 (1-351) x Q9UL88\_HUMAN (1-131)  
  
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20  
  
QY 61 TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTACGCATGAACCTGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerLysAlaTrpMetSerTrpValArgGlnAla 40  
  
QY 121 CCAGAAAGGCTTGGATTGGTGGCGCATAGAACTTAAATAATATATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValLysSerLysLeuThrAspGlyGlyThrThr 60  
  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAGAAACACG 240  
Db 61 AspTyrAlaAlaProValLysGlyArgLeuThrLysSerArgAspSerSerLysAsnThr 80  
  
QY 241 CTCTATCTGCAATGAACAGCTTGAAGTGAAGACAGACAGCGCTGATTACTGTACCAACC 300  
Db 81 LeuTyrLeuArgMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
  
QY 301 TTTTACGGTACGGTGTC-----TGCGGCCAGGGACCTGGTCACCGTCAGCTCA 318  
Db 101 -----GlyIleThrMetIleValValIleThrThrSerSerLysArgThr 116  
QY 319 -----TGCGGCCAGGGACCTGGTCACCGTCAGCTCA 351  
Db 117 -----GlyLysGlyThrLeuValThrValSerSer 117

Db 117 SerPheGluTyrTrpGlyGlnGlyThrLeuValThrValSerSer 131  
RESULT 6  
Q65ZC9\_HUMAN PRELIMINARY; PRT; 240 AA.  
AC Q65ZC9;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
CN Name=scFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=C1G/7;  
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
RA Kontermann R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies.";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL; Y13056; CAA73499.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGv; 2.  
DR PROSITE; PS50835; IG LIKE; 2.  
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FT NON\_TER 240  
FT NON\_TER 240  
SQ SEQUENCE 240 AA; 25569 MW; FDCFD03645F64B373 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.79e-42 Length: 240  
Score: 452.00 Matches: 89  
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Query Match: 71.6% Indels: 4  
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US-10-733-563-108 (1-351) x Q65ZC9\_HUMAN (1-240)  
  
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60  
Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20  
  
QY 61 TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTACGCATGAACCTGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrGlyMetHisTrpValArgGlnAla 40  
  
QY 121 CCAGAAAGGCTTGGATTGGTGGCGCATAGAACTTAAATAATATATATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValLysSerTyrAspGlySerAsn-----Lys 58  
  
QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAGAAACACG 240  
Db 59 TyrTyrAlaAspSerValLysGlyArgPheThrLysSerArgAspAsnSerLysAsnThr 78  
  
QY 241 CTCTATCTGCAATGAACAGCTTGAAGTGAAGACAGACAGCGCTGATTACTGTACCAACC 300  
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCysAlaArg 98  
  
QY 301 TTTTACGGTACGGTGTC-----TGCGGCCAGGGACCTGGTCACCGTCAGCTCA 351  
Db 99 AspTrpGlyAspSerLeuAspProTrpGlyLysGlyThrLeuValThrValSerSer 117  
RESULT 7  
HV27\_MOUSE  
ID HV27\_MOUSE STANDARD; PRT; 113 AA.  
AC P01786;  
DT 21-JUL-1986 (Rel. 01, Created)







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DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Alignment Scores:
Pred. No.: 7,69e-42 Length: 597
Score: 447.00 Matches: 89
Percent Similarity: 78.74% Conservative: 11
Best Local Similarity: 70.08% Mismatches: 15
Query Match: 70.84% Indels: 12
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q96B9_HUMAN (1-597)
QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTGATTGAGACTC 60
DB 20 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39
QY 61 TCATGTGAGCCCTCTGGATTCACTTTCAGTGTCTAGCCATGAACCTGGGTCCGCCAGGCT 120
DB 40 SerCysAlaAlaSerGlyPheSerPheSerThrAlaMetAsnTrpValArgGlnAla 59
QY 121 CCAGGAAGGGTTTGAATGGTGGCCCATAGAAGCTAAATAATTAATTATGCAACA 180
DB 60 ProGlyLysGlyLeuGluTrpValSerAlaIle-----SerGlySerGlyGlySerThr 77
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACATCTCAGAGATGATTCAAAAACAGC 240
DB 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThr 97
QY 241 CTCTATCTCAATGAACAGCTTGAAGCTGAAACCTGAGGACACAGCGTGTATTACTGTACC--- 297
DB 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117
QY 298 -----ACCTTTCAGGTAAACGGTGTCTGGGCCCGCCAGGG 330
DB 118 AspProArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyrTrpGlyGlnGly 137
QY 331 ACCCTGGTCCAGCTGAGCTCA 351
DB 138 ThrLeuValThrValSerSer 144

RESULT 11
Q96K68 HUMAN
ID Q96K68_HUMAN PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shikatori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T.,
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RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Mutsaers K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Suzuki H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh Y., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345 (1992).
DR EMBL; AK027379; BAB55072.1; -, mRNA.
DR FIR; S21205; S21205.
DR HSSP; P01876; IOWO.
DR SMR; Q96K68; 264-472.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5B5ABE4C0E CRC64;

Alignment Scores:
Pred. No.: 8.53e-42 Length: 494
Score: 446.50 Matches: 89
Percent Similarity: 79.84% Conservative: 10
Best Local Similarity: 71.77% Mismatches: 16
Query Match: 70.76% Indels: 9
DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q96K68_HUMAN (1-494)
QY 1 GAGGTGCAATGTTGAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTGATTGAGACTC 60
DB 20 GluValGlnLeuValGlnSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 39
QY 61 TCATGTGAGCCCTCTGGATTCACTTTCAGTGTCTAGCCATGAACCTGGGTCCGCCAGGCT 120
DB 40 SerCysAlaAlaSerGlyLeuSerPheSerThrTyrAlaMetAsnTrpValArgGlnAla 59
QY 121 CCAGGAAGGGTTTGAATGGTGGCCCATAGAAGCTAAATAATTAATTATGCAACA 180
DB 60 ProGlyLysGlyLeuGluTrpValSerSerIleSerSerArgSerAsp-----TyrIle 77
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACATCTCAGAGATGATTCAAAAACAGC 240
DB 78 TyrTyrArgAspSerValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSer 97
QY 241 CTCTATCTCAATGAACAGCTTGAAGCTGAAACCTGAGGACACAGCGTGTATTACTGTGT----- 294
DB 98 LeuTyrLeuGlnMetAsnSerLeuArgValAspThrAlaValTyrTyrCysAlaArg 117
QY 295 -----ACCACCTTTTACGGTAACGGTGTCTGGGCCCGCCAGGG 339
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Db      118 AppSerCysAsnGlyAlaIleCysTyrGlyPheSerProTrpGlyGlnGlyThrLeuVal 137
Qy      340 ACCGTCAGCTCA 351
Db      138 ThrValSerSer 141
RESULT 12
Q8WUK1_HUMAN
ID      Q8WUK1_HUMAN PRELIMINARY;      PRT;      613 AA.
AC      Q8WUK1.
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      IGHM protein.
GN      Name=IGHM;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Primary B-Cells;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton C., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Primary B-Cells;
RG      NIH MGC Project;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=2117273;
RA      Schroeder H.W. Jr., Wang J.Y.;
RT      "Preferential utilization of conserved immunoglobulin heavy chain
RT      variable gene segments during human fetal life.";
RL      Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150 (1990).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=1393695; DOI=10.1016/0161-5890(92)90173-U;
RA      Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;
RT      "IGM kappa/lambda EBV human B cell clone: an early step of
RT      differentiation of fetal B cells or a distinct B lineage?";
RL      Mol. Immunol. 29:1363-1373 (1992).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=1730252;
RA      Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA      Schuurman R.K.;
RT      "Restricted utilization of germ-line VH3 genes and short diverse third
RT      complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT      immunoglobulin heavy chain rearrangements.";
RL      Eur. J. Immunol. 22:247-251 (1992).
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RN      [6]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=1904154;
RA      Neale G.A., Kitchingman G.R.;
RT      "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT      chain enhancer region contain a non-translatable exon and are
RT      extremely heterogeneous at the 5' end.";
RL      Nucleic Acids Res. 19:2427-2433 (1991).
RN      [7]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA      Bird J., Gallili N., Link M., Scites D., Sklar J.;
RT      "Continuing rearrangement but absence of somatic hypermutation in
RT      immunoglobulin genes of human B cell precursor leukemia.";
RL      J. Exp. Med. 168:229-245 (1988).
RN      [8]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA      Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT      "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal
RT      B cell lines. Preferential utilization of the most JH-proximal D
RT      segment (DQ52) and two unusual VH-related rearrangements.";
RL      J. Exp. Med. 169:1391-1403 (1989).
RN      [9]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA      Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT      "The structural basis of germline-encoded VH3 immunoglobulin binding
RT      to staphylococcal protein A.";
RL      J. Exp. Med. 178:331-336 (1993).
RN      [10]
RP      NUCLEOTIDE SEQUENCE.
RX      EMBL; BC020240; AAH20240.1; -; mRNA.
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Db 60 ProGlyLysGlyLeuGluTrpValAlaValIleSerTyrAspGlySerAsn-----Lys 77
QY 181 TATTATGCCGATTCAGTGAAGACAGATTACCAATCTCAGAGATGATTCAAAAACACG 240
Db 78 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThr 97
QY 241 CTCCTATCTCAATGAACAGCTTGAAGACTGAGGACACAGCGTGTATTACTGTACCACC 300
Db 98 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 117
QY 301 TTTTACGGTAAACGGTGTCT-----TGGGGCCAGGGGACCCCTGGTCCACCGTC 345
Db 118 AspTrpSerGluGlyValGluThrPheAspIleTrpGlyGlnGlyThrMetValThrVal 137
QY 346 AGCTCA 351
Db 138 SerSer 139

RESULT 13
Q9UL71_HUMAN
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AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.,"
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -; mRNA.
DR HSP; P01852; INPD.
DR SMR; Q9UL71; 1-121.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Alignment Scores:
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Score: 446.00 Matches: 89
Percent Similarity: 81.30% Conservative: 11
Best Local Similarity: 72.36% Mismatches: 15
Query Match: 70.68% Indels: 8
DB: 2 Gaps: 3

US-10-733-563-108 (1-351) x Q9UL71_HUMAN (1-121)

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QY 61 TCATGTGAGCCCTCTGGATTCACTTTAGTGCCTAGCCCATGAATCGGTCCGCCAGGCT 120
Db 21 PheCysAlaAlaSerGlyPheThrPheAspGlyTyrAlaMetHisTrpValArgGlnAla 40
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Db 59 TyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnSer 78
QY 241 CTCCTATCTCAATGAACAGCTTGAAGACTGAGGACACAGCGTGTATTACTGT----- 294
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCysAlaLys 98
QY 295 -----ACCACCTTTTACGGTAACT---GGTGTCTGGGGCCAGGGGACCCCTGGTCCAC 342
Db 99 GlyLysValThrThrIleTyrAspArgPheAspIleTrpGlyGlnGlyThrMetValThr 118
QY 343 GTCAGCTCA 351
Db 119 ValSerSer 121

RESULT 14
HV28_MOUSE
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudnikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RT proteins.,"
RT Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -! MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds inulin.
CC -! SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; B93818; AVMS61.
CC HSP; P01783; IIGC.
CC SMR; P01797; 1-113.
CC Ensembl; ENSMUSG00000045097; Mus musculus.
CC InterPro; IPR007110; Ig-like.
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CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 >113 Ig-like.
FT DISULFID 22 98 By similarity.
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Db 41 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLysSerHisAsnTyrAlaThr 60
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Db 61 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 80
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Db 81 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGACCGTGTGTACCGTC 345
Db 101 -----GlyPheAlaTyrTrpGlyGlnGlyThrLeuValProVal 113

RESULT 15
Q80217_MOUSE
ID Q80217_MOUSE PRELIMINARY; PRT; 487 AA.
AC Q80217;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049143; AAH49143.1; -; mRNA.
DR HSSP; P01789; 1MCP.
DR SMR; Q80217; 20-242.
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DR MGI; 96486; Igh-VJ558.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

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Pred. No.: 1.64e-41 Length: 487
Score: 444.00 Matches: 85
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Best Local Similarity: 69.11% Mismatches: 15
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DB: 2 Gaps: 2

US-10-733-563-108 (1-351) x Q80217_MOUSE (1-487)
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Db 40 SerCysAlaAlaSerGlyPheThrPheSerAsnTyrTrpMetAsnTrpValArgGlnSer 59
QY 121 CCAGGAAAGGTTTGGATGGTTCGGCCGATGAAGTCAAAATAAATAATTATGCAACA 180
Db 60 ProGluLysGlyLeuGluTrpValAlaGluLeuArgLysSerHisAsnTyrAlaThr 79
QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCACATCTCCAGAGATGATTCAAAAACACG 240
Db 80 HisTyrAlaGluSerValLysGlyArgPheThrIleSerArgAspSerLysSer 99
QY 241 CTCTATCTGCAAAATGAACAGCTTGAAACTAGGACACACCGCTGTTACTGTACACC--- 297
Db 100 ValTyrLeuGlnMetAsnLeuArgAlaGluAspThrGlyIleTyrTyrCysThrArg 119
QY 298 ACCTTTTACGGTAAC-----GGTGTCTGGGGCCAGGGACCCCTGTGTACCC 342
Db 120 ArgGlyTyrGlyAspProAsnTrpTyrPheAspValTrpGlyAlaGlyThrThrValThr 139
QY 343 GTCAGCTCA 351
Db 140 ValSerSer 142

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Job time : 56.8446 secs
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 ; Search time 13.8784 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

Title: US-10-733-563-108

Perfect score: 631

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CNC 1.141 @runat 27012006 180006 4815 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2.6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	2	US-09-809-739-20
2	620	98.3	117	2	US-09-840-459-17
3	620	98.3	117	2	US-09-497-625A-17
4	620	98.3	119	2	US-09-840-459-104
5	620	98.3	119	2	US-09-497-625A-104
6	613	97.1	117	2	US-09-809-739-21
7	613	97.1	117	2	US-09-840-459-18
8	613	97.1	117	2	US-09-497-625A-18
9	604	95.7	117	2	US-09-809-739-22
10	604	95.7	117	2	US-09-840-459-19
11	604	95.7	117	2	US-09-497-625A-19
12	599	94.9	117	2	US-09-809-739-23

13	599	94.9	117	2	US-09-840-459-20	Sequence 20, Appl
14	599	94.9	117	2	US-09-497-625A-20	Sequence 20, Appl
15	548	86.8	117	2	US-09-809-739-12	Sequence 12, Appl
16	548	86.8	117	2	US-09-840-459-10	Sequence 10, Appl
17	548	86.8	117	2	US-09-497-625A-10	Sequence 10, Appl
18	548	86.8	148	2	US-09-840-459-100	Sequence 100, App
19	548	86.8	148	2	US-09-497-625A-100	Sequence 100, App
20	488.5	77.4	116	1	US-08-428-197-10	Sequence 10, Appl
21	488.5	77.4	116	4	PCT-US93-10555-10	Sequence 10, Appl
22	487	77.2	123	2	US-09-097-0558-87	Sequence 87, Appl
23	487	77.2	123	2	US-09-893-615-87	Sequence 87, Appl
24	485	76.9	125	1	US-08-428-197-9	Sequence 9, Appl
25	485	76.9	125	4	PCT-US93-10555-9	Sequence 9, Appl
26	485	76.9	127	2	US-09-840-459-71	Sequence 71, Appl
27	485	76.9	127	2	US-09-497-625A-71	Sequence 71, Appl
28	483.5	76.6	126	2	US-09-840-459-74	Sequence 74, Appl
29	483.5	76.6	126	2	US-09-497-625A-74	Sequence 74, Appl
30	482	76.4	115	2	US-08-767-128-36	Sequence 36, Appl
31	482	76.4	117	2	US-09-840-459-83	Sequence 83, Appl
32	482	76.4	117	2	US-09-497-625A-83	Sequence 83, Appl
33	480.5	76.1	126	2	US-09-840-459-73	Sequence 73, Appl
34	480.5	76.1	126	2	US-09-497-625A-73	Sequence 73, Appl
35	480.5	76.1	130	1	US-08-478-033-70	Sequence 70, Appl
36	480.5	76.1	130	1	US-08-478-039-93	Sequence 93, Appl
37	480.5	76.1	130	1	US-08-476-349A-70	Sequence 93, Appl
38	480.5	76.1	130	1	US-08-476-349A-93	Sequence 93, Appl
39	480	76.1	332	2	US-09-135-121B-7	Sequence 7, Appl
40	478	75.8	123	2	US-09-840-459-94	Sequence 94, Appl
41	478	75.8	123	2	US-09-497-625A-94	Sequence 94, Appl
42	477	75.6	119	1	US-08-428-197-11	Sequence 11, Appl
43	477	75.6	119	2	US-09-809-739-19	Sequence 19, Appl
44	477	75.6	119	2	US-09-840-459-16	Sequence 16, Appl
45	477	75.6	119	2	US-09-840-459-93	Sequence 93, Appl

ALIGNMENTS

US-09-809-739-20  
; Sequence 20, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; TITLE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-20

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Pred. No.: 1,14e-68 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

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Db 21 SerCysAlaLeuSerGlyPheThrPheSerAlaTyrAlaMetAsnTyrValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGGATTGGTGGCGCATAGAATCAAAATAATAATTATGCAACA 180  
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QY 241 CTCTATCTGCAAAATGAACAGCTTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
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## RESULT 2

US-09-840-459-17  
; Sequence 17, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-17

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Pred. No.: 1.14e-68 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
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US-10-733-563-108 (1-351) x US-09-840-459-17 (1-117)

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QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTACGCCATGAACCTGGGCTCGCCAGGCT 120  
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QY 121 CCAGAAAGGGTTTGGATTGGTGGCGCATAGAATCAAAATAATAATTATGCAACA 180  
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Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 3

US-09-497-625A-17  
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; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-497-625A-17

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Pred. No.: 1.14e-68 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-17 (1-117)

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Db 21 SerCysAlaLeuSerGlyPheThrPheSerAlaTyrAlaMetAsnTyrValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGGATTGGTGGCGCATAGAATCAAAATAATAATTATGCAACA 180  
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QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGCTGTATTACTGTACACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
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RESULT 4  
US-09-840-459-104  
; Sequence 104, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR FILING DATE: 1998-07-23  
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; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-09-840-459-104

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-104 (1-119)

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QY 121 CCAGGAAGGGTTTGAATGGTGGCCGATAGAACTTAAATAATTAATTATGCAACA 180  
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QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCAGAGATGATTCAAAAACAGC 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGCTGTATTACTGTACACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
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; Sequence 104, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: Larosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-09-497-625A-104

Alignment Scores:  
Pred. No.: 1.15e-68 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-104 (1-119)

QY 1 GAGGTGCAATGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20  
QY 61 TCATGTGACGCTCTCGATTCTACTTTTCAGTGTGCTAGCCATCAACTGAGTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAspSerValLysAspArgPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGGTTTGAATGGTGGCCGATAGAACTTAAATAATTAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCAGAGATGATTCAAAAACAGC 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGAACAGCTTGAAACTGAGGACACAGCGCTGTATTACTGTACACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuTyrThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACCGTCTCTGGGGCAGGGACCGCTCGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 6  
US-09-809-739-21  
; Sequence 21, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.



```
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-21
```

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Alignment Scores:
Pred. No.:      8.51e-68      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:     97.15%      Indels:      0
DB:              2          Gaps:          0

US-10-733-563-108 (1-351) x US-09-809-739-21 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTTCACATTTTCAGTGTCTACGCCATGAATGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCCGCATAGAACAATAAATAATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAACACG 240
DB 61 TyrTyAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTATATCTGTACCAACC 300
DB 81 LeuTyLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyTyCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyArgLysGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

```
RESULT 7
US-09-840-459-18
; Sequence 18, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
```

```
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-18

Alignment Scores:
Pred. No.:      8.51e-68      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:     97.15%      Indels:      0
DB:              2          Gaps:          0

US-10-733-563-108 (1-351) x US-09-840-459-18 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTTCACATTTTCAGTGTCTACGCCATGAATGGGTCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCCGCATAGAACAATAAATAATATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAACACG 240
DB 61 TyrTyAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTATATCTGTACCAACC 300
DB 81 LeuTyLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyTyCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyArgLysGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

```
RESULT 8
US-09-497-625A-18
; Sequence 18, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
```



```
;
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-18

Alignment Scores:
Pred. No.: 8,51e-68 Length: 117
Score: 613.00 Matches: 115
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.29% Mismatches: 0
Query Match: 97.15% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-18 (1-117)
QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTCGTTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTCGATTTCACCTTCAGTGCCTACGCCATGAATCAATCGGCTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGAATGGGTTGGCCGATGAAGCAATCAATTCAGAGATGATTCAAAAACACG 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspSerLysAsnThr 80
QY 241 CTCATCTGCAATGAACAGCTTGAAACTTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCTCGTCCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 9
US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarzan
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-19

Alignment Scores:
Pred. No.: 1.13e-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-19 (1-117)
QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTCGTTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTCGATTTCACCTTCAGTGCCTACGCCATGAATCAATCGGCTCCGCCAGGCT 120
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20
QY 121 CCAGGAAAGGGTTTGAATGGGTTGGCCGATGAAGCAATCAATTCAGAGATGATTCAAAAACACG 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80
QY 241 CTCATCTGCAATGAACAGCTTGAAACTTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCTCGTCCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 9
US-09-809-739-22
; Sequence 22, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1059-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-22

Alignment Scores:
Pred. No.: 1.13e-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-22 (1-117)
QY 1 GAGGTGCAATTGGTTCAGTCTCGAGGAGGATTCGTTGAAGCCTGGGGGTCATTGAGACTC 60
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```
Db 21 SerCysAlaAlaSerGlyPheSerPheAenAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTCGCGCATAGAAGCTTAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAenAsnTyrAlaThr 60
QY 181 TATTATGCGGATTCAGTGAACAGAGATTACCATCTCCAGAGATGATTCAAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAenThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGACTGAGGACACAGCGGTGATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAenGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 11
US-09-497-625A-19
; Sequence 19, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-19

Alignment Scores:
Pred. No.: 1,136-66 Length: 117
Score: 604.00 Matches: 113
Percent Similarity: 99.15% Conservative: 3
Best Local Similarity: 96.58% Mismatches: 1
Query Match: 95.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-497-625A-19 (1-117)
QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGAGGATTTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTCCCTACGCCATGAACCTGGCTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAenAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTCGCGCATAGAAGCTTAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAenAsnTyrAlaThr 60
QY 181 TATTATGCGGATTCAGTGAACAGAGATTACCATCTCCAGAGATGATTCAAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAenThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGACTGAGGACACAGCGGTGATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAenGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
```

```
QY 241 CTCTATCTGCAATGAACAGCTTGAAGACTGAGGACACAGCGGTGATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAenGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 12
US-09-809-739-23
; Sequence 23, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia E.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-23

Alignment Scores:
Pred. No.: 4,738-66 Length: 117
Score: 599.00 Matches: 112
Percent Similarity: 98.29% Conservative: 3
Best Local Similarity: 95.73% Mismatches: 2
Query Match: 94.93% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-23 (1-117)
QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGAGGATTTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTCCCTACGCCATGAACCTGGCTCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAenAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGAAATGGGTCGCGCATAGAAGCTTAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAenAsnTyrAlaThr 60
QY 181 TATTATGCGGATTCAGTGAACAGAGATTACCATCTCCAGAGATGATTCAAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerLysAenThr 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGACTGAGGACACAGCGGTGATTACTGTACACACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAenGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 13
US-09-840-459-20
; Sequence 20, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
```

```

: TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
:
: TITLE OF INVENTION: METHODS OF USE THEREFOR
:
: FILE REFERENCE: 1855.1052-004
:
: CURRENT APPLICATION NUMBER: US/09/497,625A
:
: CURRENT FILING DATE: 2000-02-03
:
: PRIOR APPLICATION NUMBER: 09/359,193
:
: PRIOR FILING DATE: 1999-07-22
:
: PRIOR APPLICATION NUMBER: 09/121,781
:
: PRIOR FILING DATE: 1998-07-23
:
: NUMBER OF SEQ ID NOS: 106
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 20
:
: LENGTH: 117
:
: TYPE: PRT
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Humanized sequence
:
: US-09-497-625A-20

```

Alignment Scores:		
Pred. No.:	4,738-66	Length:
Score:	\$99.00	Matches:
Percent Similarity:	98.29%	Conservative:
Best Local Similarity:	95.73%	Mismatches:
Query Match:	94.93%	Indels:
DB:	2	Gaps:
		0
US-10-733-563-108 (1-351) x US-09-497-625A-20 (1-117)		

US-10/-733-563-108 (1-351) X US-09/-497-625A-20 (1-117)

Qy		1 GAGGTGCAATTGGTTTGACTCTCGGAGGAGATTGGTGAAGCCTGGGGGTTCATTGACACTC	60
Db		1 GluValGinLeuValGlusSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu	20
Qy		61 TCATGTGCAGCCCTCGGATTCACATTCGAGTCCTACGCCCATGAAC TGGGTCCGCCAGGCT	120
	:   :   :		
Db		21 SerCysAlaIAserGlyPheSer-PheAsnAlatyrAlaMetAsnTrpValArgGlnAla	40

QY	121	CAAGAAAAGGGTTTGGAAATGGTTGGCCGCTAAGAACTAAAAATTAATTAATTAATGAACA	181	TATTTATGCGGATTCAGTGAAGACAGAGATTCCACCATCTCCAGAGATGATTCAAAAACACG	240
Db	41	ProGlyLeuGlyLeuGluTrpValAlaArgIleargThrLysAsnAenAenTyAlaThr	61	TyrTyAlaAspSerValLysAspArgTyThrIleSerArgAspAspSerLysAenThr	80
QY	241	CTCTATCTGCAAAATGAACAGCTTGGAAACTGAGAGACACAGCCGTGTATTACTGTACCAAC	301	TTTTACGGTAACGGTGTCTGGGCGCCAGGGACCCCTGCTACCGCTACGCTCA	351
Db	81	LeuTyLeuGlnMetAsnSerLeuLysThrGluAAspThrAlaValTyTyTyCysValThr	101	PheTyGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer	117

```

; TITLE OF INVENTION: Kesterosols
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Unknown
;

```

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region
; NAME/KEY: SITE
; LOCATION: (31)...(35)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (50)...(68)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12
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## Alignment Scores:

Pred. No.:	1.07e-59	Length:	117
Score:	548.00	Matches:	101
Percent Similarity:	94.87%	Conservative:	10
Best Local Similarity:	86.32%	Mismatches:	6
Query Match:	86.85%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-108 (1-351) x US-09-809-739-12 (1-117)

```
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProLysGlySerLeuLysLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTACGTGCTACGCCATGAACCTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAAGGGTTTGGATGGTTCGCCCGCATAGAACTAAAGAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAAGACACAGATTTCACCATCTCCAGAGATGATTCAAAAACACG 240
Db 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspAspSerGluSerMet 80
QY 241 CTCTATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCGGTGTATTACTGTACCACC 300
Db 81 LeuPheLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyThrGlyThrThrValThrValSerSer 117
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Search completed: January 28, 2006, 08:48:44  
Job time : 14.8784 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: January 28, 2006, 08:44:22 ; Search time 42.8649 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gaggtgcaattggttgagtc.....ccctggcaccgcagctca 351

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct  
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-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA\_Main:  
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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pcp:\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pcp:\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pcp:\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pcp:\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	3	US-09-835-087-10 Sequence 10, Appl
2	620	98.3	117	3	US-09-809-739-20 Sequence 20, Appl
3	620	98.3	117	3	US-09-840-459-17 Sequence 17, Appl
4	620	98.3	117	4	US-10-766-773-17 Sequence 17, Appl
5	620	98.3	117	4	US-10-766-610-17 Sequence 17, Appl
6	620	98.3	117	4	US-10-733-563-17 Sequence 17, Appl
7	620	98.3	117	5	US-10-662-061-20 Sequence 20, Appl
8	620	98.3	119	3	US-09-840-459-104 Sequence 104, App
9	620	98.3	119	4	US-10-766-773-104 Sequence 104, App
10	620	98.3	119	4	US-10-766-610-104 Sequence 104, App
11	620	98.3	119	4	US-10-733-563-104 Sequence 104, App

12	613	97.1	117	3	US-09-835-087-11	Sequence 11, Appl
13	613	97.1	117	3	US-09-809-739-21	Sequence 21, Appl
14	613	97.1	117	3	US-09-840-459-18	Sequence 18, Appl
15	613	97.1	117	4	US-10-766-773-18	Sequence 18, Appl
16	613	97.1	117	4	US-10-766-610-18	Sequence 18, Appl
17	613	97.1	117	4	US-10-733-563-18	Sequence 18, Appl
18	613	97.1	117	5	US-10-662-061-21	Sequence 21, Appl
19	604	95.7	117	3	US-09-835-087-12	Sequence 12, Appl
20	604	95.7	117	3	US-09-809-739-22	Sequence 22, Appl
21	604	95.7	117	3	US-09-840-459-19	Sequence 19, Appl
22	604	95.7	117	4	US-10-766-773-19	Sequence 19, Appl
23	604	95.7	117	4	US-10-766-610-19	Sequence 19, Appl
24	604	95.7	117	4	US-10-733-563-19	Sequence 19, Appl
25	604	95.7	117	5	US-10-662-061-22	Sequence 22, Appl
26	599	94.9	117	3	US-09-835-087-13	Sequence 13, Appl
27	599	94.9	117	3	US-09-809-739-23	Sequence 23, Appl
28	599	94.9	117	3	US-09-840-459-20	Sequence 20, Appl
29	599	94.9	117	3	US-10-766-773-20	Sequence 20, Appl
30	599	94.9	117	4	US-10-766-610-20	Sequence 20, Appl
31	599	94.9	117	4	US-10-733-563-20	Sequence 20, Appl
32	599	94.9	117	5	US-10-662-061-23	Sequence 23, Appl
33	548	86.8	117	3	US-09-835-087-8	Sequence 8, Appl
34	548	86.8	117	3	US-09-809-739-12	Sequence 12, Appl
35	548	86.8	117	3	US-09-840-459-10	Sequence 10, Appl
36	548	86.8	117	4	US-10-766-773-10	Sequence 10, Appl
37	548	86.8	117	4	US-10-766-610-10	Sequence 10, Appl
38	548	86.8	117	4	US-10-733-563-10	Sequence 10, Appl
39	548	86.8	117	5	US-10-662-061-12	Sequence 12, Appl
40	548	86.8	125	4	US-10-272-899A-84	Sequence 84, Appl
41	548	86.8	148	3	US-09-840-459-100	Sequence 100, App
42	548	86.8	148	4	US-10-766-773-100	Sequence 100, App
43	548	86.8	148	4	US-10-766-610-100	Sequence 100, App
44	548	86.8	148	4	US-10-733-563-100	Sequence 100, App
45	499.5	79.2	120	5	US-10-920-899-1779	Sequence 1779, Ap

ALIGNMENTS

RESULT 1  
US-09-835-087-10  
; Sequence 10, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; TITLE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-10

Alignment Scores:  
Pred. No.: 2,328-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-835-087-10 (1-117)

QY 1 GAGGTGCAATTGGTGTGAGTCTCGAGGAGGATTGGTGAACGCTGGGGGTCATTGAGACTTC 60  
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Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACTAAAAATAATTAATTCACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAAACAGC 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCCACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 2

US-09-809-739-20

; Sequence 20, Application US/09809739

; Patent No. US20020106369A1

; GENERAL INFORMATION:

; APPLICANT: Horvath, Christopher J.

; APPLICANT: Rao, Patricia E.

; TITLE OF INVENTION: Method of Inhibiting Stenosis and

; TITLE OF INVENTION: Restenosis

; FILE REFERENCE: 1855.1069-003

; CURRENT APPLICATION NUMBER: US/09/809,739

; PRIOR FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: US 09/528,267

; PRIOR FILING DATE: 2000-03-17

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized sequence

US-09-809-739-20

Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-809-739-20 (1-117)

QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACTAAAAATAATTAATTCACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAAACAGC 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCCACC 300

Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 3

US-09-840-459-17

; Sequence 17, Application US/09840459

; Patent No. US20020150576A1

; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.

; APPLICANT: Horvath, Christopher

; APPLICANT: Newman, Walter

; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa

; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 1855.1052-012

; CURRENT APPLICATION NUMBER: US/09/840,459

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/497,625

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781

; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Humanized sequence

US-09-840-459-17

Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-17 (1-117)

QY 1 GAGGTGCAATTTGGTTCAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCAATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGAGCCTCTGGATTCACTTTAGTGTGCTAGCCATGAACCTGGGTCCGCCAGGCT 120  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAGGTTTGGATGGTTCGCCGCATAGAACTAAAAATAATTAATTCACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTTCAGTGAACACAGATTCACCATCTCCAGAGATGATTCAAAAAACAGC 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATCAACAGCTTGAAACTGAGGACACAGCCGCTGATTACTGTACCCACC 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCTGGTCACCGTCAGCTCA 351

Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 4

US-10-766-773-17  
; Sequence 17, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence

## US-10-766-773-17

Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-766-773-17 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
|||  
QY 61 TCATGTGACGCTCTGGATTCACTTTCACTGCTAGCCATGAACCTGGTCCGCCAGGCT 120  
|||  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
|||  
QY 121 CCAGGAAGGGTTTGAATGGTTGGCCGCAATGAAGAACTAAAAATAATATTATGCAACA 180  
|||  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60  
|||  
QY 181 TATTATGCCGATTCACTGAGGAGGAGATTCAACATCTCCAGAGATGATTCAAAAAACAG 240  
|||  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
|||  
QY 241 CTCATCTGCAATGAACAGCTTGAATACTGAGGACACAGCCGTGATTACTGTACACCC 300  
|||  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
|||  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCAACGTCAGCTCA 351  
|||  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

US-10-733-563-108 (1-351) x US-10-766-773-17 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60  
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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
|||  
QY 61 TCATGTGACGCTCTGGATTCACTTTCACTGCTAGCCATGAACCTGGTCCGCCAGGCT 120  
|||  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
|||  
QY 121 CCAGGAAGGGTTTGAATGGTTGGCCGCAATGAAGAACTAAAAATAATATTATGCAACA 180  
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Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60  
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QY 181 TATTATGCCGATTCACTGAGGAGGAGATTCAACATCTCCAGAGATGATTCAAAAAACAG 240  
|||  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
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QY 241 CTCATCTGCAATGAACAGCTTGAATACTGAGGACACAGCCGTGATTACTGTACACCC 300  
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Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
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QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCAACGTCAGCTCA 351  
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Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 5

US-10-766-610-17  
; Sequence 17, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:

; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence

## US-10-766-610-17

Alignment Scores:  
Pred. No.: 2,32e-58 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-766-610-17 (1-117)

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Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
|||  
QY 61 TCATGTGACGCTCTGGATTCACTTTCACTGCTAGCCATGAACCTGGTCCGCCAGGCT 120  
|||  
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
|||  
QY 121 CCAGGAAGGGTTTGAATGGTTGGCCGCAATGAAGAACTAAAAATAATATTATGCAACA 180  
|||  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60  
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QY 181 TATTATGCCGATTCACTGAGGAGGAGATTCAACATCTCCAGAGATGATTCAAAAAACAG 240  
|||  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
|||  
QY 241 CTCATCTGCAATGAACAGCTTGAATACTGAGGACACAGCCGTGATTACTGTACACCC 300  
|||  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
|||  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCTGGTCAACGTCAGCTCA 351  
|||  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 6

US-10-733-563-17  
; Sequence 17, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:

; APPLICANT: Theresa  
; APPLICANT: O'Keefe, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-17

Alignment Scores:
Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-733-563-17 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGAGGAGTGGTGAAGCCTGGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTTCACCTTTTCAAGTCCCTACGCCATGAACTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaIyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCCGCATAGAAGCTAAAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAAACAGG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTTACTGTACCAACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 7
US-10-662-061-20
; Sequence 20, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-17

Alignment Scores:
Pred. No.: 2,32e-58 Length: 117
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-733-563-17 (1-117)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGAGGAGTGGTGAAGCCTGGGGGGTCATTGAGACTC 60
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGCAGCCTCTGGATTTCACCTTTTCAAGTCCCTACGCCATGAACTGGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAlaIyrAlaMetAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGGTTTGGAAATGGTTGGCCGCATAGAAGCTAAAAATAATAATTATGCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60

QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAAAACAGG 240
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80

QY 241 CTCATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTTACTGTACCAACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTyrGlyGlnGlyThrLeuValThrValSerSer 117

RESULT 8
US-09-840-459-104
; Sequence 104, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized heavy chain
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US-09-840-459-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-108 (1-351) x US-09-840-459-104 (1-119)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAACCTCGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGGCTACGCCATGAACCTGGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGGAAATGGTGGCCGCATTAAGAACTAAATAATAATTATGCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 9

US-10-766-773-104

; Sequence 104, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-773-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match:

DB: 98.26% Indels: 0  
4 Gaps: 0

US-10-733-563-108 (1-351) x US-10-766-773-104 (1-119)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAACCTCGGGGTCATTGAGACTC 60  
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGGCTACGCCATGAACCTGGGTCCGCCAGGCT 120  
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGGAAAGGGTTTGGAAATGGTGGCCGCATTAAGAACTAAATAATAATTATGCAACA 180  
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAAGACAGATTCCACATCTCAGAGATGATTCAAAAACACG 240  
DB 61 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80  
QY 241 CTCTATCTGCAATGAACAGCTTGAAACTGAGGACACAGCCGTGTATTACTGTACCACC 300  
DB 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
DB 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117

## RESULT 10

US-10-766-610-104

; Sequence 104, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain  
US-10-766-610-104

## Alignment Scores:

Pred. No.: 2,33e-58 Length: 119  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 4 Gaps: 0

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US-10-733-563-108 (1-351) x US-10-766-610-104 (1-119)
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTAGTCAGCCATGAATCGGTCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTTGGATTGGTGGCCGATGAAGTCTCAAGCACTAAATAATTAATATCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAACAGATTCACCATCTCCAGAGATGATTCACAAAACACAG 240
Db 61 TyrTyraAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAATACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 11
US-10-733-563-104
; Sequence 104, Application US/10733563
; Publication No. US2004015121A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized heavy chain
US-10-733-563-104
Alignment Scores:
Pred. No.: 2,33e-58 Length: 119
Score: 620.00 Matches: 117
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.26% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-108 (1-351) x US-10-733-563-104 (1-119)
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTAGTCAGCCATGAATCGGTCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTTGGATTGGTGGCCGATGAAGTCTCAAGCACTAAATAATTAATATCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAACAGATTCACCATCTCCAGAGATGATTCACAAAACACAG 240
Db 61 TyrTyraAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAATACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 12
US-09-835-087-11
; Sequence 11, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-11
Alignment Scores:
Pred. No.: 1,34e-57 Length: 117
Score: 613.00 Matches: 115
Percent Similarity: 100.00% Conservativeness: 2
Best Local Similarity: 98.29% Mismatches: 0
Query Match: 97.15% Indels: 0
DB: 3 Gaps: 0
US-10-733-563-108 (1-351) x US-09-835-087-11 (1-117)
QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20
QY 61 TCATGTGAGCCTCTGGATTCACTTTTCAGTGTGCTAGTCAGCCATGAATCGGTCGCCAGGCT 120
Db 21 SerCysAlaIaSerGlyPheThrPheSerAlaTyraAlaMetAsnTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTTGGATTGGTGGCCGATGAAGTCTCAAGCACTAAATAATTAATATCAACA 180
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATGCCGATTTCAGTGAACAGATTCACCATCTCCAGAGATGATTCACAAAACACAG 240
Db 61 TyrTyraAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerLysAsnThr 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAATACTGAGGACACAGCCGCTGTATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
RESULT 13
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US-09-809-739-21  
; Sequence 21, Application US/09809739  
; Patent No. US20020106369A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-21  
Alignment Scores:  
Pred. No.: 1.34e-57 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 3 Gaps: 0  
US-10-733-563-108 (1-351) x US-09-809-739-21 (1-117)  
QY 1 GAGGTGCAATGCTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGTCTACGCATCAACTGGGTCGCCAGGCT 120  
Db 21 SerCysAlaLeuSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGAATGGTTCAGTGTCTACGCATCAACTGAAATTAATAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgLeuGlyThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAACAGAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGAACAGCTTGAATACTGAGGACACAGCCGCTGATTACTGTACCTCA 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117  
RESULT 14  
US-09-840-459-18  
; Sequence 18, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-18  
Alignment Scores:  
Pred. No.: 1.34e-57 Length: 117  
Score: 613.00 Matches: 115  
Percent Similarity: 100.00% Conservative: 2  
Best Local Similarity: 98.29% Mismatches: 0  
Query Match: 97.15% Indels: 0  
DB: 3 Gaps: 0  
US-10-733-563-108 (1-351) x US-09-840-459-18 (1-117)  
QY 1 GAGGTGCAATGCTGAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGTCATTGAGACTC 60  
Db 1 GluValGlnLeuValGluSerGlyGlyLeuValLysProGlySerLeuArgLeu 20  
QY 61 TCATGTGCAGCCTCTGGATTCACTTTTCAGTGTCTACGCATCAACTGGGTCGCCAGGCT 120  
Db 21 SerCysAlaLeuSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40  
QY 121 CCAGAAAGGGTTTGAATGGTTCAGTGTCTACGCATCAACTGAAATTAATAATTATGCAACA 180  
Db 41 ProGlyLysGlyLeuGluTrpValGlyArgLeuGlyThrLysAsnAsnTyrAlaThr 60  
QY 181 TATTATGCCGATTCAGTGAACAGAGATTCCACATCTCCAGAGATGATTCAAAAACACG 240  
Db 61 TyrTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerLysAsnThr 80  
QY 241 CTCATCTGCAATGAACAGCTTGAATACTGAGGACACAGCCGCTGATTACTGTACCTCA 300  
Db 81 LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100  
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGGACCCCTGGTCACCGTCAGCTCA 351  
Db 101 PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117  
RESULT 15  
US-10-766-773-18  
; Sequence 18, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781

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; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-10-766-773-18
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Alignment Scores:
Pred. No.:      1.34e-57      Length:      117
Score:          613.00      Matches:      115
Percent Similarity: 100.00%      Conservative: 2
Best Local Similarity: 98.29%      Mismatches: 0
Query Match:     97.15%      Indels:      0
DB:              4          Gaps:          0
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US-10-733-563-108 (1-351) x US-10-766-773-18 (1-117)

```
QY      1  GAGGTGCAATTGGTTGAGTCTCGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
      |||||||
DB      1  GluValGlnLeuValGluSerGlyGlyLeuValLysProGlyGlySerLeuArgLeu 20

QY     61  TCATGTGCAGCCTCTGGATTCACTTTTCAGTGCCTACGCCATGAACCTGGGTCCGCCAGGCT 120
      |||||||
DB     21  SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40

QY     121  CCAGGAAAGGTTTGGAAATGGTTGGCGGCATAGAACTAAATAAATAATTATGCAACA 180
      |||||||
DB     41  ProGlyLysGlyLeuGluTrpValGlyArgIleArgThrLysAsnAsnAsnTyrAlaThr 60

QY     181  TATTATGCCGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAACACAG 240
      |||||||
DB     61  TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspSerLysAsnThr 80

QY     241  CTCTATCTGCAAAATGAACAGCTTGAATACTGAGGACACAGCCGCTGTTACTGTACACACC 300
      |||||||
DB     81  LeuTyrLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysThrThr 100

QY     301  TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
      |||||||
DB     101  PheTyrGlyAsnGlyValTrpGlyGlnGlyThrLeuValThrValSerSer 117
```

Search completed: January 28, 2006, 09:31:10  
Job time : 44.8649 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 4.47973 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-108  
Perfect score: 631  
Sequence: 1 gaggtgcaattggttgagtc.....ccctggtcaccgcagctca 351

Scoring table:

BLASTSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-O=/cn2\_1/USPTO\_spool\_p/US10733563/runat\_27012006\_180008\_4917/app\_query.fasta\_1.2716  
-DB=Published Applications\_AA\_New -QPM=fabcan -SUFFIX=n2p.rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USRP=US10733563 @CGN 1.1 @runat 27012006 180008 4917  
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_AA\_New:  
1: /cn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	620	98.3	117	7	US-11-075-184A-8
2	613	97.1	117	7	US-11-075-184A-9
3	604	95.7	117	7	US-11-075-184A-10
4	599	94.9	117	7	US-11-075-184A-11
5	548	86.8	117	7	US-11-075-184A-2
6	487	77.2	123	7	US-11-193-440-87
7	478.5	75.8	251	7	US-11-054-515-997
8	478.5	75.8	251	7	US-11-054-515-1346
9	476.5	75.5	139	7	US-11-125-837-24
10	475	75.3	257	7	US-11-054-515-958

11	474	75.1	244	7	US-11-054-515-1991	Sequence 1991, Ap
12	473.5	75.0	258	7	US-11-054-515-1841	Sequence 1841, Ap
13	471.5	74.7	120	6	US-10-834-397-38	Sequence 38, Appl
14	471.5	74.7	120	6	US-10-834-397-63	Sequence 63, Appl
15	471.5	74.7	256	7	US-11-054-515-1209	Sequence 1209, Ap
16	471.5	74.7	281	6	US-10-834-397-178	Sequence 178, App
17	470	74.6	250	7	US-11-054-515-1179	Sequence 1179, Ap
18	470	74.5	253	7	US-11-054-515-1650	Sequence 1650, Ap
19	469.5	74.4	256	7	US-11-054-515-843	Sequence 843, App
20	468	74.2	115	7	US-11-127-903-33	Sequence 33, Appl
21	468	74.2	470	7	US-11-144-248-46	Sequence 46, Appl
22	468	74.2	470	7	US-11-144-222-46	Sequence 46, Appl
23	467.5	74.1	116	6	US-10-925-366A-1	Sequence 1, Appl
24	467.5	74.1	240	6	US-10-925-366A-219	Sequence 219, App
25	467	74.0	117	7	US-11-127-903-32	Sequence 32, Appl
26	466.5	73.9	256	7	US-11-054-515-872	Sequence 872, App
27	466	73.9	125	7	US-11-144-248-16	Sequence 16, Appl
28	466	73.9	125	7	US-11-144-222-16	Sequence 16, Appl
29	465.5	73.8	120	6	US-10-925-366A-235	Sequence 235, App
30	465.5	73.8	250	7	US-11-054-515-1325	Sequence 1325, Ap
31	465	73.7	248	7	US-11-054-515-913	Sequence 913, App
32	465	73.7	248	7	US-11-054-515-2070	Sequence 2070, Ap
33	465	73.7	472	7	US-11-086-289-2	Sequence 2, Appl
34	464	73.5	117	6	US-10-834-397-24	Sequence 24, Appl
35	464	73.5	117	7	US-11-127-903-29	Sequence 29, Appl
36	464	73.5	117	7	US-11-127-903-30	Sequence 30, Appl
37	464	73.5	117	7	US-11-127-903-37	Sequence 37, Appl
38	463.5	73.5	254	7	US-11-054-515-1701	Sequence 1701, Ap
39	463.5	73.5	254	7	US-11-054-515-1735	Sequence 1735, Ap
40	463	73.4	119	7	US-11-127-903-31	Sequence 31, Appl
41	463	73.4	119	7	US-11-127-903-31	Sequence 31, Appl
42	462.5	73.3	248	7	US-11-054-515-921	Sequence 921, App
43	462.5	73.3	248	7	US-11-054-515-1456	Sequence 1456, Ap
44	462.5	73.3	248	7	US-11-054-515-1974	Sequence 1974, Ap
45	462	73.2	113	6	US-10-665-658-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-11-075-184A-8  
; Sequence 8, Application US/11075184A  
; Publication NO. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2 Receptor Antagonists  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE

US-11-075-184A-8  
Alignment Scores:  
Pred. No.: 1.15e-61 Length: 117  
Score: 620.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.26% Indels: 0  
DB: 7 Gaps: 0  
US-10-733-563-108 (1-351) x US-11-075-184A-8 (1-117)



```

;
; FEATURE:
; OTHER INFORMATION: Murine antibody 1D9 heavy chain variable region; presumably Mur
; OTHER INFORMATION: musculus
US-11-075-184A-2

Alignment Scores:
Pred. No.: 1.18e-53 Length: 117
Score: 548.00 Matches: 101
Percent Similarity: 94.97% Conservativeness: 10
Best Local Similarity: 86.32% Mismatches: 6
Query Match: 86.85% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-108 (1-351) x US-11-075-184A-2 (1-117)

QY 1 GAGGTGCAATGGTGTAGTCTGGAGGAGGATGGTGAAGCCCTGGGGGTCATTGAGACTC 60
DB 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProlyGlySerLeuLysLeu 20
QY 61 TCATGTGCAGCTCTGGATTCACTTTTCAGTGCCTACGCCATGAACATGGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheSerPheAsnAlaTyrAlaMetAsnTrpValArgGlnAla 40
QY 121 CAGGAAGGGTTTGGATGGTGGTGGCCGCATAGAACTAAGAACTAAATAATAATTATGCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgIleArgThrLysAsnAsnTyrAlaThr 60
QY 181 TATTATCCGATTCAGTGAAGACAGATTCCACCATCTCCAGAGATGATTCAAAAACACG 240
DB 61 TyrTyrAlaAspSerValLysAspArgTyrThrIleSerArgAspSerGluSerMet 80
QY 241 CTCTATCTGCAAAATGAACAGCTTGAAACTGAGGACACAGCCGCTGTTACTGTACCAAC 300
DB 81 LeuPheLeuGlnMetAsnAsnLeuLysThrGluAspThrAlaMetTyrTyrCysValThr 100
QY 301 TTTTACGGTAACGGTGTCTGGGGCCAGGGACCCCTGGTCACCGTCAGCTCA 351
DB 101 PheTyrGlyAsnGlyValTrpGlyThrGlyThrValThrValSerSer 117

RESULT 6
US-11-193-440-87
; Sequence 87, Application US/11193440
; Publication No. US20060002939A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; Wong, Hing
; Stinson, Jeffrey L.
; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRA
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-Aug-2005
; APPLICATION NUMBER: US/11/193,440
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Binaudi, Carol P.

```

; REGISTRATION NUMBER: 32,220  
; REFERENCE/DOCKET NUMBER: 04995.0041-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 123 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:  
US-11-193-440-87

Alignment Scores:  
Pred. No.: 7,21e-47 Length: 123  
Score: 487.00 Matches: 93  
Percent Similarity: 86.18% Conservative: 13  
Best Local Similarity: 75.61% Mismatches: 11  
Query Match: 77.18% Indels: 6  
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-193-440-87 (1-123)

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QY 1 GAGTGCATTTGGTTCAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTTCATTGAGACTC 60
DB 1 GluValMetLeuValGluSerGlyGlyGlyLeuValGlnProLysGlySerLeuLysLeu 20

QY 61 TCATGTGAGCCTCTGGATTCATTTCTAGTGCCTAGCCATCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheAsnAsnTrpValArgGlnAla 40

QY 121 CCAGAAAGGTTTGGATTTGGTTCAGTCCGCGCATAGAATCAAAATAATATATCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValAlaArgLysSerLysSerAsnAsnTrpAlaThr 60

QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCAGAGATGATTCAAAAACACG 240
DB 61 PheTyrAlaAspSerValLysAspArgPheThrLysSerArgAspSerGlnSerMet 80

QY 241 CTCATCTGCAATCAACAGCTTGAAGACTGAGGACACAGCCGCTGATTACTGTACCACC 300
DB 81 LeuTyrLeuGlnMetCAsnAsnLeuLysThrGluAspThrAlaMetCysTyrCysValArg 100

QY 301 TTTTACGGTAACGGTGTC-----TGGGGCCAGGGGACCCCTGCTCACC 342
DB 101 ArgGlyAlaSerGlyLeuAspTyrAlaMetAspTyrTrpGlyGlnGlyThrSerLeuThr 120

QY 343 GTCAGCTCA 351
DB 121 ValSerSer 123
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## RESULT 7

US-11-054-515-997  
; Sequence 997, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 997  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-997

Alignment Scores:  
Pred. No.: 6,53e-46 Length: 251  
Score: 478.50 Matches: 94  
Percent Similarity: 81.25% Conservative: 10  
Best Local Similarity: 73.44% Mismatches: 13  
Query Match: 75.83% Indels: 11  
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-997 (1-251)

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QY 1 GAGTGCATTTGGTTCAGTCTGGAGGAGGATTGGTGAAGCCCTGGGGGGTTCATTGAGACTC 60
DB 1 GluValGlnLeuValGlnSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCATTTCTAGTGCCTAGCCATCACTGGTCCGCCAGGCT 120
DB 21 SerCysAlaAlaSerGlyPheThrPheSerAspHisTyrMetAspTrpValArgGlnAla 40

QY 121 CCAGAAAGGTTTGGATTTGGTTCAGTCCGCGCATAGAATCAAAATAATATATCAACA 180
DB 41 ProGlyLysGlyLeuGluTrpValGlyArgAlaArgAsnLysAlaAsnSerTyrThrIle 60

QY 181 TATTATGCGGATTCAGTGAAGACAGATTCACCATCTCAGAGATGATTCAAAAACACG 240
DB 61 GluTyrAlaAlaSerValLysGlyArgPheThrLysSerArgAspSerLysSer 80

QY 241 CTCATCTGCAATCAACAGCTTGAAGACTGAGGACACAGCCGCTGATTACTGT----- 294
DB 81 LeuPheLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysAlaArg 100

QY 295 -----ACCACTTTTACGGTAACGGTCTGGGGCCAG 327
DB 101 AlaProTyrAspIleLeuThrGlyTyrSerAspTyrTyrGlyMetAspValTrpGlyArg 120

QY 328 GGGACCCCTGGTCCACCGTCAGCTCA 351
DB 121 GlyThrLeuValThrValSerSer 128
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## RESULT 8

US-11-054-515-1346  
; Sequence 1346, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16



```
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1346
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1346

Alignment Scores:
Pred. No.: 6,53e-46 Length: 251
Score: 478.50 Matches: 94
Percent Similarity: 81.25% Conservative: 10
Best Local Similarity: 73.44% Mismatches: 13
Query Match: 75.83% Indels: 11
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-1346 (1-251)

QY 1 GAGGTGCAATTGTTGAGTCTGAGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 1 GluValGlnLeuValGlnSerGlyGlyLeuValGlnProGlySerLeuAglLeu 20
QY 61 TCATGTGCACTCTCGATTCAGTCTGAGTCTGAGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAspHisTyrMetAspTrpValArgGlnAla 40
QY 121 CCAGGAAGGGTTGGATGGGTTGGCCGATAGAACTAAATAATTAATTATGCAACA 180
Db 41 ProGlyLeuGlyLeuGluTrpValGlyArgAlaArgAsnLysAlaSerTyrThrIle 60
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACACG 240
Db 61 GluTyrAlaAlaSerValLysGlyArgPheThrIleSerArgAspAspSerLysAsnSer 80
QY 241 CTCATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGCTGTATTACTGT 294
Db 81 LeuPheLeuGlnMetAsnSerLeuLysThrGluAspThrAlaValTyrTyrCysAlaArg 100
QY 295 -----ACCACCTTTTACGGTAACGGTCTCGGGCCAG 327
Db 101 AlaProTyrAspIleLeuThrGlyTyrSerAspTyrTyrGlyMetAspValTrpGlyArg 120
QY 328 GGGACCTGCTACCTCAGCTCA 351
Db 121 GlyThrLeuValThrValSerSer 128

RESULT 9
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
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; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Alignment Scores:
Pred. No.: 1,07e-45 Length: 139
Score: 476.50 Matches: 90
Percent Similarity: 87.50% Conservative: 15
Best Local Similarity: 75.00% Mismatches: 12
Query Match: 75.52% Indels: 3
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-125-837-24 (1-139)

QY 1 GAGGTGCAATTGTTGAGTCTGAGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 60
Db 20 GluValGlnLeuValGluThrGlyGlyLeuValGlnProLysGlySerLeuLysLeu 39
QY 61 TCATGTGCACTCTCGATTCAGTCTGAGTCTGAGGAGGAGGATTGGTGAAGCCTGGGGGGTCAATTGAGACTC 120
Db 40 SerCysAlaAlaSerGlyPheThrPheAsnThrAsnAlaMetAsnTrpValArgGlnAla 59
QY 121 CCAGGAAGGGTTGGATGGGTTGGCCGATAGAACTAAATAATTAATTATGCAACA 180
Db 60 ProGlyLeuGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAlaThr 79
QY 181 TATTATGCCGATTTCAGTGAAGACAGATTCACCATCTCCAGAGATGATTCATAAAACACG 240
Db 80 TyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspThrGlnSerMet 99
QY 241 CTCATCTGCAATGAACAGCTTGAAGAACTGAGGACACAGCCGCTGTATTACTGTAC 297
Db 100 IleTyrLeuGlnMetAsnLeuLysThrGluAspThrGlyMetTyrTyrCysValArg 119
QY 298 -----ACCTTTTACGGTAACGGTCTCGGGCCAGGACCTGTGCTCAGCTCAGCTCA 351
Db 120 GlyGlySerTyrTrpTyrPheAspValTrpGlyAlaGlyThrValThrValSerSer 139

RESULT 10
US-11-054-515-958
; Sequence 958, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 958
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-958

Alignment Scores:
Pred. No.: 1.6e-45 Length: 257
Score: 475.00 Matches: 96
Percent Similarity: 78.63% Conservative: 7
Best Local Similarity: 73.28% Mismatches: 14
Query Match: 75.28% Indels: 14
DB: 7 Gaps: 1

US-10-733-563-108 (1-351) x US-11-054-515-958 (1-257)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTACGCCATCACTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40

QY 121 CCAGGAAGGGTTTGAATGGTTGGCCGCATAGAAGTAAATAAATAATTAATGCAACA 180
Db 41 ProGlyLeuGlnLeuGluTrpValGlyArgLeuSerLeuSerLeuThrAspGlyGlyThr 60

QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACAG 240
Db 61 AspTyrAlaAlaProValGlyGlyArgPheThrIleSerArgAspSerLeuAsnThr 80

QY 241 CTCATCTGCAAAATGAACAGCTTGAAGTGAAGACAGACAGCGCTGATTACTGTACCACC 300
Db 81 LeuTyrLeuGlnMetAsnSerLeuLeuThrGluAspThrAlaValTyrCysThrThr 100

QY 301 -----TTTTACGGTAACGGTGC 318
Db 101 SerGlnAlaHisTyrAspIleLeuThrGlyTyrTyrLeuTrpSerTyrGlyMetAspVal 120

QY 319 TGGGGCCAGGGAGCCCTGTCACCTGACCTCAGCTCA 351
Db 121 TrpGlyArgGlyThrLeuValThrValSerSer 131

RESULT 11
US-11-054-515-1991
; Sequence 1991, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

US-10-733-563-108 (1-351) x US-11-054-515-1991 (1-244)

QY 1 GAGGTGCAATTGGTTGAGTCTGGAGGAGGATTGGTGAAGCCTGGGGGTCATTGAGACTC 60
Db 1 GlnValGlnLeuValGlnSerGlyGlyLeuValValProGlyGlySerLeuArgLeu 20

QY 61 TCATGTGAGCCTCTGGATTCACTTTCAGTGCCTACGCCATCACTGGTCCGCCAGGCT 120
Db 21 SerCysAlaAlaSerGlyPheThrPheSerAsnAlaTrpMetSerTrpValArgGlnAla 40

QY 121 CCAGGAAGGGTTTGAATGGTTGGCCGCATAGAAGTAAATAAATAATTAATGCAACA 180
Db 41 ProGlyLeuGlnLeuGluTrpValSerSerLeuSerLeuSerHis-----Ile 58

QY 181 TATTATGCGGATTTCAGTGAAGACAGATTCCACATCTCCAGAGATGATTCAAAAACAG 240
Db 59 TyrTyrAlaAspSerValGlyGlyArgPheThrIleSerArgAspAsnAlaValAsnSer 78

QY 241 CTCATCTGCAAAATGAACAGCTTGAAGTGAAGACAGACAGCGCTGATTACTGTACCACC 300
Db 79 LeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98

QY 301 TTTTACGGTAACGGTGCCTGTCACCTGACCTCAGCTCA 351
Db 99 ValHisSerSerGlySerTrpGlyGlnGlyThrLeuValThrValSerSer 115

RESULT 12
US-11-054-515-1841
; Sequence 1841, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
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QY      301 -----TTTACGGTAACGGTGTCTGG 321
Db      101 AspProGlyAsnTyrAspIleLeuThrGlyTyrTyrTyrTyrGlyMetAspValTrp 120
QY      322 GGCACGGGACCTGGTCACCGTCAGCTCA 351
Db      121 GlyGlnGlyThrMetValThrValSerSer 130
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Search completed: January 28, 2006, 09:32:13  
Job time : 6.47973 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:12:21 ; Search time 52.4685 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

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Perfect score: 590  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	590	100.0	112	4	Aae06949 Humanised
2	590	100.0	112	4	Aau09921 Humanised
3	590	100.0	112	5	Abg75530 Humanised
4	590	100.0	112	5	Aao14973 Humanised
5	590	100.0	112	5	Adf98233 Humanised
6	590	100.0	112	8	Adq98234 Humanised
7	590	100.0	112	9	Aeb09507 Humanised
8	584	99.0	114	4	Aae07035 Humanised
9	584	99.0	114	8	Adq99328 Humanised

10	584	99.0	114	9	Aeb09601 Humanised
11	577	97.8	112	4	Aae06950 Humanised
12	577	97.8	112	4	Aau09922 Humanised
13	577	97.8	112	5	Abg75531 Humanised
14	577	97.8	112	5	Adf98234 Humanised
15	577	97.8	112	8	Adq98233 Humanised
16	577	97.8	112	9	Aeb09508 Humanised
17	572	96.9	112	4	Aae07036 Humanised
18	572	96.9	112	4	Aau09925 Humanised
19	572	96.9	112	5	Abg75534 Humanised
20	572	96.9	112	5	Adf98237 Humanised
21	572	96.9	112	5	Adq99329 Humanised
22	572	96.9	112	8	Aeb09602 Humanised
23	570	96.6	112	4	Aae06951 Humanised
24	570	96.6	112	4	Aau09923 Humanised
25	570	96.6	112	5	Abg75532 Humanised
26	570	96.6	112	5	Adf98235 Humanised
27	570	96.6	112	8	Adq98236 Humanised
28	570	96.6	112	9	Aeb09509 Humanised
29	569	96.4	112	8	Adq31290 Humanised
30	566	95.9	112	8	Adq31289 Humanised
31	565	95.8	112	4	Aae06952 Humanised
32	565	95.8	112	4	Aau09924 Humanised
33	565	95.8	112	5	Abg75533 Humanised
34	565	95.8	112	5	Aao14976 Humanised
35	565	95.8	112	5	Adf98236 Humanised
36	565	95.8	112	8	Adq98237 Humanised
37	565	95.8	112	9	Aeb09510 Humanised
38	559	94.7	113	6	Abp58270 Humanised
39	559	94.7	219	6	Abp58272 Humanised
40	559	94.7	239	6	Abp58274 Humanised
41	557.5	94.5	111	5	Aao14977 Humanised
42	554.5	94.0	111	5	Aao14975 Humanised
43	544	92.2	110	5	Aao14974 Humanised
44	542	91.9	132	5	Abg76931 Humanised
45	542	91.9	132	8	Adr88415 Humanised

ALIGNMENTS

RESULT 1  
AAE06949  
ID AAE06949 standard; protein; 112 AA.

XX AC AAE06949;  
XX AC  
DT 11-SEP-2003 (revised)  
DT 16-OCT-2001 (first entry)  
XX  
DE Humanised murine 1D9 antibody kappa light chain variable region, 1D9KA.  
XX  
KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; stenosis; allograft rejection; anaphylaxis; malignancy; inflammation; stenosis; acquired immune deficiency syndrome; AIDS; fibrotic disease; angioplasty; vascular intervention; 1D9 antibody; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neonatal hyperplasia; VK; kappa light chain variable region; 1D9KA.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.

Key	Location/Qualifiers
FT Region	23..39
FT	/label= CDR1
FT	/note= "Complementarity determining region 1"
FT	55..61
FT	/label= CDR2
FT	/note= "Complementarity determining region 2"
FT Region	94..102

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FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO200157226-A1.
XX 09-AUG-2001.
XX 02-FEB-2001; 2001WO-US003537.
XX 03-FEB-2000; 2000US-00497625.
XX (MILL-) MILLENNIUM PHARM INC.
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX WPI; 2001-488888/53.
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
XX disorder in a patient, comprises a binding specificity for CCR2, and a
XX non-human antigen binding region and human immunoglobulin.
XX Claim 61; Fig 11; 183pp; English.
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
XX comprising an antigen binding region of non-human origin and at least a
XX portion of an immunoglobulin of human origin. The humanised antibodies
XX are useful for inhibiting the interaction of a cell expressing CCR2. They
XX are useful for inhibiting or treating HIV infection. The proteins of the
XX invention are useful for inhibiting leukocyte trafficking, for treating
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune
XX disorders such as rheumatoid arthritis and multiple sclerosis,
XX atherogenesis and atherosclerosis, and for inhibiting restenosis. They
XX are useful in therapy or diagnosis, and in the manufacture of a
XX medicament for treating CCR-2 mediated disease. They are also useful for
XX treating allergy, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and IgE-mediated allergic reaction, shock,
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
XX associated with vascular intervention, including angioplasty and/or stent
XX placement in a mammal. Humanised antibodies are also useful for
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
XX neointimal hyperplasia of a vessel in a mammal, preferably associated
XX with vascular intervention. The present sequence is humanised murine 1D9
XX antibody kappa light chain variable (VK) region, 1D9RKA. (Updated on 11-
XX SEP-2003 to standardise OS field)
XX SQ Sequence 112 AA;

Alignment Scores:
Pred. No.: 3.74e-59 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x AA06949 (1-112)
QY 1 GATGTAGTGATGACCCAGCTCTCCACTCTCTGCGCCGTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCCTCTAGATAGTGATGGAACACACATTTTGAATTGG 120
Db 21 ILeserCyLySerSerGlnSerLeuLeuLeuSerAspGlyLySerThrPheLeuLeuTrp 40
QY 121 TTTCAGCAGAGCCAGCCAGCTCTCAAGCGCCCTAAATCTATCTGGTCTCTAAATCGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuLeuLeuLeuValSerLeuLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTGACGGCGAGTCAGCGAGTCAGGACAGATTTACACTGAATTC 240
Db 181 TCTGGAGTCCCTGACAGGTTGACGGCGAGTCAGCGAGTCAGGACAGATTTACACTGAATTC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTCCGACCAAGGACCCGACTCGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 2
AAU09921
ID AAU09921 standard; protein; 112 AA.
XX AC AAU09921;
XX 18-JUN-2002 (first entry)
XX Humanised 1D9 light chain variable region, 1D9RKA protein sequence.
XX Human; mouse; 1D9 light chain variable region; vasotropic;
XX antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
XX insulin-dependent diabetes mellitus; inflammatory bowel disease;
XX ulcerative colitis; HF-21/28; graft rejection; allergic disease;
XX antipsoriatic; 1D9RKA; antiarthritic; nephrotropic; antithyroid;
XX restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;
XX vascular injury; autoimmune disease; immunoglobulin;
XX complementarity determining region; CDR; CD18; CCR2; atherosclerosis;
XX mutant; mutein.
XX Homo sapiens.
XX Mus sp.
XX Synthetic.
XX Chimeric.
XX Key Location/Qualifiers
XX Region 24..39
XX /note= "Complementarity determining region 1 (CDR1),
XX grafted from mouse mAb 1D9 light chain sequence
XX (AAU09918)"
XX Region 55..61
XX /note= "Complementarity determining region 2 (CDR2),
XX grafted from mouse mAb 1D9 light chain sequence
XX (AAU09918)"
XX Region 94..102
XX /note= "Complementarity determining region 3 (CDR3),
XX grafted from mouse mAb 1D9 light chain sequence
XX (AAU09918)"
XX Misc-difference 112
XX /note= "Addition of Lys residue normally present in mouse
XX mAb 1D9 sequence and absent in human antibody HF-21/28
XX sequence (AAU09920)"
XX WO200170266-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008266.
XX 17-MAR-2000; 2000US-00528267.
XX (MILL-) MILLENNIUM PHARM INC.
XX Horvath CJ, Rao PE;
XX WPI; 2001-607511/69.
XX Inhibiting stenosis or restenosis of a blood vessel following vascular
XX injury or angioplasty in a subject by administering agent which inhibits
XX recruitment or adhesion of neutrophils, mononuclear cells to injury site.
XX Claim 32; Fig 17; 108pp; English.
XX
```



CC The present invention relates to a new method of inhibiting stenosis or  
CC restenosis of a blood vessel following vascular injury in a subject. The  
CC new method comprises administering to the subject agents which inhibit  
CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
CC site of vascular injury by binding CD18 or CCR2. The method of the  
CC invention inhibits stenosis or restenosis of a blood vessel following  
CC vascular injury arising from a vascular intervention procedure such as  
CC vascular by-pass or transplantation surgery. The method is also useful  
CC for treating a subject having an inflammatory disease or condition  
CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
CC graft versus host disease. Chronic inflammatory diseases of the lung,  
CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
CC treated. The method is further useful for treating inflammatory bowel  
CC diseases, such as ulcerative colitis. Additional diseases or conditions  
CC include inflammatory or allergic diseases and conditions, including  
CC systemic anaphylaxis of hypersensitivity responses, drug allergies,  
CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
CC arthritis, graft rejection and other diseases including atherosclerosis.  
CC The present sequence represents the variable region of one of several  
CC humanised 1D9 light chains (AAU09921-AAU09925). These light chains were  
CC used in the invention for the production of anti-CCR2 antibody or antigen  
CC -binding fragment  
XX  
SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 3,74e-59 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x AAU09921 (1-112)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTCGCCGTTACCTTGGACAGCAGCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGCCAGTCAGTCTCAAGCGCCTAATCTATCTGTGTCTAAATCGGAC 180  
DB 41 PheGlnGlnArgProGlyGlnSerProArgGlnLeuTyrLeuValSerIysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGCAGTCAGTCAGGACAGATTTCACCTGAAATTC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGCTGAGGATGTGGAGTTATTATTGTCGCAAGGTACACATTTTCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGCAAGGACCCGACTGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 3  
ABG75530  
ID ABG75530 standard; protein; 112 AA.  
XX  
AC ABG75530;  
DT 16-APR-2003 (first entry)  
XX  
DE Humanised mouse mAb 1D9 light chain variable region, 1D9RKAVK.  
KW Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
KW antigen binding fragment; cellular adhesion molecule; adhesion;  
KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
KW percutaneous transluminal coronary angioplasty; PTCA; stent;

KW vascular by-pass surgery; vascular grafting; endarterectomy; atherectomy;  
KW endovascular stenting; prosthetic valve; transplantation;  
KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
KW chronic bronchitis; asthma; graft-versus-host disease;  
KW chronic inflammatory disease; hypersensitivity pneumonitis;  
KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HP-21/28;  
KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RKAVK;  
KW light chain variable region; VK; complementarity determining region; CDR;  
KW mutant; mutein.  
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OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 24..39  
FT CDR1 /note= "Mouse complementarity determining region 1  
FT Region 55..61  
FT CDR2 /note= "Mouse complementarity determining region 2  
FT Region 94..102  
FT CDR3 /note= "Mouse complementarity determining region 3  
FT Misc-difference 112  
FT /note= "Lys derived from the mouse 1D9 mAb sequence"  
PN US2002106369-A1.  
XX 08-AUG-2002.  
XX 15-MAR-2001; 2001US-00809739.  
PR 17-MAR-2000; 2000US-00528267.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Horvath CJ, Rao PE;  
XX WPI; 2002-697861/75.  
XX  
XX Inhibiting (re)stenosis of blood vessel following vascular injury, by  
XX administering first and second agents that inhibit adhesion and/or  
XX recruitment of neutrophils and mononuclear cells, respectively to site of  
XX vascular injury.  
PS Claim 32; Fig 17; 59pp; English.  
XX  
CC The invention discloses a method for inhibiting stenosis or restenosis of  
CC a blood vessel following vascular injury in a subject. The method  
CC involves administering to the subject a first therapeutic agent, which  
CC comprises an antibody or its antigen binding fragment which binds a  
CC cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
CC of neutrophils to a site of vascular injury and a second therapeutic  
CC agent, which comprises an antagonist of CCR2 function, that inhibits  
CC adhesion and/or recruitment of mononuclear cells to a site of vascular  
CC injury. The vascular injury arises from a vascular intervention procedure  
CC such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
CC (PTCA) or angioplasty including placement of a stent), vascular by-pass  
CC surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
CC stenting, insertion of a prosthetic valve and transplantation of organs,  
CC diseases or conditions mediated by early neutrophil activity and later  
CC mononuclear cell activity. Preferably, the method is useful for treating  
CC a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
CC asthma and graft-versus-host disease, chronic inflammatory disease of  
CC lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
CC other idiopathic conditions, pancreatitis and insulin dependent diabetes  
CC mellitus. The method is also useful for treating inflammatory bowel  
CC disease, Crohn's disease, inflammatory or allergic diseases (such as

CC psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
 CC (such as arthritis and multiple sclerosis), graft rejection,  
 CC atherosclerosis and myositis. The method enables simultaneous inhibition  
 CC of neutrophil and mononuclear cell participation in response to vascular  
 CC injury or inhibition of neutrophil participation followed by inhibition  
 CC of mononuclear cell participation, and thus provides superior therapy for  
 CC inhibiting stenosis or restenosis following vascular injury. The sequence  
 CC presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
 CC chain variable region (VK), 1D9RKAVK, which is comprised of the mouse 1D9  
 CC mAb complementarity determining regions (CDR's) linked by human HF-21/28  
 CC mAb VK regions with a mouse derived Lys at position 112  
 XX  
 SQ Sequence 112 AA;

Alignment Scores:  
 Pred. No.: 3.74e-59 Length: 112  
 Score: 590.00 Matches: 112  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ABG75530 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCCACTCTCTTGGCCGTTACCTTGGACAGCCCTCC 60  
 Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
 QY 61 ATCTCTTCCAAAGTCAAGTCAGAGCCTCTAGATAGTGTGATGGAAGACATTTTGAATTGG 120  
 Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
 QY 121 TTTTCAGCAGAGCCAGCCAGCTCTCCAGGGCCCTTAATCTCTGGTGTCTAAACTGGAC 180  
 Db 41 PheGlnGlnArgProGlyGlnSerProArgGlnLeuLeuValSerLysLeuAsp 60  
 QY 181 TCTGGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTACACTGAAATC 240  
 Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTTCCG 300  
 Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTTCGACAGGACCCGACTGGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluLysIle 112

RESULT 4

AAO14973  
 ID AAO14973 standard; protein; 112 AA.

AC AAO14973;

XX 05-SEP-2002 (first entry)

DT 05-SEP-2002 (first entry)

XX Humanised murine light chain variable region (1D9Rka Vk).

DE Mouse; graft rejection; CC chemokine receptor 2 antagonist; mutant;  
 KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;  
 KW lung transplant; heart-lung transplant; pancreas transplant; mutein;  
 KW bowel transplant; heart transplant; graft versus host disease;  
 KW chronic graft rejection; antibody light chain variable region; 1D9Rka Vk.

XX Mus musculus.

OS Synthetic.

XX US2002042370-A1.

FN 11-APR-2002.

XX 13-APR-2001; 2001US-00835087.

XX

PR 14-APR-2000; 2000US-00549448.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Hancock WW;  
 PI WPI; 2002-351265/38.  
 XX  
 DR Inhibiting graft rejection, graft versus host disease or chronic  
 XX rejection of a transplanted graft, involves administering a CCR2  
 PT antagonist.  
 PT  
 XX Claim 26; Fig 1; 16pp; English.

XX The invention comprises a method of inhibiting graft rejection, graft  
 CC versus host disease or chronic rejection of a transplanted graft. The  
 CC method involves administering an antagonist of CC chemokine receptor 2  
 CC (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may  
 CC be an anti-CCR2 antibody (i.e. containing light and heavy chain  
 CC complementarity determining regions from various non-human origins). CCR2  
 CC is known to be involved in the rejection of transplanted grafts. The  
 CC method of the invention is useful for inhibiting graft rejection -  
 CC particularly allografts such as kidney, liver, lung, heart-lung,  
 CC pancreas, bowel and heart. The method of the invention is also useful for  
 CC inhibiting graft versus host disease and for inhibiting chronic rejection  
 CC of a transplanted graft. The present amino acid sequence represents a  
 CC humanised murine antibody light chain variable region (1D9Rka Vk)

SQ Sequence 112 AA;

Alignment Scores:

Pred. No.: 3.74e-59 Length: 112  
 Score: 590.00 Matches: 112  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x AAO14973 (1-112)

QY 1 GATGTAGTGTGACCCAGCTCCACTCTCTTGGCCGTTACCTTGGACAGCCCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTCTTCCAAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATTTTGAATTGG 120

Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTTCAGCAGAGCCAGCCAGCTCTCCAGGGCCCTTAATCTCTGGTGTCTAAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgGlnLeuLeuValSerLysLeuAsp 60

QY 181 TCTGGAGTCCCTGACAGGTTTCCAGCGCAGTGTGATCAGGACAGATTTACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTTCCG 300

Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTTCGACAGGACCCGACTGGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluLysIle 112

RESULT 5

ADP98233

ID ADP98233 standard; protein; 112 AA.

XX AC ADP98233;

XX 26-FEB-2004 (first entry)

DT 26-FEB-2004 (first entry)

XX Humanised 1D9 light chain variable region, 1D9Rka V kappa, SEQ ID 3.

DE

```
XX Immunosuppressive; CCR2 function inhibitor; graft rejection;
KW graft verses host disease; CC chemokine receptor 2; CCR2;
KW anti-CCR2 antibody.
XX Synthetic.
OS Mus musculus.
OS Homo sapiens.
XX WO200178653-A2.
XX 25-OCT-2001.
XX 13-APR-2001; 2001WO-US012139.
XX 14-APR-2000; 2000US-00549448.
XX (WILL-) MILLENNIUM PHARM INC.
XX Hancock WW;
XX WPI; 2002-017543/02.
XX Inhibition of rejection of graft e.g. heart or graft verses host disease
PT involves use of CC chemokine receptor 2 inhibitor.
XX Claim 26; Fig 1; 44pp; English.
XX The present invention relates to a method for inhibiting graft rejection
CC or graft verses host diseases. The method comprises administration of a
CC CC chemokine receptor 2 (CCR2) function antagonist to a subject or
CC recipient of a transplanted graft. The CCR2 function antagonist is an
CC anti-CCR2 antibody or its antigen-binding fragment (ADP98233-ADF98237,
CC ADF98240-ADF98249). The method is useful for inhibiting rejection,
CC particularly chronic rejection of a graft, particularly an allograft of
CC kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for
CC inhibiting graft verses host disease for a bone marrow graft.
XX Sequence 112 AA;
SQ
Alignment Scores:
Pred. No.: 3,74e-59 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-733-563-109 (1-336) x ADF98233 (1-112)
QY 1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGCGTTTACCTTGGACAGCCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAAGTCCAGAGCTCTTAGATGATGGAAGACATTTTGAATTGG 120
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCAAGCGGCTTAATCTATCTGTGTCTAACTGAGAC 180
DB 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCTGAGTCAAGGACAGATTTTCACCTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACCAGAGTGGAGCTGAGGATGTGGAGTTATTATTGCTGGCAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTyrGlnGlyThrHisPhePro 100
QY 301 TACACGTTGGACAGGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
```

```
RESULT 6
ADQ89234
ID ADQ89234 standard; protein; 112 AA.
XX AC ADQ89234;
XX DT 21-OCT-2004 (first entry)
XX DE Humanised immunoglobulin protein #1.
XX KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;
KW inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX OS Synthetic.
XX PN US2004151721-A1.
XX PD 05-AUG-2004.
XX PF 10-DEC-2003; 2003US-00733563.
XX PR 19-OCT-2001; 2001US-0350166P.
XX PR 26-JUN-2002; 2002US-0392364P.
XX PR 17-OCT-2002; 2002US-00272899.
XX PA (KSEF/) O'KEEFE T.
XX PA (PONA/) PONATH P.
XX PI O'keefe T, Ponath P;
XX WPI; 2004-580175/56.
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX Claim 5; SEQ ID NO 12; 128pp; English.
XX The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
CC infection and atherosclerosis. This sequence represents a humanised
CC immunoglobulin protein of the invention.
XX Sequence 112 AA;
SQ
Alignment Scores:
Pred. No.: 3,74e-59 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-733-563-109 (1-336) x ADQ89234 (1-112)
QY 1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGCGTTTACCTTGGACAGCCAGCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAAGTCCAGAGCTCTTAGATGATGGAAGACATTTTGAATTGG 120
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
```

QY 121 TTTCAGCAGAGCCAGCCAGCTCTCCAGGCGCCTAATCTATCTGGTGTCTAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyLeuValSerIysLeuAsp 60  
QY 181 TCTGAGTCCCTGACACAGGTTTCAGCGCAGTGGATCAGGACAGATTTCACACTGAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGAAGGTACACATTTCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 100  
QY 301 TACAGTTTCGACAGAGGACCGGACTCGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

## RESULT 7

AEBO9507  
ID AEBO9507 standard; protein; 112 AA.

XX AC  
XX AEBO9507;

XX DT  
XX 08-SEP-2005 (first entry)

XX DE  
XX Humanized ID9 kappa light chain variable region SEQ ID NO 12.

XX KW  
XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
XX antibody engineering; therapeutic; diagnosis; inflammation;  
XX autoimmune disease; immune disorder; graft rejection; HIV infection;  
XX infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
XX light chain variable region.

XX OS  
XX Homo sapiens.

XX OS  
XX Mus musculus.

XX OS  
XX Synthetic.

XX PN  
XX WO2005060368-A2.

XX XX  
XX 07-JUL-2005.

XX PD  
XX 10-DEC-2003; 2003WO-US039599.

XX PF  
XX 10-DEC-2003; 2003WO-US039599.

XX PR  
XX (MILL-) MILLENNIUM PHARM INC.

XX XX  
XX Okeefe T, Ponath P;

XX PI  
XX WPI; 2005-488561/49.

XX DR  
XX New humanized immunoglobulin or its antigen binding portion having

XX PT  
XX binding specificity for CC-chemokine receptor 2 and having a heavy chain  
XX and light chain, for treating inflammatory diseases, HIV, and autoimmune  
XX diseases.

XX PS  
XX Claim 1; SEQ ID NO 12; 192pp; English.

XX XX  
XX The invention describes a humanized immunoglobulin (I) or its antigen  
XX binding portion having binding specificity for CC-chemokine receptor 2  
XX (CCR2) and having a heavy chain and a light chain, where the heavy chain  
XX comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
XX sequence, given in specification or its portion, and the light chain  
XX comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
XX in specification. Also described are: a humanized immunoglobulin heavy  
XX chain, or its antigen binding fragment, having binding specificity for  
XX CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
XX amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
XX immunoglobulin light chain, or its antigen binding fragment, having  
XX binding specificity for CCR2 and comprising the amino acid sequence of  
XX (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
XX sequence, given in specification. The following are disclosed: isolated  
XX nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
XX construct comprising nucleic acid molecule encoding (I); and host cell

CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response, for use in the treatment of diseases  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocytic-mediated disorders such as atherosclerosis. (I) Is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of a humanized ID9  
CC kappa light chain variable region used in the creation of a humanized  
CC anti-CCR2-antibody.

XX SQ  
XX Sequence 112 AA;

## Alignment Scores:

Pred. No.: 3,74e-59 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-733-563-109 (1-336) x AEBO9507 (1-112)

QY 1 GATGTAGTGTATGACCCAGTCTCCACTCTCTCTGCGCGTTACCTTGGACAGCCCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20

QY 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGTATGTAAGAAAGACATTTTGAATTGG 120

Db 21 IleSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyIysThrPheLeuAsnTrp 40

QY 121 TTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTAATCTATCTGGTGTCTAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleIysLeuValSerIysLeuAsp 60

QY 181 TCTGAGTCCCTGACAGGTTTCAGCGCAGTGGATCAGGACAGATTTCACACTGAAATC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIysIle 80

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGAAGGTACACATTTCG 300

Db 81 SerArgValGluAlaGluAspValGlyValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 100

QY 301 TACAGTTTCGACAGAGGACCGGACTCGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleIys 112

## RESULT 8

AAE07035

ID AAE07035 standard; protein; 114 AA.

XX AC  
XX AAE07035;

XX XX  
XX 11-SEP-2003 (revised)

XX DT  
XX 16-OCT-2001 (first entry)

XX XX  
XX Humanised murine antibody light chain ID9RKA protein.

XX XX  
XX Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
XX neuroprotective; immunosuppressive; human immunodeficiency virus;  
XX HIV infection; cytostatic; vasotrophic; leukocyte trafficking; allergy;  
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
XX multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
XX fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
XX neointimal hyperplasia; antibody ID9 light chain; ID9RKA.

XX OS  
XX Mus sp.

XX OS  
XX Homo sapiens.

XX OS  
XX Chimeric.

XX WO200157226-A1.  
XX 09-AUG-2001.  
XX 02-FEB-2001; 2001WO-US003537.  
XX 03-FEB-2000; 2000US-00497625.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;  
XX WPI; 2001-488888/53.  
XX N-PSDB; AAD13180.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated  
XX disorder in a patient, comprises a binding specificity for CCR2, and a  
XX non-human antigen binding region and human immunoglobulin.  
XX Disclosure; Fig 24; 183pp; English.  
XX The patent discloses a humanised antibody or its antigen-binding  
XX fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),  
XX comprising an antigen binding region of non-human origin and at least a  
XX portion of an immunoglobulin of human origin. The humanised antibodies  
XX are useful for inhibiting the interaction of a cell expressing CCR2. They  
XX are useful for inhibiting or treating HIV infection. The proteins of the  
XX invention are useful for inhibiting leukocyte trafficking, for treating  
XX CCR2-mediated disorders such as inflammatory disorder, autoimmune  
XX disorders such as rheumatoid arthritis and multiple sclerosis,  
XX atherosclerosis and arteriosclerosis, and for inhibiting restenosis. They  
XX are useful in therapy or diagnosis, and in the manufacture of a  
XX medicament for treating CCR-2 mediated disease. They are also useful for  
XX treating allergy, anaphylaxis, malignancy, chronic and acute  
XX inflammation, histamine and IgE-mediated allergic reaction, shock,  
XX stenosis, allograft rejection, fibrotic disease, asthma, inflammatory  
XX glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis  
XX associated with vascular intervention, including angioplasty and/or stent  
XX placement in a mammal. Humanised antibodies are also useful for  
XX inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting  
XX neointimal hyperplasia of a vessel in a mammal, preferably associated  
XX with vascular intervention. The present sequence is humanised murine  
XX antibody light chain region, 1D9RKA. (Updated on 11-SEP-2003 to  
XX standardise OS field)  
XX Sequence 114 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 1.86e-58 Length: 114  
XX Score: 584.00 Matches: 111  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 98.98% Indels: 0  
XX DB: 4 Gaps: 0  
XX  
XX US-10-733-563-109 (1-336) x AAE07035 (1-114)  
XX  
XX 4 GTAGTGATGACCCAGTCTCCATCTCTCTGCGGTACCTTGGACAGCCAGCTTCATC 63  
XX 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
XX  
XX 64 TCTTCGACGTCAAGTCAGAGCTCTTAGATAGTGTGAGAAACACATTTTGAATTGGTTT 123  
XX 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
XX  
XX 124 CAGCAGAGCCAGGCGAGTCTCCAGGCGCCCTAAATCTATCTGGTGTCTAAACTGGACTCT 183  
XX 42 GlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAspSer 61  
XX  
XX 184 GGAGTCCCTCAGAGGTTTCAGCGCGAGTGGATCAGGACAGATTCACACTGAAATCAGC 243  
XX 62 GlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIleSer 81

QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCTGCAAGGTACACATTTCCGTAC 303  
DB 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTCGGACAGGAGCCGACCTGGAGATCAAG 336  
DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 9  
ADQ89328  
ID ADQ89328 standard; protein; 114 AA.  
XX  
AC ADQ89328;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Humanised immunoglobulin protein #10.  
XX  
KW Immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2;  
KW inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
OS Synthetic.  
XX  
PN US2004151721-A1.  
XX  
PD 05-AUG-2004.  
XX  
PF 10-DEC-2003; 2003US-00733563.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
XX  
PR 26-JUN-2002; 2002US-0392364P.  
XX  
PR 17-OCT-2002; 2002US-00272899.  
XX  
XX (OKEE/) O'KEEFE T.  
XX (PONA/) PONA P.  
XX  
XX O'keefe T, Ponath P;  
XX  
XX WPI; 2004-580175/56.  
XX  
XX N-PSDB; ADQ89320.  
XX  
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
XX useful for diagnosing and/or treating inflammatory or autoimmune  
XX diseases, and HIV infection.  
XX  
XX Disclosure; SEQ ID NO 106; 128pp; English.  
XX  
XX The invention relates to humanised immunoglobulin heavy and light chains  
XX which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
XX immunoglobulin or its antigen binding fragment comprising the chains. The  
XX humanised immunoglobulin or its antigen binding fragment comprising preferably  
XX comprises two heavy chains and two light chains. The humanised  
XX immunoglobulin and its heavy and light chains are useful for the  
XX diagnosis, prevention and/or treatment of diseases or conditions  
XX associated with aberrant expression or activity of the CCR2 polypeptide,  
XX such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
XX infection and atherosclerosis. This sequence represents a humanised  
XX immunoglobulin protein of the invention.  
XX  
XX Sequence 114 AA;  
XX  
XX Alignment Scores:  
XX Pred. No.: 1.86e-58 Length: 114  
XX Score: 584.00 Matches: 111  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 98.98% Indels: 0  
XX DB: 8 Gaps: 0  
XX  
XX US-10-733-563-109 (1-336) x ADQ89328 (1-114)

QY 4 GTAGTGATGACCACTCTCCACTCTCTTGTCCCGTTACCTTGGACAGCCAGCTCCATC 63  
 Db ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
 QY 64 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGAAGACATTTTGAATGGTTT 123  
 Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
 QY 124 CAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAACTCTATCTGGTCTCTAAACTGCACACT 183  
 Db 42 GlnGlnArgProGlyGlnSerProArgArgLeuLeuIleThrLeuValSerLysLeuAspSer 61  
 QY 184 GGAGTCCCTGACAGCTTCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAATCAGC 243  
 Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
 QY 244 AGAGTGGAGGCTGAGGATTTGGAGTTTATTTCTGCTGCAAGGTACACATTTTCCGTAC 303  
 Db 82 ArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPheProTyr 101  
 QY 304 ACGTTCCGACAGGACCGACTCGAGATCAAG 336  
 Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
 RESULT 10  
 AEB09601  
 ID AEB09601 standard; protein; 114 AA.  
 XX  
 AC AEB09601;  
 XX  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE Humanized light chain 1D9RKA.  
 XX  
 DE antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW light chain variable region.  
 XX  
 OS Synthetic.  
 XX  
 FN WO2005060368-A2.  
 XX  
 PD 07-JUL-2005.  
 XX  
 PP 10-DEC-2003; 2003WO-US039599.  
 XX  
 PR 10-DEC-2003; 2003WO-US039599.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Okeefe T, Ponath P;  
 XX  
 DR WPI; 2005-488561/49.  
 DR N-PSDB; AEB09593.  
 XX  
 XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.  
 XX  
 PS Disclosure; SEQ ID NO 106; 192pp; English.  
 XX  
 CC The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for

CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (i); a  
 CC construct comprising nucleic acid molecule encoding (i); and host cell  
 CC comprising the nucleic acid molecule. (i) is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocyte-mediated disorders such as atherosclerosis. (i) is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of humanized light  
 CC chain 1D9RKA.  
 XX

SQ Sequence 114 AA;

Alignment Scores:  
 Pred. No.: 1.86e-58 Length: 114  
 Score: 584.00 Matches: 111  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.98% Indels: 0  
 DB: 9 Gaps: 0

US-10-733-563-109 (1-336) x AEB09601 (1-114)

QY 4 GTAGTGATGACCACTCTCCACTCTCTTGTCCCGTTACCTTGGACAGCCAGCTCCATC 63  
 Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerile 21  
 QY 64 TCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGAAGACATTTTGAATGGTTT 123  
 Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
 QY 124 CAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAACTCTATCTGGTCTCTAAACTGCACACT 183  
 Db 42 GlnGlnArgProGlyGlnSerProArgArgLeuLeuIleThrLeuValSerLysLeuAspSer 61  
 QY 184 GGAGTCCCTGACAGGTTTCAGGCGCAGTGGATCAGGACAGATTTTCCACTGAAATCAGC 243  
 Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
 QY 244 AGAGTGGAGGCTGAGGATTTGGAGTTTATTTCTGCTGCAAGGTACACATTTTCCGTAC 303  
 Db 82 ArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPheProTyr 101  
 QY 304 ACGTTCCGACAGGACCGACTCGAGATCAAG 336  
 Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 11

AAE06950  
 ID AAE06950 standard; protein; 112 AA.

XX AC AAE06950;

XX 11-SEP-2003 (revised)  
 DT 16-OCT-2001 (first entry)

XX Humanised murine 1D9 antibody kappa light chain variable region, 1D9RKB.  
 XX  
 DE Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;  
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
 KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;  
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;



KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;  
 KW inflammatory glomerulopathy; vascular intervention; ID9 antibody;  
 KW neonatal hyperplasia; VK; kappa light chain variable region; ID9RKB.

OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.

XX Key Location/Qualifiers  
 FT 23..39  
 FT Region /label= CDR1  
 FT /note= "Complementarity determining region 1"  
 FT 55..61  
 FT Region /label= CDR2  
 FT /note= "Complementarity determining region 2"  
 FT 94..102  
 FT Region /label= CDR3  
 FT /note= "Complementarity determining region 3"

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003537.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

XX Claim 61; Fig 11; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is humanised murine ID9 antibody kappa light chain variable (VK) region, ID9RKB. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 112 AA;

#### Alignment Scores:

Pred. No.: 1.19e-57 Length: 112  
 Score: 577.00 Matches: 110  
 Percent Similarity: 98.21% Conservative: 0  
 Best Local Similarity: 98.21% Mismatches: 2  
 Query Match: 97.80% Indels: 0  
 DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x AAE06950 (1-112)

QY 1 GATGTAGTGTATGACCCAGTCTCCACTCTCTTCCGCTTACCTTGGACAGCCAGCTCC 60

DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnGlnProAlaSer 20

QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120

DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40

QY 121 TTTTACGAGAGCCAGCCAGTCTCCAGGCGCCCTAATCTATCTGTGTCTAACTGGAC 180

DB 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLeuAsp 60

QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGTCAGTGTGATCAGGACAGATTTACACTGAAATC 240

DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuIle 80

QY 241 AGCAGATGGAGGCTGAGGATGTTGGAGTTTATTCTGTCGAAGGTACACATTTTCG 300

DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100

QY 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336

DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

#### RESULT 12

AAU09922

ID AAU09922 standard; protein; 112 AA.

XX AC AAU09922;

XX 18-JUN-2002 (first entry)

XX DE Humanised ID9 light chain variable region, ID9RKB protein sequence.

XX KW Human; mouse; ID9 light chain variable region; vasotropic; antiinflammatory; collagen disease; immunosuppressive; antiasthmatic; insulin-dependent diabetes mellitus; inflammatory bowel disease; ulcerative colitis; HP-21/28; graft rejection; allergic disease; antipsoriatic; ID9RKB; antiarthritic; nephrotropic; antithyroid; restenosis; dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury; autoimmune disease; immunoglobulin; complementarity determining region; CDR; CD18; CCR2; atherosclerosis; mutant; mutein.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Synthetic.

XX OS Chimeric.

XX Key Location/Qualifiers

XX 24..39

XX Region

FT /note= "Complementarity determining region 1 (CDR1), grafted from mouse mAb ID9 light chain sequence (AAU09918)"

FT Misc-difference 41

FT /note= "Substitution of Phe residue normally present in human HF-21/28 sequence (AAU09920) by Leu residue normally present in mouse mAb ID9 light chain sequence (AAU09918)"

FT Misc-difference 42

FT /note= "Substitution of Gln residue normally present in human HF-21/28 sequence (AAU09920) by Leu residue normally present in mouse mAb ID9 light chain sequence (AAU09918)"

FT 55..61

FT Region

FT /note= "Complementarity determining region 2 (CDR2), grafted from mouse mAb ID9 light chain sequence (AAU09918)"

FT 94..102

FT Region

FT /note= "Complementarity determining region 3 (CDR3), grafted from mouse mAb ID9 light chain sequence

FT Misc-difference 112 (AAU09918) "  
 FT /note= "Addition of Lys residue normally present in mouse  
 FT mAb 1D9 sequence and absent in human antibody HF-21/28  
 FT sequence (AAU09920) "  
 XX  
 PN WO200170266-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 15-MAR-2001; 2001WO-US008266.  
 XX  
 PR 17-MAR-2000; 2000US-00528267.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX PA Horvath CJ, Rao PE;  
 XX  
 XX PI WPI; 2001-607511/69.  
 DR  
 XX  
 XX Inhibiting stenosis or restenosis of a blood vessel following vascular  
 PT injury or angioplasty in a subject by administering agent which inhibits  
 PT recruitment or adhesion of neutrophils, mononuclear cells to injury site.  
 XX  
 XX Claim 32; Fig 17; 108pp; English.  
 XX  
 CC The present invention relates to a new method of inhibiting stenosis or  
 CC restenosis of a blood vessel following vascular injury in a subject. The  
 CC new method comprises administering to the subject agents which inhibit  
 CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a  
 CC site of vascular injury by binding CD18 or CCR2. The method of the  
 CC invention inhibits stenosis or restenosis of a blood vessel following  
 CC vascular injury arising from a vascular intervention procedure such as  
 CC vascular by-pass or transplantation surgery. The method is also useful  
 CC for treating a subject having an inflammatory disease or condition  
 CC mediated by neutrophil and mononuclear cell activity e.g. asthma and  
 CC graft versus host disease. Chronic inflammatory diseases of the lung,  
 CC collagen diseases, and insulin-dependent diabetes mellitus can also be  
 CC treated. The method is further useful for treating inflammatory bowel  
 CC diseases, such as ulcerative colitis. Additional diseases or conditions  
 CC include inflammatory or allergic diseases and conditions, including  
 CC systemic anaphylaxis or hypersensitivity responses, drug allergies,  
 CC psoriasis and inflammatory dermatoses, autoimmune diseases such as  
 CC arthritis, graft rejection and other diseases including atherosclerosis.  
 CC The present sequence represents the variable region of one of several  
 CC humanised 1D9 light chains (AAU0921-AAU0925). These light chains were  
 CC used in the invention for the production of anti-CCR2 antibody or antigen  
 CC -binding fragment  
 XX  
 SQ Sequence 112 AA;  
 Alignment Scores:  
 Pred. No.: 1.19e-57 Length: 112  
 Score: 577.00 Matches: 110  
 Percent Similarity: 98.21% Conservative: 0  
 Best Local Similarity: 98.21% Mismatches: 2  
 Query Match: 97.80% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-733-563-109 (1-336) x AAU09922 (1-112)  
 QY 1 GATGTAGTGTGACCCAGTCTCCATCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60  
 Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
 QY 61 ATCTCTTCGACAGTCAAGTCAGAGCTCTTAGTACTGTAGTGGAAAGACATTTTGAATTGG 120  
 Db 21 IleSerCysLysSerSerGlnSerLeuLeuAepSerAepGlyLysThrPheLeuAenTrp 40  
 QY 121 TTTCAGCAGAGCCAGGCGAGTCTCCAGGCGCCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
 Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuIleTyrLeuValSerLysLeuAep 60

QY 181 TCTGGAGTCCCTGACAGGTTCCAGCGGCGAGTCAGGACAGATTCACACTGAAATC 240  
 Db 61 SerGlyValProAaspArgPheSerGlySerGlySerGlyThrAaspPheThrLeuLysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTGTATTATTGCTGCGCAGGTACACATTTCCG 300  
 Db 81 SerArgValGluAlaGluAaspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
 QY 301 TACAGTTTCGACAGGAGGACCCGACTGAGATCAAG 336  
 Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112  
 RESULT 13  
 AEG75531  
 ID AEG75531 standard; protein; 112 AA.  
 XX  
 AC AEG75531;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 XX Humanised mouse mAb 1D9 light chain variable region, 1D9RKBVK.  
 DE Mouse; stenosis; restenosis; blood vessel; vascular injury; antibody;  
 KW antigen binding fragment; cellular adhesion molecule; adhesion;  
 KW recruitment; neutrophil; antagonist; CCR2; mononuclear cell; angioplasty;  
 KW percutaneous transluminal coronary angioplasty; PTCA; stent;  
 KW endovascular stenting; vascular grafting; endarterectomy; atherectomy;  
 KW inflammatory disease; mastitis; vaginitis; cholecystitis;  
 KW chronic bronchitis; asthma; graft-versus-host disease;  
 KW chronic inflammatory disease; hypersensitivity pneumonitis;  
 KW collagen disease; sarcoidosis; idiopathic; pancreatitis; HF-21/28;  
 KW insulin dependent; diabetes mellitus; inflammatory bowel disease;  
 KW Crohn's disease; allergic disease; psoriasis; atopic dermatitis; human;  
 KW allergic rhinitis; autoimmune disease; arthritis; multiple sclerosis;  
 KW graft rejection; atherosclerosis; myositis; therapy; 1D9; 1D9RKBVK;  
 KW light chain variable region; VK; complementarity determining region; CDR;  
 KW mutant; mutein.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 24..39  
 FT /note= "Mouse complementarity determining region 1  
 FT (CDR1) "  
 FT Misc-difference 41..42  
 FT /note= "Leu's derived from the mouse 1D9 mAb sequence"  
 FT Region 55..61  
 FT /note= "Mouse complementarity determining region 2  
 FT (CDR2) "  
 FT Region 94..102  
 FT /note= "Mouse complementarity determining region 3  
 FT (CDR3) "  
 FT Misc-difference 112  
 FT /note= "Lys derived from the mouse 1D9 mAb sequence"  
 XX  
 PN US2002106369-A1.  
 XX  
 XX 08-AUG-2002.  
 XX  
 XX 15-MAR-2001; 2001US-00809739.  
 XX  
 PR 17-MAR-2000; 2000US-00528267.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX PA Horvath CJ, Rao PE;  
 XX  
 XX PI WPI; 2002-697861/75.  
 DR  
 XX Inhibiting (re)stenosis of blood vessel following vascular injury, by



PT administering first and second agents that inhibit adhesion and/or  
PT recruitment of neutrophils and mononuclear cells, respectively to site of  
PT vascular injury.

PS Claim 32; Fig 17; 59pp; English.

XX The invention discloses a method for inhibiting stenosis or restenosis of  
XX a blood vessel following vascular injury in a subject. The method  
XX involves administering to the subject a first therapeutic agent, which  
XX comprises an antibody or its antigen binding fragment which binds a  
XX cellular adhesion molecule, that inhibits the adhesion and/or recruitment  
XX of neutrophils to a site of vascular injury and a second therapeutic  
XX agent, which comprises an antagonist of CCR2 function, that inhibits  
XX adhesion and/or recruitment of mononuclear cells to a site of vascular  
XX injury. The vascular injury arises from a vascular intervention procedure  
XX such as angioplasty (e.g. percutaneous transluminal coronary angioplasty  
XX (PTCA) or angioplasty including placement of a stent), vascular by-pass  
XX surgery, vascular grafting, endarterectomy, atherectomy, endovascular  
XX stenting, insertion of a prosthetic valve and transplantation of organs,  
XX tissues or cells. The method is also useful for treating inflammatory  
XX diseases or conditions mediated by early neutrophil activity and later  
XX mononuclear cell activity. Preferably, the method is useful for treating  
XX a subject having mastitis, vaginitis, cholecystitis, chronic bronchitis,  
XX asthma and graft-versus-host disease, chronic inflammatory disease of  
XX lung, hypersensitivity pneumonitis, collagen diseases, sarcoidosis and  
XX other idiopathic conditions, pancreatitis and insulin dependent diabetes  
XX mellitus. The method is also useful for treating inflammatory bowel  
XX disease, Crohn's disease, inflammatory or allergic diseases (such as  
XX psoriasis, atopic dermatitis and allergic rhinitis), autoimmune diseases  
XX (such as arthritis and multiple sclerosis), graft rejection,  
XX atherosclerosis and myositis. The method enables simultaneous inhibition  
XX of neutrophil and mononuclear cell participation in response to vascular  
XX injury or inhibition of neutrophil participation followed by inhibition  
XX of mononuclear cell participation, and thus provides superior therapy for  
XX inhibiting stenosis or restenosis following vascular injury. The sequence  
XX presented is the humanised mouse monoclonal antibody (mAb), 1D9, light  
XX chain variable region (VK), 1D9K8VK, which is comprised of the mouse 1D9  
XX mAb complementarity determining regions (CDR's) linked by human HF-21/28  
XX MAB VK regions with a mouse derived Lys at position 112 and Leu's at  
XX positions 41 and 42

SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 1.19e-57 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ABG75531 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTGCGGTACCTTGGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGATGGAACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAAATCTATCTGTGTCTAAACTGGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuLeuTyLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTCAGCAGGTTACGCGCACTGGATCAGGACAGATTTTCACATGAAAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 ACAGAGTGGAGCTTGAGATCTTGGAGTTTATTATTGCTGCGCAGGTACACATTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyTyTyCysTrpGlnGlyThrHisPhePro 100

QY 301 TACAGTTTCGACAAAGGACCCGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 14

ADF98234  
ID ADF98234 standard; protein; 112 AA.

XX ADF98234;

XX 26-FEB-2004 (first entry)

XX Humanised 1D9 light chain variable region, 1D9RKB V kappa, SEQ ID 4.  
XX Immunosuppressive; CCR2 function inhibitor; graft rejection;  
XX graft verses host disease; CC chemokine receptor 2; CCR2;  
XX anti-CCR2 antibody.

XX Synthetic.

XX Mus musculus.

XX Homo sapiens.

XX WO2001178653-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US0121139.

XX 14-APR-2000; 2000US-00549448.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hancock WI;

XX WPI; 2002-017543/02.

XX Inhibition of rejection of graft e.g. heart or graft verses host disease  
XX involves use of CC chemokine receptor 2 inhibitor.

XX Claim 26; Fig 1; 44pp; English.

XX The present invention relates to a method for inhibiting graft rejection  
XX or graft verses host diseases. The method comprises administration of a  
XX CC chemokine receptor 2 (CCR2) function antagonist to a subject or  
XX recipient of a transplanted graft. The CCR2 function antagonist is an  
XX anti-CCR2 antibody or its antigen-binding fragment (ADF98233-ADF98237,  
XX ADF98240-ADF98249). The method is useful for inhibiting rejection,  
XX particularly chronic rejection of a graft, particularly an allograft of  
XX kidney, liver, lung, heart-lung, pancreas, bowel and heart, and for  
XX inhibiting graft verses host disease for a bone marrow graft.

SQ Sequence 112 AA;

Alignment Scores:  
Pred. No.: 1.19e-57 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 5 Gaps: 0

US-10-733-563-109 (1-336) x ADF98234 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTGCGGTACCTTGGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGATGGAACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAAATCTATCTGTGTCTAAACTGGAC 180



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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:20:11 ; Search time 9.16516 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590  
Sequence: 1 gatgtagtgtgaccagtc.....ggaccgactggagatcaag 336

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	531	90.0	113	2 F30560	Ig kappa chain V r
2	530	89.8	132	2 C32513	Ig kappa chain pre
3	526	89.2	133	2 S23230	Ig kappa chain pre
4	526	89.2	142	2 S22902	Ig kappa chain V r
5	517	87.6	112	2 A36259	Ig kappa chain V r
6	514	87.1	133	1 K2HURP	Ig kappa chain pre
7	513.5	87.0	114	2 S49572	Ig kappa chain pre
8	512	86.8	111	2 S20709	Ig kappa chain V r
9	512	86.8	112	2 A55491	Ig kappa chain V r
10	506	85.8	133	1 A24452	proteolytic antibo
11	505.5	85.7	140	2 S22658	Ig kappa chain pre
12	505	85.6	133	2 S40324	Ig kappa chain pre
13	503	85.3	131	2 S31577	Ig kappa chain V r
14	501	84.9	112	2 PL0273	Ig kappa chain V r

15	501	84.9	133	2	S42611	HUNVK protein prec
16	499	84.6	118	2	S40374	Ig kappa chain - h
17	499	84.6	122	2	S40338	Ig kappa chain - h
18	496.5	84.2	114	2	B49002	Ig kappa chain V r
19	491	83.2	132	2	S40322	Ig kappa chain - h
20	488	82.7	101	2	A37330	Ig kappa chain V r
21	477	80.8	126	2	S40312	Ig kappa chain - h
22	470	79.7	120	2	S42268	Ig kappa chain V r
23	470	79.7	120	2	S42267	Ig kappa chain V r
24	461.5	78.2	134	2	S40376	Ig kappa chain - h
25	457	77.5	103	2	PH1056	Ig light chain V r
26	457	77.5	112	2	A31807	Ig kappa chain V r
27	456	77.3	103	2	PH1055	Ig light chain V r
28	456	77.3	219	2	S16112	Ig kappa chain V r
29	454	76.9	115	2	S38715	Ig kappa chain V r
30	452	76.6	131	2	B39276	Ig kappa chain V r
31	450	76.3	113	1	K2HUTW	Ig light chain pre
32	449	76.1	113	1	K2HUPF	Ig kappa chain V-I
33	448.5	76.0	130	2	S40321	Ig kappa chain V-I
34	448	75.9	113	2	PL0203	Ig kappa chain - h
35	447	75.8	114	2	A32967	anti-DNA autoantib
36	446	75.6	112	2	E27887	Ig kappa chain V-I
37	445	75.4	91	2	S42186	Ig kappa chain V r
38	445	75.4	131	2	B32513	Ig kappa chain pre
39	444	75.3	219	2	S52028	Ig kappa chain - m
40	443	75.1	111	2	PL0257	Ig kappa chain V r
41	443	75.1	112	2	S58207	Ig light chain V r
42	443	75.1	131	2	B30577	Ig kappa chain pre
43	443	75.1	136	2	S40357	Ig kappa chain V-J
44	442.5	75.0	115	1	K2HUCM	Ig kappa chain V-I
45	442	74.9	115	2	S60066	Ig kappa chain V r

ALIGNMENTS

RESULT 1

F30560  
Ig kappa chain V region (28.4.10A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C:Accession: F30560  
R:Matsumura, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon

A:Reference number: A30560; MUID:89110062; PMID:2464028

A:Accession: F30560

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Cross-references: UNIPARC:UPI0000114824; GB:M24273; NID:g197081; PIDN:AAAG3370.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7.63e-48 Length: 113  
Score: 531.00 Matches: 99  
Percent Similarity: 95.54% Conservative: 8  
Best Local Similarity: 88.39% Mismatches: 5  
Query Match: 90.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x F30560 (1-113)

Qy	1	GATGTAGTGTACCCAGTCTCCACTCTCTCGCGTTACCTTGGACAGCAGCTCC	60
Db	1	AspValValMetThrGlnIleProLeuThrLeuSerValThrIleGlyGlnProAlaSer	20
Qy	61	ATCTCTTGCAGTCAAGTCAGCAGCTCTTAGATAGTGAAGACACATTTTGAATGG	120
Db	21	IleSerCysLysSerSerGlnSerLeuAspSerAspGlyLysThrTyrLeuAsnTrp	40

QY 121 TTTTCAGCAGGCCAGCCAGCTCCCAAGGCGCCTAATCTATCTGTGTCTAAACTGGAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGGATGTGGAGTTTATTTATTGCTGGCAAGGTACACATTTTCGG 300  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 101 HisThrPheGlyGlyThrLysLeuGluIleLys 112  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 2  
C32513  
Ig kappa chain precursor V region (BXW14) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: C32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.B.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 82, 852-860, 1988  
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID: 88331394; PMID:3138286  
A:Accession: C32513  
A:Molecule type: DNA  
A:Residues: 1-132 <KOF>  
A:Cross-references: UNIPARC:UPI0000114D99; GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 9.75e-48 Length: 132  
Score: 530.00 Matches: 99  
Percent Similarity: 95.54% Conservative: 8  
Best Local Similarity: 88.39% Mismatches: 5  
Query Match: 89.83% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x C32513 (1-132)  
QY 1 GATGTAGTGATGACCCAGTCTCCACTCTCCTGTCGCCGTACCCCTTGACAGCCAGCCTCC 60  
Db 21 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 40  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ATCTCTTGCAAGTCAAGTCAAGGCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGG 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 41 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrTyrLeuAsnTrp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 TTTTCAGCAGGCCAGCCAGTCTCCCAAGGCGCCTAATCTATCTGTGTCTAAACTGGAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGGATGTGGAGTTTATTTATTGCTGGCAAGGTACACATTTTCGG 300  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 101 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 ArgThrPheGlyGlyThrLysLeuGluIleLys 132  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 3  
S23230  
Ig kappa chain precursor V-J region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S23230  
R:Kennedy, M.A.  
J. Exp. Med. 173, 1033-1036, 1991  
A:Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light  
A:Reference number: S23230; MUID:91178438; PMID:1840606  
A:Accession: S23230  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <KEN>  
A:Cross-references: UNIPARC:UPI0000115EA9; EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:  
C:Genetics:  
A:Introns: 17/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2.57e-47 Length: 133  
Score: 526.00 Matches: 101  
Percent Similarity: 93.75% Conservative: 4  
Best Local Similarity: 90.18% Mismatches: 7  
Query Match: 89.15% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-109 (1-336) x S23230 (1-133)  
QY 1 GATGTAGTGATGACCCAGTCTCCACTCTCCTGTCGCCGTACCCCTTGACAGCCAGCCTCC 60  
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 ATCTCTTGCAAGTCAAGTCAAGGCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGG 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 41 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrHisLeuAsnTrp 60  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 TTTTCAGCAGGCCAGCCAGTCTCCCAAGGCGCCTAATCTATCTGTGTCTAAACTGGAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 TCTGGAGTCCCTGCACAGGTTTCAGCGGCAGTGGATCAGGGACAGATTTTCACACTGAAAATC 240  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 AGCAGAGTGAGGCTGAGGATGTGGAGTTTATTTATTGCTGGCAAGGTACACATTTTCGG 300  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 120  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 TACACGTTCCGACAAAGGACCCGACTGGAGATCAAG 336  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 TyrThrPheGlyGlnGlyThrLysLeuGluIleLys 132  
|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||  
RESULT 4  
S22902  
Ig kappa chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C:Accession: S22902  
R:Chastagner, P.; Theze, J.; Zouali, M.  
Gene 101, 305-306, 1991  
A:Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region usi  
A:Reference number: S22902; MUID:91276289; PMID:1905262  
A:Accession: S22902  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-142 <CHA>  
A:Cross-references: UNIPARC:UPI0000176CAB; EMBL:X56510  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-126/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2.58e-47 Length: 142  
Score: 526.00 Matches: 100  
Percent Similarity: 94.59% Conservative: 5

Best Local Similarity: 90.09% Mismatches: 6  
Query Match: 89.15% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x S22902 (1-142)

```
OY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCTCC 60
DB 32 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 51
OY 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120
DB 52 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 71
OY 121 TTTTACAGAGCCAGCCAGCCAGCTCTCAAGCCGCTTAATCTATCTGCTGCTAAACTGGAC 180
DB 72 PheGlnGlnArgProGlnSerProArgArgLeuLeuTyrLysValSerAsnArgAsp 91
OY 181 TCTGGAGTCCCTGACAGCTTCAGCGGAGTGCATCAGGACAGATTCACACTGAAATC 240
DB 92 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 111
OY 241 AGCAGAGTGGAGCTGAGGATCTTGAGTTTATTATTGCTGCGAAGGTACACATTTCCG 300
DB 112 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 131
OY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATC 333
DB 132 PheThrPheGlyGlnGlyThrArgLeuGluile 142
```

## RESULT 5

A36259  
ig kappa chain V region (TE34) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 21-Jan-2000  
C:Accession: A36259  
R:Zilber, B.; Scherff, T.; Levitt, M.; Anglistter, J.  
Biochemistry 29, 10032-10041, 1990  
A:Title: NMR-derived model for a peptide-antibody complex.  
A:Reference number: A36259; MUID:91104915; PMID:2271636  
A:Accession: A36259  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <ZIL>  
A:Cross-references: UNIPARC:UPI000176AFD; GB:M30458; GB:M30459; GB:M30480; GB:M30481; G  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 2,286-46 Length: 112  
Score: 517.00 Matches: 97  
Percent Similarity: 93.75% Conservative: 8  
Best Local Similarity: 86.61% Mismatches: 7  
Query Match: 87.63% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x A36259 (1-112)

```
OY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCTCC 60
DB 1 AspValValMetIleGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20
OY 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120
DB 21 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyLysThrTyrLeuAsnTrp 40
OY 121 TTTTACAGAGCCAGCCAGCCAGCTCTCAAGCCGCTTAATCTATCTGCTGCTAAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuLeuTyrLysValSerLysLeuAsp 60
OY 181 TCTGGAGTCCCTGACAGCTTCAGCGGAGTGCATCAGGACAGATTCACACTGAAATC 240
```

```
DB 61 SerGlyValProThrArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysile 80
OY 241 AGCAGAGTGGAGCTGAGGATCTTGGAGTTTATTATTGCTGCGAAGGTACACATTTCCG 300
DB 81 SerArgValGluAlaGluAspGlyGlyValTyrCysTrpGlnGlyThrHisPhePro 100
OY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
DB 101 TrpThrPheGlyGlyGlyThrLysLeuGluileLys 112
```

## RESULT 6

K2HURP

ig kappa chain precursor V-II region (RPMI) - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C:Accession: A01890  
R:Klobeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.  
Nucleic Acids Res. 13, 6499-6513, 1985  
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.  
A:Reference number: A93588; MUID:86041852; PMID:2997711  
A:Accession: A01890  
A:Molecule type: DNA  
A:Residues: 1-133 <KLO>  
A:Cross-references: UNIPROT:P06310; UNIPARC:UPI000012E159  
A:Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

A:Introns: 17/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 161  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

P:1-20/Domain: signal sequence #status predicted <SIG>

P:21-133/Product: ig kappa chain V-II region (RPMI) #status predicted <MAT>

P:21-43/Region: framework 1

P:36-115/Domain: immunoglobulin homology <IMM>

P:44-59/Region: complementarity-determining 1

P:60-74/Region: framework 2

P:75-81/Region: complementarity-determining 2

P:82-113/Region: framework 3

P:114-122/Region: complementarity-determining 3

P:123-133/Region: framework 4

P:43-113/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.: 4,74e-46 Length: 133  
Score: 514.00 Matches: 98  
Percent Similarity: 93.75% Conservative: 7  
Best Local Similarity: 87.50% Mismatches: 7  
Query Match: 87.12% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x K2HURP (1-133)

```
OY 1 GATGTAGTGTGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCTCC 60
DB 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
OY 61 ATCTCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120
DB 41 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
OY 121 TTTTACAGAGCCAGCCAGCTCTCCAGCGGCTTAATCTATCTGCTGCTAAACTGGAC 180
DB 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuTyrLysValSerAsnArgAsp 80
OY 181 TCTGGAGTCCCTGACAGCTTCAGCGGAGTGCATCAGGACAGATTCACACTGAAATC 240
DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysile 100
OY 241 AGCAGAGTGGAGCTGAGGATCTTGGAGTTTATTATTGCTGCGAAGGTACACATTTCCG 300
```

Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120  
:::|||||  
Qy 301 TACAGTTCGACAGGACCCGACTGGAGATCAAG 336  
:::|||||  
Db 121 TrpThrPheGlyGlnGlyThrLysValGluLeuLys 132  
:::|||||  
RESULT 7  
S49572  
Ig kappa chain precursor - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S49572  
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.  
submitted to the EMBL Data Library, November 1994  
A;Description: K-1+ dual receptor B cells are present in the human peripheral repertoire  
A;Reference number: S49571  
A;Accession: S49572  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <GIA>  
A;Cross-references: UNIPARC:UPI0000116709; EMBL:Z46626; NID:9575261; PIDN:CAA86596.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 5.34e-46 Length: 114  
Score: 513.50 Matches: 99  
Percent Similarity: 93.81% Conservative: 7  
Best Local Similarity: 87.61% Mismatches: 6  
Query Match: 87.03% Indels: 1  
DB: 2 Gaps: 1  
US-10-733-563-109 (1-336) x S49572 (1-114)  
Qy 1 GATGTAGTGTAGTACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGTATGATGAGAAAGACATTTTGAATTGG 120  
Db 21 IleSerCysArgSerSerGlnSerLeuValTyrThrAspGlyAsnThrTyrLeuAsnTrp 40  
Qy 121 TTTCCAGAGAGCCAGGACCCAGTCTCCAGGCGCTATCTATCTGCTGCTTAACTCGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgGluLeuIleTyrLysValSerAsnArgAsp 60  
Qy 181 TCTGGAGTCCCTGACAGGTTCCAGCGGCGAGTGGATCAGGACAGATTTTCACACTGAAAAATC 240  
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGGCAGGATACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyIleTyrCysIleGlnGlyThrHisTrpPro 100  
Qy 301 ---TACAGTTCGACAGGACCCGACTGGAGATCAAG 336  
Db 101 GlnTyrThrPheGlyGlnGlyThrLysLeuGluLeuLys 113  
RESULT 8  
S20709  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S20709  
R;Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osh  
submitted to the EMBL Data Library, April 1992  
A;Description: Binding specificity and variable region sequences of two monoclonal anti  
A;Reference number: S20706  
A;Accession: S20709  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-111 <BRE>

A;Cross-references: UNIPARC:UPI00001163E1; EMBL:Z11917; NID:952655; PIDN:CAA77975.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7.68e-46 Length: 111  
Score: 512.00 Matches: 95  
Percent Similarity: 93.69% Conservative: 9  
Best Local Similarity: 85.59% Mismatches: 7  
Query Match: 86.78% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x S20709 (1-111)

Qy 1 GATGTAGTGTAGTACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspIleGlnLeuThrGlnSerProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGTATGATGAGAAAGACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuHisSerAspGlyLysThrTyrLeuAsnTrp 40  
Qy 121 TTTCCAGCAGAGGCGCAGCCAGTCTCCAGGCGCTATCTATCTGCTGCTTAACTCGAC 180  
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60  
Qy 181 TCTGGAGTCCCTGACAGGTTCCAGCGGCGAGTGGATCAGGACAGATTTTCACACTGAAAAATC 240  
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
Qy 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGGCAGGATACACATTTTCCG 300  
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
Qy 301 TACAGTTCGACAGGACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCTCC 333  
Db 101 GlnThrPheGlyGlyThrLysLeuGluLeu 111

RESULT 9  
A55491  
proteolytic antibody light chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A55491  
R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.;  
J. Biol. Chem. 269, 32389-32393, 1994  
A;Title: Molecular cloning of a proteolytic antibody light chain.  
A;Reference number: A55491; MUID:95096089; PMID:7798238  
A;Accession: A55491  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <GAO>  
A;Cross-references: UNIPROT:Q8K0R8; UNIPARC:UPI0000176CC8; GB:L34775  
A;Note: authors translated the codon TAT for residue 37 as Thr  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-95/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 7.69e-46 Length: 112  
Score: 512.00 Matches: 96  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 85.71% Mismatches: 7  
Query Match: 86.78% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x A55491 (1-112)

Qy 1 GATGTAGTGTAGTACCCAGTCTCCACTCTCTGCGCGTACCCCTTGACAGCCAGCTCC 60  
Db 1 AspValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20  
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGTATGATGAGAAAGACATTTTGAATTGG 120

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Db 21 ILeSerCysValSerSerGlnSerLeuLeuHisThrAspGlyLysThrTyrLeuIleTrp 40
Qy 121 TTTTCCAGCAGAGCCAGGCGCAGTCTCCAGGGCCCTAAATCTATCTGCTGCTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGGACAGAGATTTTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAGGACCGGACTCGGAGATCAAG 336
Db 101 GlnThrPheGlyGlyThrLysLeuGluLys 112
RESULT 10
A24452
Ig kappa chain precursor V-II region (RPMI 6410) - human
C:Species: Homo sapiens (man)
C:Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: A24452
R:Weir, L.; Leder, P.
Nucleic Acids Res. 14, 3957-3970, 1986
A:Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A:Reference number: A24452; MUID:86232631; PMID:3086847
A:Accession: A24452
A:Molecule type: DNA
A:Residues: 1-133 <WEI>
A:Cross-references: UNIPARC:UPI000113B46; GB:M36859; NID:G185932; PID:AA58920.1; PID:
A:Note: this sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted
Alignment Scores:
Pred. NO.: 3.3e-45 Length: 133
Score: 506.00 Matches: 97
Percent Similarity: 92.86% Conservative: 7
Best Local Similarity: 86.61% Mismatches: 8
Query Match: 85.76% Indels: 0
DB: 1 Gaps: 0
US-10-733-563-109 (1-336) x A24452 (1-133)
Qy 1 GATCTAGTGTGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
Qy 61 ATCTCTTGCAGTCAAGTCCAGGCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGG 120
Db 41 ILeSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
Qy 121 TTTTCCAGCAGGCGCAGGCTCTCCAGGCGCTTAATCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGGCTTCCAGGCGCAGTCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGGACAGAGATTTTCACACTGAAATC 240
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100
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Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTCCG 300
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120
Qy 301 TACAGTTCGGACAGGACCGGACTCGGAGATCAAG 336
Db 121 TrpThrPheGlyGlnGlyThrLysValGluLys 132
RESULT 11
S22658
Ig kappa chain precursor V region (O-81VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C:Accession: S22658
R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 2601, 1992
A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as
A:Reference number: S22657; MUID:92285150; PMID:1598223
A:Accession: S22658
A:Molecule type: mRNA
A:Residues: 1-140 <HIR>
A:Cross-references: UNIPROT:Q8TCD0; UNIPARC:UPI00001769CF; EMBL:X59135
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. NO.: 3.73e-45 Length: 140
Score: 505.50 Matches: 99
Percent Similarity: 92.04% Conservative: 5
Best Local Similarity: 87.61% Mismatches: 8
Query Match: 85.68% Indels: 1
DB: 2 Gaps: 1
US-10-733-563-109 (1-336) x S22658 (1-140)
Qy 1 GATCTAGTGTGACCCAGTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCGCTCC 60
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40
Qy 61 ATCTCTTGCAGTCAAGTCCAGGCTCTTAGATAGTGTGATGAGAAAGACATTTTGAATGG 120
Db 41 ILeSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 60
Qy 121 TTTTCCAGCAGGCGCAGGCTCTCCAGGCGCTTAATCTATCTGCTGCTTAAACTGGAC 180
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrArgValSerAsnArgAsp 80
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCGAGTGGATCAGGGACAGAGATTTTCACACTGAAATC 240
Db 81 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 100
Qy 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTTATCTGCTGCGCAAGGTACACATTTT 297
Db 101 SerArgValGluAlaGluAspValGlyLeuTyrCysMetGlnHisThrHisTrpSer 120
Qy 298 CCGTACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
Db 121 ProIleThrPheGlyGlnGlyThrArgLeuGluLys 133
RESULT 12
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
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QY 241 AGCAGAGTGGAGGCTGAGGATCTTGAGTTTATTATTGCTGCAAGGTACACATTTTCGG 300  
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Db 81 SerArgValGluAlaGluAsePLeuGlyValTyrCysValGlnGlyThrHisPhePro 100  
|||||  
QY 301 TACAGGTTTCGACACAGGACCGAGCTGAGTGCATCAAG 336  
|||||  
Db 101 TrpThrPheGlyGlyGlyThrLysLeuGluIleLys 112  
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## RESULT 15

S42611  
HUNVK protein precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42611  
R:Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.  
J. Neuroimmunol. 36, 29-39, 1992  
A:Title: DNA sequence analysis and comparison of the variable heavy and light chain regi  
A:Reference number: S42610; MUID:92138794; PMID:1370957  
A:Accession: S42611  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-133 <SPA>  
A:Cross-references: UNIPARC:UPI000011378B; EMBL:X54137; NID:G433889; PIDN:CMA38072.1; PI  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:36-115/Domain: immunoglobulin homology <IMM>

## Alignment Scores:

Pred. No.:	1..11e-44	Length:	133
Score:	501.00	Matches:	95
Percent Similarity:	91.89%	Conservative:	7
Best Local Similarity:	85.59%	Mismatches:	9
Query Match:	84.92%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-109 (1-336) x S42611 (1-133)

QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTTGCCCGTTACCCCTTGAGCAGCCGCTCC 60  
|||||  
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
|||||  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGTAGTATGATGGAAGACATTTTGAATTGG 120  
|||||  
Db 41 IleSerCysArgSerSerGlnSerLeuValPheSerAspGlyAsnThrTyrLeuAsnTrp 60  
|||||  
QY 121 TTTCAGCAGAGCCAGGCCAGTCTCAAGGCCCTAATCTATCTGCTGTCTAAACTGGAC 180  
|||||  
Db 61 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLysValSerAsnArgAsp 80  
|||||  
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGGCAGTGGATCAGGGACAGATTTCACACTGAAATC 240  
|||||  
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
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QY 241 AGCAGAGTGGAGGCTGAGAGTGTGGAGTTTATTATTGCTGCAAGGTACACATTTTCGG 300  
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Db 101 SerArgValGluAlaGluAsePLeuGlyIleTyrCysMetGlnGlyAlaHisTrpPro 120  
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QY 301 TACAGGTTTCGACACAGGACCGAGCTGAGATC 333  
|||||  
Db 121 LeuThrPheGlyGlyGlyThrLysValGluIle 131  
|||||

Search completed: January 28, 2006, 08:45:57  
Job time : 11.1652 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 51.5435 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590

Sequence: 1 gatgtagtgtgaccagtc.....ggaccgactggagatcaag 336

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO\_spool\_p/US10733563/runat\_27012006\_180005\_4782/app\_query.fasta.1.2716  
-DB=UniProt -QMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -PART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 -CGEN 1.1 632 @runat\_27012006\_180005\_4782 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	87.1	133	1 KV2P_HUMAN	P06310 homo sapien
2	511	86.6	239	2 QTCDD_HUMAN	Q8CDD0 homo sapien
3	496.5	84.2	114	2 Q9UL80_HUMAN	Q9UL80 homo sapien
4	491	83.2	239	2 Q58EU8_MOUSE	Q58EU8 mus musculus
5	459	77.8	239	2 Q6P491_HUMAN	Q6P491 homo sapien
6	450	76.3	113	1 KV2D_HUMAN	P01617 homo sapien
7	449	76.1	113	1 KV2B_HUMAN	P01615 homo sapien
8	447	75.8	239	2 Q9NEK0_HUMAN	Q9NEK0 homo sapien
9	445	75.4	248	2 Q65ZQ7_MOUSE	Q65ZQ7 mus sp. b3(
10	442.5	75.0	115	1 KV2A_HUMAN	P01614 homo sapien
11	438	74.2	117	1 KV2E_HUMAN	P06309 homo sapien
12	430.5	73.0	115	2 Q5F2I0_MOUSE	Q5F2I0 mus musculus
13	430	72.9	113	1 KV2G_MOUSE	P01631 mus musculus
14	428	72.5	112	2 Q53VP8_MOUSE	Q53VP8 mus musculus
15	418	70.8	219	2 Q65ZC0_MOUSE	Q65ZC0 mus musculus
16	417.5	70.8	240	2 Q6PIH6_HUMAN	Q6PIH6 homo sapien

17	411	69.7	234	2 Q5XKG4_MOUSE	Q5XKG4 mus musculus
18	405.5	68.7	112	1 KV2C_HUMAN	P01616 homo sapien
19	402	68.1	113	1 KV2E_MOUSE	P03976 mus musculus
20	397	67.3	113	1 KV2C_MOUSE	P01628 mus musculus
21	396	67.1	112	1 KV2D_MOUSE	P01629 mus musculus
22	396	67.1	113	1 KV2F_MOUSE	P01630 mus musculus
23	390	66.1	112	1 KV2A_MOUSE	P01626 mus musculus
24	390	66.1	112	2 Q6LEM8_MOUSE	Q6LEM8 mus musculus
25	386.5	65.5	134	1 KV4C_HUMAN	P06314 homo sapien
26	385.5	65.3	108	1 KV1CANFA	P01618 canis fami
27	380.5	64.5	114	1 KV4A_HUMAN	P01625 homo sapien
28	378.5	64.2	111	1 KV3L_MOUSE	P01664 mus musculus
29	378.5	64.2	111	1 KV3M_MOUSE	P01665 mus musculus
30	377.5	64.0	111	1 KV3O_MOUSE	P01667 mus musculus
31	372.5	63.1	111	1 KV3Q_MOUSE	P01669 mus musculus
32	371.5	63.0	111	1 KV3N_MOUSE	P01665 mus musculus
33	370	62.7	86	2 Q723Y5_HUMAN	Q723Y5 homo sapien
34	368.5	62.5	111	1 KV3H_MOUSE	P01660 mus musculus
35	366	62.0	110	1 KV3P_MOUSE	P01668 mus musculus
36	365.5	61.9	111	1 KV3J_MOUSE	P01662 mus musculus
37	364.5	61.8	111	2 Q811U6_MOUSE	Q811U6 mus musculus
38	363	61.5	120	1 KV2B_MOUSE	P01627 mus musculus
39	361.5	61.3	111	2 Q920E9_MOUSE	Q920E9 mus musculus
40	360.5	61.1	131	1 KV3I_MOUSE	P01661 mus musculus
41	360.5	61.1	255	2 Q6KB05_MOUSE	Q6KB05 mus musculus
42	359	60.8	133	1 KV4B_HUMAN	P06313 homo sapien
43	356.5	60.4	111	1 KV3K_MOUSE	P01663 mus musculus
44	356.5	60.4	111	1 KV3U_MOUSE	P01673 mus musculus
45	355.5	60.3	240	2 Q52L64_MOUSE	Q52L64 mus musculus

ALIGNMENTS

RESULT 1  
KV2P\_HUMAN  
ID KV2P\_HUMAN STANDARD; PRT; 133 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-II region RPMI 6410 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=85041852; PubMed=2997711;  
RA Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and III.";  
RL Nucleic Acids Res. 13:6499-6513(1985).

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CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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CC EMBL; Z00020; CAA77315.1; -; Genomic\_DNA.  
DR PIR; A01890; K2HURP.  
DR HSSP; Q99M37; 1191.  
DR SMR; P06310; 21-133.  
DR Ensembl; ENSG00000173758; Homo sapiens.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 20  
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.  
FT REGION 21 43 Framework-1.  
FT REGION 44 59 Complementarity-determining-1.  
FT REGION 60 74 Framework-2.  
FT REGION 75 81 Complementarity-determining-2.  
FT REGION 82 113 Framework-3.  
FT REGION 114 122 Complementarity-determining-3.  
FT REGION 123 132 Framework-4.  
FT DISULFID 43 113 By similarity.  
FT NON TER 133 133  
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009BE CRC64;

Alignment Scores:  
Pred. No.: 2,37e-53 Length: 133  
Score: 514.00 Matches: 98  
Percent Similarity: 93.75% Conservativeness: 7  
Best Local Similarity: 87.50% Mismatches: 7  
Query Match: 87.12% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2P\_HUMAN (1-133)  
Qy 1 GATCTAGTACCCAGTCTCCACTCTCTGTCGCGTTACCTTGGACGACGCTCC 60  
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 40  
Qy 61 ATCTCTTGGAGTCAAGTCAAGCTCTTAGATAGTATGATGAAAGACATTTTGAATGG 120  
Db 41 IleSerCysArgSerSerGlnSerLeuValTySerAspGlyAsnThrTyrLeuAsnTrp 60  
Qy 121 TTTTCAGCAGAGGCGGAGTCTCCAGGCGCTTATCTATCTGCTGCTTAACTCGAC 180  
Db 61 PheGlnGlnArgProGlyGlnSerProArgGluLeuIleTyrLysValSerAsnArgAsp 80  
Qy 181 TCTGGAGTCTCCAGTTCAGCGGTCAGCGGAGTGGATCAGGAGCAGATTTTCACTCAAAATC 240  
Db 81 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 100  
Qy 241 AGCAGAGTGGAGGCTGAGGAGTGTGGAGTTTATTTATTTGCTGGCAGGTACACATTTCCG 300  
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpSer 120  
Qy 301 TACAGTTCGACAGGAGGCGGAGTGGAGTCAAG 336  
Db 121 TrpThrPheGlnGlyThrLysValGluIleLys 132

RESULT 2  
Q8TCD0\_HUMAN  
ID Q8TCD0\_HUMAN PRELIMINARY; PRT; 239 AA.  
AC Q8TCD0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Narasina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1598223;  
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;  
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus  
RT nephritis-associated idiotype.";  
RL Nucleic Acids Res. 20:2601-0(1992).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1551402;  
RA Lautner-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,  
RA Thiebe R., Zocher I., Zachau H.G.;  
RT "The human immunoglobulin kappa locus. Characterization of the  
RT duplicated A regions.";  
RL Eur. J. Immunol. 22:1023-1029(1992).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8258341;  
RA Klein R., Jaenichen R., Zachau H.G.;  
RT "Expressed human immunoglobulin kappa genes and their hypermutation.";  
RL Eur. J. Immunol. 23:3248-3262(1993).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
RT distributed over a large portion of the V kappa locus and do not show  
RT somatic mutation.";  
RL Eur. J. Immunol. 23:391-397(1993).  
DR EMBL; BC022362; AAH22362.1; -; mRNA.  
DR PIR; S22658; S22658.  
DR PIR; S34095; S34095.  
DR PIR; S40324; S40324.  
DR PIR; S40374; S40374.  
DR PIR; S42267; S42267.  
DR PIR; S42268; S42268.  
DR HSSP; P01834; I172.  
DR SMR; Q8TCD0; 21-237.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 239 AA; 26235 MW; FAGEDC3A3B03871D CRC64;

Alignment Scores:  
Pred. No.: 6,12e-53 Length: 239  
Score: 511.00 Matches: 97  
Percent Similarity: 93.75% Conservativeness: 8  
Best Local Similarity: 86.61% Mismatches: 7  
Query Match: 86.61% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q8TCD0\_HUMAN (1-239)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTCTGCCCCGTTACCTTGGACAGCCAGCTCC 60  
 DB |||||  
 DB 21 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 40  
 QY 61 ATCTTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
 DB |||||  
 DB 41 IleSerCysArgSerThrGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 60  
 QY 121 TTTTACAGAGCCAGGCGAGCTCTCAAGGGCCCTAATCTATCTGCTGCTCTAACTGAC 180  
 DB |||||  
 DB 61 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 80  
 QY 181 TCTGGAGTCCCTGACAGGTCAGCGGCGAGTGGATCAGGAGCAGATTTTCACTGAAATC 240  
 DB |||||  
 DB 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100  
 QY 241 AGCAGAGTGGAGGCTGAGATGTTGGAGTTTATTTATTTCTGCTGAGGATGATCTCCG 300  
 DB |||||  
 DB 101 ThrArgValGluAlaGluAspValGlyValTyrPheCysMetGlnGlyThrHisTrpPro 120  
 QY 301 TACAGCTTCCGACAGGCGAGCCGAGCTGCGAGATCAAG 336  
 DB |||||

# RESULT 3

Q9UL80\_HUMAN  
 ID Q9UL80\_HUMAN PRELIMINARY; PRT; 114 AA.  
 AC Q9UL80;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1322670;  
 RA Stuber P., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,  
 RA Gaskin F., Fu S.M.;  
 RT "A rheumatoid factor from a normal individual encoded by VH2 and V  
 RT kappa II gene segments";  
 RL Arthritis Rheum. 35:900-904(1992).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=8436174;  
 RA Wagner S.D., Iuzzatto L.;  
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are  
 RT distributed over a large portion of the V kappa locus and do not show  
 RT somatic mutation";  
 RL Eur. J. Immunol. 23:391-397(1993).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1601042;  
 RA Huber C., Klobbeck H.G., Zachau H.G.;  
 RT "Ongoing V kappa-J kappa recombination after formation of a productive  
 RT V kappa-J kappa coding joint";  
 RL Eur. J. Immunol. 22:1561-1565(1992).  
 DR EMBL; AF035034; AAD56270.1; -; mRNA.  
 DR PIR; B49002; B49002.

DR PIR; S23638; S23638.  
 DR PIR; S34094; S34094.  
 DR PIR; S34095; S34095.  
 DR HSSP; P01625; 1LVE.  
 DR SMR; Q9UL80; 1-114.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS08335; IG\_LIKE; 1.  
 FT NON\_TER 1 114  
 FT NON\_TER 114 114  
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

## Alignment Scores:

Pred. No.: 3,16e-51 Length: 114  
 Score: 496.50 Match: 97  
 Percent Similarity: 92.04% Conservative: 7  
 Best Local Similarity: 85.84% Mismatches: 8  
 Query Match: 84.15% Indels: 1  
 DB: 2 Gaps: 1

US-10-733-563-109 (1-336) x Q9UL80\_HUMAN (1-114)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTCTGCCCCGTTACCTTGGACAGCCAGCTCC 60  
 DB |||||  
 DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuArgGlnProAlaSer 20  
 QY 61 ATCTTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120  
 DB |||||  
 DB 21 IleSerCysArgSerGlnSerProValTyrSerAspGlyAsnThrTyrLeuAsnTrp 40  
 QY 121 TTTTACAGAGCCAGGCGAGCTCTCAAGGGCCCTAATCTATCTGCTGCTCTAACTGAC 180  
 DB |||||  
 DB 41 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 60  
 QY 181 TCTGGAGTCCCTGACAGGTCAGCGGCGAGTGGATCAGGAGCAGATTTTCACTGAAATC 240  
 DB |||||  
 DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
 QY 241 AGCAGAGTGGAGGCTGAGATGTTGGAGTTTATTTATTTCTGCTGCGAGGATGATCTCC 297  
 DB |||||  
 DB 81 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHisTrpPro 100  
 QY 298 CCGTACAGCTTCCGACAGGCGAGGCGAGCTGAGATCAAG 336  
 DB |||||  
 DB 101 ProTrpThrPheGlyGlnGlyThrLysValGluLys 113

## RESULT 4

Q58EU8\_MOUSE  
 ID Q58EU8\_MOUSE PRELIMINARY; PRT; 239 AA.  
 AC Q58EU8;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Igk-C protein.  
 GN Name=Igk-C;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,





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DR HSSP; Q99M37; 1191.
DR SMR; P01615; 1-109.
DR GO; GO:0005573; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 39
FT REGION 40 54
FT REGION 55 61
FT REGION 62 93
FT REGION 94 102
FT REGION 103 112
FT REGION 112 113
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Alignment Scores:
Pred. No.: 1,99e-45 Length: 113
Score: 449.00 Matches: 84
Percent Similarity: 85.71% Conservative: 12
Best Local Similarity: 75.00% Mismatches: 16
Query Match: 76.10% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2B_HUMAN (1-113)
Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCTGTCGCGTACCTTGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnSerProLeuPheLeuProValThrLeuGlyGluProAlaSer 20
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTGAAGAAAGACATTTTGAATTGG 120
Db 21 IleGlnCysArgSerGlnSerLeuValThrArg***Gly***ThrTyrLeu***Tyr 40
Qy 121 TTTCAGCAGAGCCAGCCAGTCTCCAGGCGCTAATCTATCTGCTGTCTAACTCGAC 180
Db 41 TyrLeuGlnLysProGlyGlnSerProGluLeuLeuLetyrLeuSerSerTyrArgAsp 60
Qy 181 TCTGGAGTCCCTGACAGGTTTCAGCGGAGTGATCAGGACAGATTTTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerAspSerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGCAAGGTACACATTTTCCG 300
Db 81 ThrArgValGlnAlaGluAspValIGlyValTyrTyrCysMetGlnAlaThr***SerPro 100
Qy 301 TACACGTTCCGACAAAGGACCCGACTCGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrLysLeu***IleLys 112

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## RESULT 8

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Q8NEKO_HUMAN
ID Q8NEKO_HUMAN PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8258341;
RA Klein R., Jaenichen R., Zachau H.G.;
RT "Expressed human immunoglobulin kappa genes and their hypermutation."
RL Eur. J. Immunol. 23:3248-3262(1993).
DR EMBL; BC030814; AAH30814.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 117Z.
DR SMR; Q8NEKO; 21-237.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

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Alignment Scores:
Pred. No.: 4e-45 Length: 239
Score: 447.00 Matches: 85
Percent Similarity: 86.61% Conservative: 12
Best Local Similarity: 75.89% Mismatches: 15
Query Match: 75.76% Indels: 0
DB: 2 Gaps: 0

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US-10-733-563-109 (1-336) x Q8NEKO_HUMAN (1-239)
Qy 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60
Db 21 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
Qy 61 ATCTCTTCAAGTCAGTCAAGCTCTTAGATAGTGTAGAAAGACATTTTGAATTGG 120
Db 41 IleSerCysArgSerSerGlnSerLeuLeuHisSerAspGlyTyrAsnTyrLeuAspTrp 60
Qy 121 TTTCAGACAGCCAGCCAGCTCTCCAGGCGCTTAATCTATCTGCTGCTCTAACTGGAC 180
Db 61 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlySerAsnArgAla 80
Qy 181 TCTGAGTCCCTGACAGCTTTCAGGCGCAGTGGATGATGAGGACAGATTTTACACTGAAAATC 240
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTCCG 300
Db 101 SerLysValGluAlaGluAspValGlyIleTyrCysMetGlnGlyLeuGlnThrPro 120
Qy 301 TACAGCTTCGACAGGAGGACCCGACTGGAGATCAAG 336
Db 121 GlnThrPheGlyGlnGlyThrLysValGluLys 132

RESULT 9
Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3(Fv)-PE40 (Fragment).
GN Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Wittingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
PL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB19971.2; -; mRNA.
DR SMR; Q65ZQ7; 4-247.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Alignment Scores:
Pred. No.: 7,07e-45 Length: 248
Score: 445.00 Matches: 83
Percent Similarity: 87.50% Conservative: 15
Best Local Similarity: 74.11% Mismatches: 14
Query Match: 75.42% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q65ZQ7_9MURI (1-248)
Qy 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACAGCCAGCTCC 60
Db 136 AsplleValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 155
Qy 61 ATCTCTTCAAGTCAGTCAAGCTCTTAGATAGTGTAGAAAGACATTTTGAATTGG 120
```

```
Db 156 IleSerCysArgSerSerGlnIleValHisSerAsnGlyAsnThrTyrLeuGluTrp 175
Qy 121 TTTCAGACAGCCAGCCAGCTCTCCAGGCGCTTAATCTATCTGCTGCTCTAACTGGAC 180
Db 176 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuIleTyrLysValSerAsnArgPhe 195
Qy 181 TCTGAGTCCCTGACAGCTTTCAGGCGCAGTGGATGATGAGGACAGATTTTACACTGAAAATC 240
Db 196 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 215
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGCTGGCAGGTACACATTTCCG 300
Db 216 SerArgValGluAlaGluAspLeuGlyValTyrCysPheGlnGlySerHisValPro 235
Qy 301 TACAGCTTCGACAGGAGGACCCGACTGGAGATCAAG 336
Db 236 PheThrPheGlySerGlyThrLysLeuGluLys 247

RESULT 10
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region Cmu.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP SEQUENCE REVISION TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; B91639; K2HUCM.
DR HSSP; P01751; 1NOB.
DR SMR; P01614; 2-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 24 95
FT NON TER 115 115 By similarity.
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Alignment Scores:
Pred. No.: 1.24e-44 Length: 115
Score: 442.50 Matches: 86
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Percent Similarity: 86.73% Conservative: 12
Best Local Similarity: 76.11% Mismatches: 14
Query Match: 75.00% Indels: 1
DB: 1 Gaps: 1

US-10-733-563-109 (1-336) x KV2A_HUMAN (1-115)
Qy 1 GATGTAGTATGACCCAGCTCTCCACTCTCCCTGCGCGTTCACCTTGGACAGCCAGCTCC 60
Db 2 AspIleValMetThrGlnThrProLeuSerLeuProValThrProGlyGluProAlaSer 21
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGT---GATGGAAGACATTTTGAAT 117
Db 22 IleserCysArgSerSerGlnSerLeuLeuAspSerGlyAspGlyAsnThrTyrluAsn 41
Qy 118 TGGTTTCAGCAGAGCCAGGCGAGTCCTCCAGAGCGCTTAATCTATCTGCTCTAAACTG 177
Db 42 TrpTyrluGlnLysAlaGlyGlnSerProGlnLeuLeuIleTyrluSerTyrluArg 61
Qy 178 GACTCTGGAGTCCCTGACAGGCTTCAGCGGCGAGTCAGGACGATCAGGACGATTTTCACTGAAA 237
Db 62 AlaSerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLys 81
Qy 238 ATCAGCAGAGTGGAGGTGAGGATGTTGGAGTCTTATTATTCTGCTGGCAAGGTACACATTTT 297
Db 82 IleserArgValGlnAlaGluAspValGlyValTyrluTyrluSerMetGlnArgLeuGluIle 101
Qy 298 CCGTACAGCTTCGACAGAGGACCGAGCTGAGATCAAG 336
Db 102 ProTyrluPheGlyGlnGlyThrLysLeuGluIleArg 114

RESULT 11
KV2E_HUMAN
ID - KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC ENBL; 200009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A01889; K2HUGM.
DR HSP; Q99M37; 1191.
DR SMR; P06309; 5-117.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL <1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT REGION 5 27 Framework-1.
FT
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DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D3E8B8007 CRC64;

Alignment Scores:
Pred. No.: 3,63e-43 Length: 115
Score: 430.50 Matches: 84
Percent Similarity: 86.73% Conservative: 14
Best Local Similarity: 74.34% Mismatches: 14
Query Match: 72.97% Indels: 1
DB: 2 Gaps: 1

US-10-733-563-109 (1-336) x Q5P210_MOUSE (1-115)
QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTTGGCCGTTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTCTAGATAGTGTGATGATGATGATGATGATGATG 120
Db 21 IleserCysArgSerSerGlnSerLeuValHisSerAenGlyAenThrTyLeuHisTrp 40
QY 121 TTTCCAGCAGAGCCAGGCGAGTCTCCAGGCGCCCTAATCTATCTGCTGTCTAAACTGGAC 180
Db 41 TyrLeuGlnLysProGlyGlnSerProLysLeuLeuLeuTyLeuValSerAsnArgPhe 60
QY 181 TCTGGAGTCCCTGACAGGTTTCCAGGCGAGTGTGATGATGATGATGATGATGATGATG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGly 80
QY 241 AGCAGAGTGGAGGTGAGAGTGTGGAGTGTATTTATTTCTGCTGGCAGGTACACATTT 297
Db 81 SerArgValGluAlaGluAspLeuGlyValTyPheCysSerGlnThrHisValPro 100
QY 298 CCGTACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
Db 101 ProTyThrPheGlyGlyThrLysLeuGluMetLys 113

RESULT 13
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01914; KVM526.
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DR HSSP; Q9NM37; 1I91.
DR Ensembl; ENSMUSG0000055315; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin domain;
KW Immunoglobulin V region; Monoclonal antibody.
FT REGION 1 23 Framework-1.
FT REGION 24 39 Complementarity-determining-1.
FT REGION 40 54 Framework-2.
FT REGION 55 61 Complementarity-determining-2.
FT REGION 62 93 Framework-3.
FT REGION 94 102 Complementarity-determining-3.
FT REGION 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Alignment Scores:
Pred. No.: 4.17e-43 Length: 113
Score: 430.00 Matches: 83
Percent Similarity: 85.71% Conservative: 13
Best Local Similarity: 74.11% Mismatches: 16
Query Match: 72.88% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-109 (1-336) x KV2G_MOUSE (1-113)
QY 1 GATGTAGTGTGACCCAGTCTCCACTCTCTTGGCCGTTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnThrProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20
QY 61 ATCTCTTCAAGTCAAGTCAAGTCTCTAGATAGTGTGATGATGATGATGATGATGATG 120
Db 21 IleserCysArgSerSerGlnSerLeuValHisSerAenGlyAenThrTyLeuHisTrp 40
QY 121 TTTCCAGCAGAGCCAGGCGAGTCTCCAGGCGCCCTAATCTATCTGCTGTCTAAACTGGAC 180
Db 41 TyrLeuGlnLysAlaGlyGlnSerProLysLeuLeuLeuTyLeuValSerAsnArgPhe 60
QY 181 TCTGGAGTCCCTGACAGGTTTCCAGGCGAGTGTGATGATGATGATGATGATGATGATG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlySerGlySerGlySerGly 80
QY 241 AGCAGAGTGGAGGTGAGAGTGTGGAGTGTATTTATTTCTGCTGGCAGGTACACATTT 300
Db 81 SerArgValGluAlaGluAspLeuGlyValTyPheCysSerGlnThrHisValPro 100
QY 301 TACACGTTCCGACCAAGGACCCGACTGGAGATCAAG 336
Db 101 ProThrPheGlyGlyThrLysLeuGluLeuLys 112

RESULT 14
Q53VP8_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q53VP8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Kappa chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigen encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RT
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RL EMBL J. 4:3681-3688 (1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 108-109.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X03386; CAA27113.1; -, mRNA.  
FT NON\_TER 1 112  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12266 MW; C844B7881A89C18A CRC64;

Alignment Scores:  
Pred. No.: 7.3e-43 Length: 112  
Score: 428.00 Matches: 81  
Percent Similarity: 84.92% Conservative: 14  
Best Local Similarity: 72.32% Mismatches: 17  
Query Match: 72.54% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q53VP8\_MOUSE (1-112)

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Qy 1 GATGTAGTATGACCCAGTCTCCACTCTCCTTGCCGTTACCTTGAGCAGCCAGCTCC 60
Db 1 AspIleValMetThrGlnProLeuSerLeuProValSerLeuGlyAspGlnAlaSer 20
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120
Db 21 IleserCysArgSerGlnSerIleValIleSerAenGlyPheThrTyLeuGluTrp 40
Qy 121 TTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTGCTCTAAACTGGAC 180
Db 41 TyrLeuGlnLysProGly*****LysLeuLeuIleTyGlyIleSerAsnArgPhe 60
Qy 181 TCTGGAGTCCCTGACAGTTTCAGGCGCAGTGGATGATGAGGACAGATTTTCACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGTGAGGATGTTGGAGTTATATTATCTGGCAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyIleTyrcysPheGlnGlyIleHisValPro 100
Qy 301 TACACGTTCCGACAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112
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## RESULT 15

Q65ZC0\_MOUSE  
ID Q65ZC0\_MOUSE PRELIMINARY; PRT; 219 AA.  
AC Q65ZC0;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Kappa light chain C region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Spleen;  
RX MEDLINE=96319505; PubMed=8768802;  
RA Kipp B., Schlaak M., Becker W.M.;  
RT "cloning and expression of a recombinant mouse Fab-fragment  
recognizing a defined linear epitope of Chironomus thummi thummi major  
allergen Chi t I.";  
RL Int. Arch. Allergy Immunol. 110:348-353 (1996).  
DR EMBL; Z37499; CAA85724.1; -, mRNA.  
DR SMR; Q65ZC0; 1-219  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
FT NON\_TER 1 219  
FT NON\_TER 219 219  
SQ SEQUENCE 219 AA; 23944 MW; 7B1B82A14EAF8445 CRC64;

Alignment Scores:  
Pred. No.: 1.37e-41 Length: 219  
Score: 418.00 Matches: 80  
Percent Similarity: 85.71% Conservative: 16  
Best Local Similarity: 71.43% Mismatches: 16  
Query Match: 70.85% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x Q65ZC0\_MOUSE (1-219)

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Db 1 GlulLeuValMetThrGlnSerProLeuSerLeuSerValSerLeuGlyAspGlnAlaSer 20
Qy 61 ATCTCTTGCAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120
Db 21 IleserCysArgSerGlnSerLeuValIleThrAenGlyAenThrTyLeuHisValPro 40
Qy 121 TTTCAGCAGAGGCGCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTGCTCTAAACTGGAC 180
Db 41 TyrLeuGlnLysProGlyLeuSerProLysLeuLeuIleTyrlleValSerAsnArgPhe 60
Qy 181 TCTGGAGTCCCTGACAGTTTCAGGCGCAGTGGATGATGAGGACAGATTTTCACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGTGAGGATGTTGGAGTTATATTATCTGGCAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrcysSerGlnSerThrHisValPro 100
Qy 301 TACACGTTCCGACAGGACCCGACTGGAGATCAAG 336
Db 101 GlyThrPheGlyGlyThrLysLeuGluIleLys 112
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Search completed: January 28, 2006, 08:43:57  
Job time : 52.5435 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 / Search time 13.2853 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

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Perfect score: 590  
Sequence: 1 gatgtagtgtgacccagtc.....ggaccgactggagatcaag 336

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPEXT=0 -UNITITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10733563 @CGN 1 1 141 @runat 27012006\_180006\_4815 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGESQRY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	112	2	US-09-809-739-14
2	590	100.0	112	2	US-09-840-459-12
3	590	100.0	112	2	US-09-497-625A-12
4	584	99.0	114	2	US-09-840-459-106
5	584	99.0	114	2	US-09-497-625A-106
6	577	97.8	112	2	US-09-809-739-15
7	577	97.8	112	2	US-09-809-739-13
8	577	97.8	112	2	US-09-497-625A-13
9	572	96.9	112	2	US-09-809-739-18
10	572	96.9	112	2	US-09-840-459-107
11	570	96.6	112	2	US-09-809-739-16
12	570	96.6	112	2	US-09-840-459-14

13	570	96.6	112	2	US-09-497-625A-14	Sequence 14, Appl
14	565	95.8	112	2	US-09-809-739-17	Sequence 17, Appl
15	565	95.8	112	2	US-09-840-459-15	Sequence 15, Appl
16	565	95.8	112	2	US-09-497-625A-15	Sequence 15, Appl
17	536	90.8	112	2	US-09-809-739-11	Sequence 11, Appl
18	536	90.8	112	2	US-09-840-459-9	Sequence 9, Appl
19	536	90.8	112	2	US-09-497-625A-9	Sequence 9, Appl
20	536	90.8	112	2	US-09-840-459-102	Sequence 102, App
21	536	90.8	142	2	US-09-497-625A-102	Sequence 102, App
22	527	89.3	257	2	US-09-419-788-113	Sequence 113, App
23	526	89.2	111	2	US-09-809-739-13	Sequence 13, Appl
24	526	89.2	111	2	US-09-840-459-59	Sequence 59, Appl
25	526	89.2	111	2	US-09-497-625A-11	Sequence 11, Appl
26	526	89.2	111	2	US-09-497-625A-59	Sequence 59, Appl
27	526	89.2	112	1	US-08-477-281A-89	Sequence 89, Appl
28	526	89.2	112	1	US-08-477-989B-89	Sequence 89, Appl
29	526	89.2	112	1	US-08-477-989B-89	Sequence 89, Appl
30	526	89.2	112	2	US-09-462-140D-97	Sequence 97, Appl
31	524	88.8	113	2	US-09-698-705-7	Sequence 7, Appl
32	524	88.8	218	2	US-09-698-705-12	Sequence 12, Appl
33	521	88.3	112	2	US-09-840-459-54	Sequence 54, Appl
34	521	88.3	112	2	US-09-497-625A-54	Sequence 54, Appl
35	521	88.3	112	2	US-09-254-180C-8	Sequence 8, Appl
36	521	88.3	353	2	US-09-203-958A-4	Sequence 4, Appl
37	520	88.1	111	2	US-09-840-459-11	Sequence 11, Appl
38	520	88.1	112	2	US-09-840-459-58	Sequence 58, Appl
39	520	88.1	112	2	US-09-497-625A-58	Sequence 58, Appl
40	518	87.8	112	2	US-09-647-468-149	Sequence 149, App
41	518	87.8	112	2	US-09-647-468-150	Sequence 150, App
42	518	87.8	131	2	US-09-647-468-163	Sequence 163, App
43	518	87.8	131	2	US-09-647-468-164	Sequence 164, App
44	518	87.8	243	2	US-09-297-181-2	Sequence 2, Appl
45	516	87.5	535	2	US-08-983-035A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-09-809-739-14  
; Sequence 14, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.  
; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-14

Alignment Scores:  
Pred. No.: 5,84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-14 (1-112)

QY 1 GATGTAGTGTGACCCAGTCCTCCACTCTCTTCCCGCTTACCCCTTGACAGCCCTCC 60  
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Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTGACGAGAGCCAGGCGAGTCTCAAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTATTTGCTGCAAGGTACACATTTTCGG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGGACAAGGACCGAGCTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 2

US-09-840-459-12  
; Sequence 12, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-12

Alignment Scores:  
Pred. No.: 5,84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-12 (1-112)

QY 1 GATGTAGTAGTACCCAGCTCTCCACTCTCTTGGCCCGTTACCCCTGGACAGCAGCCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40

QY 121 TTTGACGAGAGCCAGGCGAGTCTCCAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTATTTGCTGCAAGGTACACATTTTCGG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGGACAAGGACCGAGCTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 3

US-09-497-625A-12  
; Sequence 12, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-497-625A-12

Alignment Scores:  
Pred. No.: 5,84e-70 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-497-625A-12 (1-112)

QY 1 GATGTAGTAGTACCCAGCTCTCCACTCTCTTGGCCCGTTACCCCTGGACAGCAGCCTCC 60  
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGGAAGACACATTTTGAATTGG 120  
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40  
QY 121 TTTGACGAGAGCCAGGCGAGTCTCCAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTGAGTCCCTGACAGGCTTCAAGCGCAGTGTGATCAGGACAGATTTTACACTGGAATC 240  
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 ACCAGTGGAGGCTGAGATGTTGGAGTTATTATTGCTGCAAGGTACACATTTCCG 300  
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTTCGGAACAGGACCGGACTGGAGATCAAG 336  
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 4  
US-09-840-459-106  
; Sequence 106, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: Larrosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US/09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-09-840-459-106

Alignment Scores:  
Pred. No.: 3,728-69 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-106 (1-114)

QY 4 GTAGTGATGACCCAGCTCTCCACTCTCCTTGCCCGTTACCTTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGTGATGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerArgGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGGCGCAGCTCTCAAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGCTTTCAGGGCAGTGGATCAGGACAGATTTACACTGAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCGAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTTCGGAACAGGACCGGACTGGAGATCAAG 336

Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112  
RESULT 5  
US-09-497-625A-106  
; Sequence 106, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: Larrosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-09-497-625A-106

Alignment Scores:  
Pred. No.: 3,728-69 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-497-625A-106 (1-114)

QY 4 GTAGTGATGACCCAGCTCTCCACTCTCCTTGCCCGTTACCTTGGACAGCCAGCTCCATC 63  
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTCAAGTCAAGTCAGAGCTCTTAGATAGTGTGATGAAAGACATTTTGAATTGGTTT 123  
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerArgGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGGCGCAGCTCTCCAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGCTTTCAGGGCAGTGGATCAGGACAGATTTACACTGAAATCAGC 243  
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTATTATTCTGCGAAGGTACACATTTCCGTAC 303  
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACGTTTCGGAACAGGACCGGACTGGAGATCAAG 336  
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 6  
US-09-739-15  
; Sequence 15, Application US/09809739  
; Patent No. 6663863  
; GENERAL INFORMATION:  
; APPLICANT: Horvath, Christopher J.



; APPLICANT: Rao, Patricia E.  
; TITLE OF INVENTION: Method of Inhibiting Stenosis and  
; FILE OF INVENTION: Restenosis  
; FILE REFERENCE: 1855.1069-003  
; CURRENT APPLICATION NUMBER: US/09/809,739  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: US 09/528,267  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-809-739-15

Alignment Scores:  
Pred. No.: 3.18e-68 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-15 (1-112)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACGCCAGCCCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGCCAGCTCTCCAGGCGCTATCTATCTGTGTCCTAAACTGGAC 180  
DB 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTCGAGTCCCTGACAGGTTTCAGGCGCAGTGCAGGACAGATTTTCACACTGAAATC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTCTGCGCAAGGTACACATTTTCCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGAGCCGACTGGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 7

US-09-840-459-13  
; Sequence 13, Application US/09840459  
; Patent No. 6696550  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840,459  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193

; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-840-459-13

Alignment Scores:  
Pred. No.: 3.18e-68 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-13 (1-112)

QY 1 GATGTAGTATGACCCAGCTCTCCACTCTCTTGGCCGTTACCTTGGACGCCAGCCCTCC 60  
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20  
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTATGATGGAAGACATTTTGAATTGG 120  
DB 21 IleSerCysIysSerSerGlnSerLeuLeuAspSerAspGlyLeuThrPheLeuAsnTrp 40  
QY 121 TTTCAGCAGAGCCAGCCAGCTCTCCAGGCGCTATCTATCTGTGTCCTAAACTGGAC 180  
DB 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60  
QY 181 TCTCGAGTCCCTGACAGGTTTCAGGCGCAGTGCAGGACAGATTTTCACACTGAAATC 240  
DB 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80  
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTCTGCGCAAGGTACACATTTTCCG 300  
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGTTCGACAGGAGCCGACTGGAGATCAAG 336  
DB 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

## RESULT 8

US-09-497-625A-13  
; Sequence 13, Application US/09497625A  
; Patent No. 6727349  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-004  
; CURRENT APPLICATION NUMBER: US/09/497,625A  
; CURRENT FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence



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;
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-13

Alignment Scores:
Pred. No.: 3,18e-68 Length: 112
Score: 577.00 Matches: 110
Percent Similarity: 98.21% Conservative: 0
Best Local Similarity: 98.21% Mismatches: 2
Query Match: 97.80% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-497-625A-13 (1-112)
QY 1 GATGTAGTATGATGACCCAGGCTCCACTCTCTTGGCCGTTACCCCTTGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAGAGCCCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGGCTTCAAGCGCCTTAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTACGGCAGTCAGGACGATGATGACGACAGATTTTCACATG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 9
US-09-809-739-18
; Sequence 18, Application US/09809739
; Patent No. 663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-18

Alignment Scores:
Pred. No.: 1,48e-67 Length: 112
Score: 572.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.95% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-18 (1-112)
QY 1 GATGTAGTATGATGACCCAGGCTCCACTCTCTTGGCCGTTACCCCTTGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAAGTCAGAGCCCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGGCTTCAAGCGCCTTAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTACGGCAGTCAGGACGATGATGACGACAGATTTTCACATG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 10
US-09-840-459-107
; Sequence 107, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-107

Alignment Scores:
Pred. No.: 1,48e-67 Length: 112
Score: 572.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.95% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-107 (1-112)
QY 1 GATGTAGTATGATGACCCAGGCTCCACTCTCTTGGCCGTTACCCCTTGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 61 ATCTCTTGAAGTCAAGTCAAGTCAGAGCCCTCTTAGATAGTGTGGAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
QY 121 TTTTCAGCAGAGCCAGGCTTCAAGCGCCTTAATCTATCTGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgGluLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTACGGCAGTCAGGACGATGATGACGACAGATTTTCACATG 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 ACAGAGTGGAGCTGAGGATCTTGAGTTTATTATGCTGCGCAGGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAAAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
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Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTCAGCAGAGCCAGCCAGCTCTCAAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGACAGATTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCCTGCGAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAAGGACCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 11
US-09-809-739-16
; Sequence 16, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-16

Alignment Scores:
Pred. No.: 2.73e-67 Length: 112
Score: 570.00 Matches: 109
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-16 (1-112)
Qy 1 GATGTAGTATGATGACCCAGCTCTCCACTCTCTGCGCGTTACCTTGGACAGCCAGCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
Qy 61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGATAGTATGATGAAAGACATTTTGAATTGG 120
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTCAGCAGAGCCAGCCAGCTCTCAAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGACAGATTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCCTGCGAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAAGGACCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 13
US-09-497-625A-14
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Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

RESULT 12
US-09-840-459-14
; Sequence 14, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-14

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Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-14 (1-112)
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Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTCAGCAGAGCCAGCCAGCTCTCAAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuValSerLysLeuAsp 60
Qy 181 TCTGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGACAGATTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGAGTTCGGAGTTTATTATTCCTGCGAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAAGGACCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

RESULT 13
US-09-497-625A-14
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; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

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Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: 2 Gaps: 0

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QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCT 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuTyrLeuValSerLysLeuAsp 60
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; Sequence 15, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0

; Sequence 14, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
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; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanized sequence
US-09-497-625A-14

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Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: 2 Gaps: 0

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Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 20
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Db 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyThrLeuValSerLysLeuAsp 40
QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCT 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGTTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTCAGGTC 240
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QY 241 AGCAGAGTGGAGCTGAGGATGTTGAGTGTATTTATTTCTGCTGCAAGTACACATTTTCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlyThrArgLeuGluLeuLys 112

RESULT 14
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; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
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; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-15

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QY  121  TTCAGCAGAGCCAGGCCAGTCTCCAAGGCGCCTTAATCTATCTGGTGTCTAAACTGGAC 180
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   41  LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60
QY  181  TCTGGAGTCCCTGACAGGTTTCAGCGGCAGTGGATCAGGGACAGATTTCACACTGAAATC 240
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QY  241  AGCAGAGTGGAGGCTTGAGATCTTGGAGTCTTATTATTCTGTCAGAGGTACACATTTTCGG 300
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   81  SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY  301  TACAGGTTCCGACAGGAGCCGACTGGAGATCAAG 336
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Job time : 15.2853 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Database : Published Applications AA Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	590	100.0	112	4	US-10-766-773-12
5	590	100.0	112	4	US-10-766-610-12
6	590	100.0	112	4	US-10-733-563-12
7	590	100.0	112	5	US-10-662-061-14
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14	577	97.8	112	3	US-09-840-459-13	Sequence 13, Appl
15	577	97.8	112	4	US-10-766-773-13	Sequence 13, Appl
16	577	97.8	112	4	US-10-766-610-13	Sequence 13, Appl
17	577	97.8	112	4	US-10-733-563-13	Sequence 13, Appl
18	577	97.8	112	5	US-10-662-061-15	Sequence 15, Appl
19	572	96.9	112	3	US-09-835-087-7	Sequence 7, Appl
20	572	96.9	112	3	US-09-809-739-18	Sequence 18, Appl
21	572	96.9	112	3	US-09-840-459-107	Sequence 107, App
22	572	96.9	112	4	US-10-766-610-107	Sequence 107, App
23	572	96.9	112	4	US-10-733-563-107	Sequence 107, App
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26	570	96.6	112	3	US-09-809-739-16	Sequence 16, Appl
27	570	96.6	112	3	US-09-840-459-14	Sequence 14, Appl
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32	565	95.8	112	3	US-09-835-087-6	Sequence 6, Appl
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36	565	95.8	112	4	US-10-766-610-15	Sequence 15, Appl
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ALIGNMENTS

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; Sequence 3, Application US/09835087  
; Patent No. US20020042370A1  
; GENERAL INFORMATION:  
; APPLICANT: Wayne W. Hancock  
; TITLE OF INVENTION: Method of Treating Graft Rejection Using  
; TITLE OF INVENTION: Inhibitors of CCR2 Function  
; FILE REFERENCE: 1855.2008-003  
; CURRENT APPLICATION NUMBER: US/09/835,087  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/549,448  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-09-835-087-3

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; Sequence 14, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-14
Alignment Scores:
Pred. No.: 1.76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-733-563-109 (1-336) x US-09-809-739-14 (1-112)
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RESULT 3
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; Sequence 12, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-840-459-12
Alignment Scores:
Pred. No.: 1.76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-733-563-109 (1-336) x US-09-840-459-12 (1-112)
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Qy 181 TCTGAGTCCCTGACAGGCTTACGGCGCAGTGTGATCAGGACAGATTTTCACACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATTTTGGAGTTTATTGCTGGCAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
Qy 301 TACAGTTCGGACAAGGACCGAGCTGGAGATCAAG 336
```

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 4

US-10-766-773-12

Sequence 12, Application US/10766773

Publication No. US20040126851A1

GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

FILE REFERENCE: 1855.1052-028

CURRENT APPLICATION NUMBER: US/10/766,773

CURRENT FILING DATE: 2004-01-27

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 106

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 112

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized sequence

US-10-766-773-12

Alignment Scores:

Pred. No.:	176e-55	Length:	112
Score:	590.00	Matches:	112
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-733-563-109 (1-336) x US-10-766-773-12 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTGCCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProIleSer 20

QY 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAenTtp 40

QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAap 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATTC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGCTGAGGATGTGGAGTTATTATTGCTGCAAGGTACACATTTTCG 300

Db 81 SerArgValGluAlaGluAaspValGlyValTyrCysTyrGlnGlyThrHisPhePro 100

QY 301 TACAGTTCGGACAGGGACCCGACTGGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 5

US-10-766-610-12

Sequence 12, Application US/10766610

Publication No. US20040132980A1

GENERAL INFORMATION:

APPLICANT: LaRosa, Gregory J.

APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter

APPLICANT: Jones, S. Tarran

APPLICANT: O'Brien, Siobhan H.

APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

FILE REFERENCE: 1855.1052-029

CURRENT APPLICATION NUMBER: US/10/766,610

CURRENT FILING DATE: 2004-01-27

PRIOR APPLICATION NUMBER: 09/840,459

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: PCT/US01/03537

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/497,625

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: 09/359,193

PRIOR FILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/121,781

PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 107

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 112

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Humanized sequence

US-10-766-610-12

Alignment Scores:

Pred. No.:	176e-55	Length:	112
Score:	590.00	Matches:	112
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-733-563-109 (1-336) x US-10-766-610-12 (1-112)

QY 1 GATGTAGTATGATGACCCAGTCTCCACTCTCTTGCCCGTTACCTTGGACAGCCAGCTCC 60

Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProIleSer 20

QY 61 ATCTCTTGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120

Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAenTtp 40

QY 121 TTTTCAGCAGAGCCAGCCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180

Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAap 60

QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGGATCAGGACAGATTTTCACACTGAAATTC 240

Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80

QY 241 AGCAGAGTGGAGCTGAGGATGTGGAGTTATTATTGCTGCAAGGTACACATTTTCG 300

Db 81 SerArgValGluAlaGluAaspValGlyValTyrCysTyrGlnGlyThrHisPhePro 100

QY 301 TACAGTTCGGACAGGGACCCGACTGGAGATCAAG 336

Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 6

US-10-733-563-12

Sequence 12, Application US/10733563

Publication No. US20040151721A1

GENERAL INFORMATION:

APPLICANT: O'Keefe, Theresa

APPLICANT: Ponath, Paul

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12
Alignment Scores:
Pred. No.: 1,76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-109 (1-336) x US-10-733-563-12 (1-112)
QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCCGTTACCCCTTGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTAGTAGTATGATGGAAGACATTTTGAATTGG 120
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTCAAGAGAGCCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGCGAGTGAGTATGATGAGGACAGATTTCACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCCTGCGAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTTCGACAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112
RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-733-563-12
Alignment Scores:
Pred. No.: 1,76e-55 Length: 112
Score: 590.00 Matches: 112
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-109 (1-336) x US-10-733-563-12 (1-112)
QY 1 GATGTAGTATGACCCAGTCTCCACTCTCTGCGCCGTTACCCCTTGGACAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTAGTAGTATGATGGAAGACATTTTGAATTGG 120
Db 21 IleserCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTCAAGAGAGCCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTGTCTAAACTGGAC 180
Db 41 PheGlnGlnArgProGlyGlnSerProArgArgLeuLeuTyrLeuValSerLysLeuAsp 60
QY 181 TCTGAGTCCCTGACAGGTTTCAGCGGCGAGTGAGTATGATGAGGACAGATTTCACTGAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCCTGCGAAGGTACACATTTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACACGTTTCGACAGGACCCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112
RESULT 7
US-10-662-061-14
; Sequence 14, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain
```



US-09-840-459-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-840-459-106 (1-114)

QY 4 GTAGTGTATGACCCAGTCTCCACTCTCTTCCCGGTACCCCTGGAGCAGCCCTCCATC 63  
DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAACACATTTTGAATTGGTTT 123  
DB 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGCCAGTCTCCAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
DB 42 GlnGlnArgProGlyGlnSerProArgAGLeuIleTyLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTCACACTGAAATCAGC 243  
DB 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGCGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTCCGTAC 303  
DB 82 ArgValGluAlaGlnAspValGlyValTyTyrcystTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACCTTCGGACAAAGGACCCGACTGGAGATCAAG 336  
DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 9

US-10-766-773-106  
; Sequence 106, Application US/10766773  
; Publication No. US20040126851A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-028  
; CURRENT APPLICATION NUMBER: US/10/766,773  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-10-766-773-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.98% Indels: 0  
DB: 4 Gaps: 0  
US-10-733-563-109 (1-336) x US-10-766-773-106 (1-114)

QY 4 GTAGTGTATGACCCAGTCTCCACTCTCTTCCCGGTACCCCTGGAGCAGCCCTCCATC 63  
DB 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSerIle 21  
QY 64 TCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTAGTGAAGAACACATTTTGAATTGGTTT 123  
DB 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41  
QY 124 CAGCAGAGCCAGCCAGTCTCCAGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183  
DB 42 GlnGlnArgProGlyGlnSerProArgAGLeuIleTyLeuValSerLysLeuAspSer 61  
QY 184 GGAGTCCCTGACAGGTTGACGGCAGTGTGATCAGGACAGATTTCACACTGAAATCAGC 243  
DB 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81  
QY 244 AGAGTGGAGCGCTGAGGATGTTGGAGTTTATTATTCGTCGCAAGGTACACATTTCCGTAC 303  
DB 82 ArgValGluAlaGlnAspValGlyValTyTyrcystTrpGlnGlyThrHisPheProTyr 101  
QY 304 ACCTTCGGACAAAGGACCCGACTGGAGATCAAG 336  
DB 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112

RESULT 10

US-10-766-610-106  
; Sequence 106, Application US/10766610  
; Publication No. US20040132980A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; FILE REFERENCE: 1855.1052-029  
; CURRENT APPLICATION NUMBER: US/10/766,610  
; CURRENT FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: 09/840,459  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 106  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized light chain  
US-10-766-610-106

Alignment Scores:  
Pred. No.: 7,98e-55 Length: 114  
Score: 584.00 Matches: 111  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.98% Indels: 0  
DB: 4 Gaps: 0

```
US-10-733-563-109 (1-336) x US-10-766-610-106 (1-114)
QY 4 GTAGTGATGACCCAGCTCTCCACTCTCTTCCCGGTACCCCTTGAGCAGCCAGCCTCCATC 63
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerIle 21
QY 64 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGGTTT 123
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41
QY 124 CAGCAGAGCGCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGGACTCT 183
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleIleIleIleIleIleIleIleIle 61
QY 184 GGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGAGCAGATTTTCCACTGAAAATCAGC 243
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81
QY 244 GGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGAGCAGATTTTCCACTGAAAATCAGC 243
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGCAAGGTACACATTTCCGTAC 303
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101
QY 304 ACGTTCGACAGGACCGGACCGACTGGAGATCAAG 336
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112
RESULT 11
US-10-733-563-106
; Sequence 106, Application US/10733563
; Publication No. US2004015121A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized light chain
US-10-733-563-106
Alignment Scores:
Pred. No.: 7,98e-55 Length: 114
Score: 584.00 Matches: 111
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.98% Indels: 0
Gaps: 4
US-10-733-563-109 (1-336) x US-10-733-563-106 (1-114)
QY 4 GTAGTGATGACCCAGCTCTCCACTCTCTTCCCGGTACCCCTTGAGCAGCCAGCCTCCATC 63
Db 2 ValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSerIle 21
QY 64 TCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGGTTT 123
Db 22 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrpPhe 41
QY 124 CAGCAGAGCGCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGGACTCT 183
Db 42 GlnGlnArgProGlyGlnSerProArgLeuIleIleIleIleIleIleIleIleIle 61
QY 184 GGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGAGCAGATTTTCCACTGAAAATCAGC 243
Db 62 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIleSer 81
QY 244 AGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGCAAGGTACACATTTCCGTAC 303
Db 82 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProTyr 101
QY 304 ACGTTCGACAGGACCGGACCGACTGGAGATCAAG 336
Db 102 ThrPheGlyGlnGlyThrArgLeuGluIleLys 112
RESULT 12
US-09-835-087-4
; Sequence 4, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-835-087-4
Alignment Scores:
Pred. No.: 4.62e-54 Length: 112
Score: 577.00 Matches: 110
Percent Similarity: 98.21% Conservative: 0
Best Local Similarity: 98.21% Mismatches: 2
Query Match: 97.80% Indels: 0
Gaps: 3
US-10-733-563-109 (1-336) x US-09-835-087-4 (1-112)
QY 1 GATGTAGTGATGACCCAGCTCTCCACTCTCTTCCCGGTACCCCTTGAGCAGCCAGCCTCC 60
Db 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlnProAlaSer 20
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGATAGTGTGAAAGACATTTTGAATTGG 120
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTGAGCAGAGCGCAGGCGCAGTCTCCAGGCGCCTAATCTATCTGGTCTCTAAACTGGAC 180
Db 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleIleIleIleIleIleIleIleIle 60
QY 181 TCTGAGTCCCTGACAGGTTCCAGCGCAGTGGATCAGGAGCAGATTTTCCACTGAAAATC 240
Db 61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGCGCAAGGTACACATTTCCG 300
Db 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGCAAGGACCGGACCGACTGGAGATCAAG 336
Db 101 TyrThrPheGlyGlnGlyThrArgLeuGluIleLys 112
RESULT 13
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US-09-809-739-15
; Sequence 15, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-15

Alignment Scores:
Pred. No.: 4,62e-54 Length: 112
Score: 577.00 Matches: 110
Percent Similarity: 98.21% Conservative: 0
Best Local Similarity: 98.21% Mismatches: 2
Query Match: 97.80% Indels: 0
DB: 3 Gaps: 0

US-10-733-563-109 (1-336) x US-09-809-739-15 (1-112)
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QY 61 ATCTCTTGAAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGGAAGACATTTTGAATTGG 120
DB 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTCAGCAGAGCCAGCCAGCTCCAGGCGCCTTAATCTATCTGGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTACGGCAGTGTGATCAGGACAGATTTTCACTGAAATC 240
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QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTTATTATTGCTGCAAGGTACACATTTTCG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTTGGACAGGAGCCGACTGGAGATCAAG 336
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US-09-840-459-13
; Sequence 13, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02

US-09-809-739-13
; Sequence 13, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
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; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 112  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized sequence  
US-10-766-773-13

Alignment Scores:  
Pred. No.: 4.62e-54 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-109 (1-336) x US-10-766-773-13 (1-112)

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   21 IleSerCysLysSerSerGlnSerLeuLeuAapSerAspGlyLysThrPheLeuAsnTrp 40
Qy 121 TTTCAGCAGAGCCAGCCAGCTCTCCAGGCGCCTAATCTATCTGGTCTAAACTGGAC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   41 LeuLeuGlnArgProGlyGlnSerProArgArgLeuIleTyrLeuValSerLysLeuAap 60
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Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCTGGCAAGGTACACATTTTCCG 300
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   81 SerArgValGluAlaGluAapValGlyValTyrCysTrpGlnGlyThrHisPhePro 100
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: January 28, 2006, 09:31:11  
Job time : 42.033 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 4.28829 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-109

Perfect score: 590

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=PublishedApplications\_AA\_New -QFMT=faetan -SUFFIX=n2p.rapbn -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications\_AA\_New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	572	96.9	112	7	US-11-075-184A-7
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5	565	95.8	112	7	US-11-075-184A-6
6	542	91.9	132	6	US-10-789-273-11
7	536	90.8	112	7	US-11-075-184A-1
8	536	90.8	132	6	US-10-789-273-5
9	520	88.1	132	6	US-10-789-273-2
10	510	86.4	253	7	US-11-054-515-1964
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					Sequence 4, Appli
					Sequence 7, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 11, Appli
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 2, Appli

11	507	85.9	112	6	US-10-477-950-4	Sequence 4, Appli
12	491.5	83.3	244	7	US-11-054-515-1991	Sequence 1991, Ap
13	490.5	83.1	261	7	US-11-056-825-2	Sequence 2, Appli
14	485.5	82.3	259	7	US-11-056-825-7	Sequence 7, Appli
15	483	81.9	113	7	US-11-054-689-122	Sequence 122, App
16	480	81.4	139	7	US-11-128-900-25	Sequence 25, Appl
17	480	81.4	139	7	US-11-128-900-114	Sequence 114, App
18	474	80.3	132	6	US-10-489-866-30	Sequence 30, Appl
19	470	79.7	100	7	US-11-054-669-75	Sequence 75, Appl
20	470	79.7	100	7	US-11-054-669-76	Sequence 76, Appl
21	470	79.7	100	7	US-11-084-584-103	Sequence 103, App
22	470	79.7	100	7	US-11-084-584-107	Sequence 107, App
23	470	79.7	100	7	US-11-128-900-113	Sequence 113, App
24	470	79.7	100	7	US-11-004-590-82	Sequence 82, Appl
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26	459	77.8	112	7	US-11-012-353-57	Sequence 57, Appl
27	457	77.5	112	7	US-11-012-353-61	Sequence 61, Appl
28	457	77.5	131	7	US-11-012-353-63	Sequence 63, Appl
29	456	77.3	112	7	US-11-012-353-65	Sequence 65, Appl
30	456	77.3	131	7	US-11-012-353-67	Sequence 67, Appl
31	451	76.4	112	7	US-11-012-353-60	Sequence 60, Appl
32	451	76.4	113	6	US-10-834-397-15	Sequence 15, Appl
33	447	75.8	113	6	US-10-932-334-60	Sequence 60, Appl
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36	446	75.6	113	6	US-10-932-334-59	Sequence 59, Appl
37	445	75.4	112	7	US-11-012-353-55	Sequence 55, Appl
38	445	75.4	112	7	US-11-012-353-56	Sequence 56, Appl
39	445	75.4	263	7	US-11-089-286-66	Sequence 66, Appl
40	444	75.3	144	7	US-11-055-163-16	Sequence 16, Appl
41	443	75.1	113	6	US-10-932-334-61	Sequence 61, Appl
42	443	75.1	149	7	US-11-089-266-2	Sequence 2, Appli
43	443	75.1	239	7	US-11-139-499-6	Sequence 6, Appli
44	441	74.7	113	6	US-10-489-866-20	Sequence 20, Appl
45	441	74.7	116	7	US-11-065-943-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-11-075-184A-3  
; Sequence 3, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; TITLE OF INVENTION: Receptor Antagonists  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RA  
US-11-075-184A-3

Alignment Scores:  
Pred. No.: 2.96e-57 Length: 112  
Score: 590.00 Matches: 112  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-3 (1-112)

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QY 301 TACAGCTTCGGACAAGGACCGGACTCGAGATCAAG 336  
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## RESULT 2

US-11-075-184A-4  
; Sequence 4, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-4

Alignment Scores:  
Pred. No.: 7,81e-56 Length: 112  
Score: 577.00 Matches: 110  
Percent Similarity: 98.21% Conservative: 0  
Best Local Similarity: 98.21% Mismatches: 2  
Query Match: 97.80% Indels: 0  
DB: 7 Gaps: 0

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QY 181 TCTGGAGTCCCTGACAGGCTTCACAGGCTTCAGCGGCGAGTGGATCAGGACAGATTTTCACACTGAAATC 240

Db |||||  
61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80  
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81 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 100  
QY 301 TACAGCTTCGGACAAGGACCGGACTCGAGATCAAG 336  
Db |||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112

## RESULT 3

US-11-075-184A-7  
; Sequence 7, Application US/11075184A  
; Publication No. US20050260139A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: PAIRET, Michel  
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2  
; FILE REFERENCE: 1/1669  
; CURRENT APPLICATION NUMBER: US/11/075,184A  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: EP 04 007 635.8  
; PRIOR FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,  
; OTHER INFORMATION: 1D9RKE  
US-11-075-184A-7

Alignment Scores:  
Pred. No.: 2,75e-55 Length: 112  
Score: 572.00 Matches: 109  
Percent Similarity: 97.32% Conservative: 0  
Best Local Similarity: 97.32% Mismatches: 3  
Query Match: 96.95% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-7 (1-112)

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QY 121 TTTCAGCAGAGCCAGGCGCAGTCTCAAGGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180  
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QY 301 TACAGCTTCGGACAAGGACCGGACTCGAGATCAAG 336  
Db |||||  
101 TyrThrPheGlyGlnGlyThrArgLeuGluLeuLys 112

## RESULT 4

US-11-075-184A-5  
; Sequence 5, Application US/11075184A

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; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; US-11-075-184A-5

Alignment Scores:
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Score: 570.00 Matches: 109
Percent Similarity: 97.32% Conservativeness: 0
Best Local Similarity: 97.32% Mismatches: 3
Query Match: 96.61% Indels: 0
DB: Gaps: 0

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QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAGTGAAGACATTTTGAATTGG 120
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
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QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTATTATTGCTGCAAGGTACACATTTTCGG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
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RESULT 5
; Sequence 6, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
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; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized Murine 1D9 antibody kappa light chain variable region,
; US-11-075-184A-6

Alignment Scores:
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Score: 565.00 Matches: 108
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Best Local Similarity: 96.43% Mismatches: 4
Query Match: 95.76% Indels: 0
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-6 (1-112)
QY 1 GATGTAGTGTGATGACCCAGGCTCTCCACTCTCTTGGCCCGTTACCTTGGACAGCAGCCTCC 60
DB 1 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyHisProAlaSer 20
QY 61 ATCTCTTGCAGTCAAGTCAGAGCCTCTTAGATAGTGTGATGAGTGAAGACATTTTGAATTGG 120
DB 21 IleSerCysLeuSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
QY 121 TTTTCAGCAGAGCCAGGCGCAGTCTCCAGGCGCCTTAATCTATCTGTGTCTAACTGGAC 180
DB 41 LeuLeuGlnArgProGlyGlnSerProArgLeuIleTyrLeuValSerLysLeuAsp 60
QY 181 TCTGGAGTCCCTGACAGGTTTCAGCGCAGTGTGATCAGGACAGATTTTCACACTGAAATC 240
DB 61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGAGTTATTATTGCTGCAAGGTACACATTTTCGG 300
DB 81 SerArgValGluAlaGluAspValGlyValTyrTyrCysTrpGlnGlyThrHisPhePro 100
QY 301 TACAGTTCGGACAGGACCCGACTGGAGATCAAG 336
DB 101 TyrThrPheGlyGlyThrArgLeuGluIleLys 112

RESULT 6
US-10-789-273-11
; Sequence 11, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELM-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-789-273-11
```

Alignment Scores:  
Pred. No.: 5,26e-52 Length: 132  
Score: 542.00 Matches: 102  
Percent Similarity: 96.43% Conservative: 6  
Best Local Similarity: 91.07% Mismatches: 4  
Query Match: 91.86% Indels: 0  
DB: 6 Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-11 (1-132)

```
QY 1 GATGTAGTGAACCCAGCTCTCCACTCTCTGGCCGCTTACCTTGGACAGCCAGCCCTCC 60
   |||
Db 21 AspValValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 40
   |||
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGTAGTGTGATGGAAGACATTTTGAATTGG 120
   |||
Db 41 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrTyrLeuAsnTrp 60
   |||
QY 121 TTTGAGGAGGCGAGGCGAGCTCTCAAGGCGCCTTAATCTATCTGGTGTCTAAACTGGAC 180
   |||
Db 61 LeuLeuGlnLysProGlyGlnSerProGlnArgLeuIleTyrLeuValSerLysLeuAsp 80
   |||
QY 181 TCTGAGTCCCTGACAGCTTACAGGCGAGTGTGATCAGGACAGATTTTACACTGAAATC 240
   |||
Db 81 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 100
   |||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTTGCTGCGAAGGTACACATTTCCG 300
   |||
Db 101 SerArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPhePro 120
   |||
QY 301 TACAGTTCGACAGGACCGGACTGGAGATCAAG 336
   |||
Db 121 ArgThrPheGlyGlnGlyThrLysValGluLys 132
```

## RESULT 7

```
US-11-075-184A-1
; Sequence 1, Application US/11075184A
; Publication No. US20050260139A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: PAIRET, Michel
; TITLE OF INVENTION: Pharmaceutical Compositions based on Anticholinergics and CCR2
; TITLE OF INVENTION: Receptor Antagonists
; FILE REFERENCE: 1/1669
; CURRENT APPLICATION NUMBER: US/11/075,184A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: EP 04 007 635.8
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Murine 1D9 antibody kappa light chain variable (VK) region;
; OTHER INFORMATION: presumably Mus musculus
US-11-075-184A-1
```

Alignment Scores:  
Pred. No.: 2,38e-51 Length: 112  
Score: 536.00 Matches: 100  
Percent Similarity: 95.54% Conservative: 7  
Best Local Similarity: 89.29% Mismatches: 5  
Query Match: 90.85% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-109 (1-336) x US-11-075-184A-1 (1-112)

```
QY 1 GATGTAGTGAACCCAGCTCTCCACTCTCTGGCCGCTTACCTTGGACAGCCAGCCCTCC 60
   |||
Db 1 AspValValMetThrGlnThrProLeuThrLeuSerValThrValGlyHisProAlaSer 20
   |||
```

```
QY 61 ATCTCTTCAAGTCAAGTCAGAGCCTCTTAGTAGTGTGATGGAAGACATTTTGAATTGG 120
   |||
Db 21 IleSerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrPheLeuAsnTrp 40
   |||
QY 121 TTTGAGGAGGCGAGGCGAGCTCTCAAGGCGCCTTAATCTATCTGGTGTCTAAACTGGAC 180
   |||
Db 41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerLysLeuAsp 60
   |||
QY 181 TCTGAGTCCCTGACAGGTTTACAGGCGAGTGTGATCAGGACAGATTTTACACTGAAATC 240
   |||
Db 61 SerGlyValProAspArgPheThrGlySerGlyThrAspPheThrLeuLysIle 80
   |||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGAGTTTATTATTTGCTGCGAAGGTACACATTTCCG 300
   |||
Db 81 SerArgValGluAlaGluAspLeuGlyValTyrCysTrpGlnGlyThrHisPhePro 100
   |||
QY 301 TACAGTTCGACAGGACCGGACTGGAGATCAAG 336
   |||
Db 101 TyrThrPheGlyGlyThrLysLeuGluLys 112
```

## RESULT 8

```
US-10-789-273-5
; Sequence 5, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-789-273-5
```

Alignment Scores:  
Pred. No.: 2,38e-51 Length: 132  
Score: 536.00 Matches: 101  
Percent Similarity: 96.40% Conservative: 6  
Best Local Similarity: 90.99% Mismatches: 4  
Query Match: 90.85% Indels: 0  
DB: 6 Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-5 (1-132)

```
QY 4 GTAGTGAACCCAGCTCTCCACTCTCTGGCCGCTTACCTTGGACAGCCAGCCCTCCATC 63
   |||
Db 22 ValValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSerIle 41
   |||
QY 64 TCTTGAAGTCAAGTCAGAGCCTCTTAGTAGTGTGATGGAAGACATTTTGAATTGGTTT 123
   |||
Db 42 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrTyrLeuAsnTrpLeu 61
   |||
QY 124 CAGCAGGCGAGGCGAGCTCTCAAGGCGCCTTAATCTATCTGGTGTCTAAACTGGACTCT 183
   |||
Db 62 LeuGlnLysProGlyGlnSerProGlnArgLeuIleTyrLeuValSerLysLeuAspSer 81
   |||
```



```
QY 184 GGAGTCCCTGACAGGTTACGGCGCAGTGTGATCAGGACAGATTTCACACTGAAATCAGC 243
Db |||||
82 GlyValProAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuIleSer 101
QY 244 AGAGTGGAGCGCTGAGGATCTGGAGTTTATTATTCCTGCGCAGGTACACATTTCCGTAC 303
Db |||||
102 ArgValGluAlaGluAspValGlyValTyrCysTrpGlnGlyThrHisPheProArg 121
QY 304 ACGTTTCGGAACAAGGACCGGACTGGAGATCAAG 336
Db |||||
122 ThrPheGlyGlnGlyThrIysValGluIleLys 132

RESULT 9
US-10-789-273-2
; Sequence 2, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurik
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-789-273-2

Alignment Scores:
Pred. No.: 1,34e-49 Length: 132
Score: 520.00 Matches: 96
Percent Similarity: 95.50% Conservative: 10
Best Local Similarity: 86.43% Mismatches: 5
Query Match: 88.14% Indels: 0
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-10-789-273-2 (1-132)
QY 4 GTAGTGTGATGATGACCCAGTCTCCACTCTCTGCGGTACCTTGGACAGCAGCCTCCATC 63
Db |||||
22 ValValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSerIle 41
QY 64 TCTTGAAGTCAAGTCAGAGCTCTTAGATAGTGTGAAAGACACATTTTGAATTGGTTT 123
Db |||||
42 SerCysLysSerSerGlnSerLeuLeuAspSerAspGlyLysThrLeuAsnTrpLeu 61
QY 124 CAGCAGAGCCAGCGGCGAGTCTCAAGCGCCTAAATCTATCTGGTGTCTAAACTGGACTCT 183
Db |||||
62 LeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuValSerIysLeuAspSer 81
QY 184 GGAGTCCCTGACAGGTTACGGCGCAGTGTGATCAGGACAGATTTCACACTGAAATCAGC 243
Db |||||
82 GlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuIleSer 101
QY 244 AGAGTGGAGCGCTGAGGATCTGGAGTTTATTATTCCTGCGCAGGTACACATTTCCGTAC 303
Db |||||
102 ArgIleGluAlaGluAspLeuGlyLeuTyrCysTrpGlnGlyThrHisPheProArg 121
QY 304 ACGTTTCGGAACAAGGACCGGACTGGAGATCAAG 336
```

```
Db |||||
122 ThrPheGlyGlyGlyThrIysLeuGluIleLys 132

RESULT 10
US-11-054-515-1964
; Sequence 1964, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1964
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1964

Alignment Scores:
Pred. No.: 1.67e-48 Length: 253
Score: 510.00 Matches: 97
Percent Similarity: 92.86% Conservative: 7
Best Local Similarity: 86.61% Mismatches: 8
Query Match: 86.44% Indels: 0
DB: Gaps: 0

US-10-733-563-109 (1-336) x US-11-054-515-1964 (1-253)
QY 1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGGTACCTTGGACAGCAGCCTCC 60
Db |||||
141 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 160
QY 61 ATCTCTTGAAGTCAAGTCAGAGCTCTTAGATAGTGTGAAAGACACATTTTGAATTGG 120
Db |||||
161 IleSerCysArgSerSerGlnSerLeuValTyrSerAspGlyAsnThrTyrLeuAsnTrp 180
QY 121 TTTTCAGCAGAGCCAGCGCAGTCTCAAGCGCCTAAATCTATCTGGTGTCTAAACTGGAC 180
Db |||||
181 PheGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 200
QY 181 TCTGAGTCCCTGACAGGTTACGGCGCAGTGTGATCAGGACAGATTTCACACTGAAATC 240
Db |||||
201 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuIleSer 220
QY 241 AGCAGAGTGGAGCGCTGAGGATCTGGAGTTTATTATTCCTGCGCAGGTACACATTTCCG 300
Db |||||
221 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnAlaThrArgTrpPro 240
QY 301 TACACGTTCGGAACAAGGACCGGACTGGAGATCAAG 336
Db |||||
```

```

Db      241 PheThrPheGlyGlnGlyThrLysMetGluLeuLys 252
RESULT 11
US-10-477-950-4
; Sequence 4, Application US/10477950
; Publication No. US20050260207A1
; GENERAL INFORMATION:
; APPLICANT: Krka tovarna zdravil, d.d., Novo mesto
; TITLE OF INVENTION: Monoclonal antibody neutralising Cathepsin B activity
; FILE REFERENCE: 28880
; CURRENT APPLICATION NUMBER: US/10/477,950
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: SI/P200100132
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mouse
US-10-477-950-4

Alignment Scores:
Pred. No.:      3,548-48      Length:      112
Score:          507.00      Matches:      95
Percent Similarity: 94.64%      Conservative: 11
Best Local Similarity: 84.82%      Mismatches: 6
Query Match:      85.93%      Indels:      0
DB:              6          Gaps:      0

US-10-733-563-109 (1-336) x US-10-477-950-4 (1-112)
QY      1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGCGTTACCTTGGACGAGCCCTCC 60
      112
Db      1 AspLeuValMetThrGlnThrProLeuThrLeuSerValThrIleGlyGlnProAlaSer 20
      112
QY      61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGTAGTGTAGTGAAGACATTTTGAATTGG 120
      120
Db      21 IleSerCysLeuSerSerGlnSerLeuLeuTyrSerAsnGlyLysThrTyrLeuAsnTrp 40
      40
QY      121 TTTCAGCAGAGCCGAGCCAGTCTCCAGGCGCTCAAGCGCCTAATCTATCTGCTCTAACTGGAC 180
      180
Db      41 LeuLeuGlnArgProGlyGlnSerProLysArgLeuIleTyrLeuLeuSerLysLeuAsp 60
      60
QY      181 TCTGAGTCCCTGACAGGTTGACGGCGAGTGTGATCAGGACAGATTTTCACACTGAAAATC 240
      240
Db      61 SerGlyValProAspArgPheThrGlySerGlySerGlyThrAspPheThrLeuLysIle 80
      80
QY      241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGGCAAGGTACACATTTCCG 300
      300
Db      81 SerArgValGluAlaGluAspLeuGlyValTyrCysValGlnGlyThrHisPhePro 100
      100
QY      301 TACAGTTCCGACAGGACCCGACTGGAGATCAAG 336
      336
Db      101 TyrThrPheGlyGlyGlyThrLysLeuGluLeuLys 112
      112
RESULT 12
US-11-054-515-1991
; Sequence 1991, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoespecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1991

Alignment Scores:
Pred. No.:      1,76e-46      Length:      244
Score:          491.50      Matches:      98
Percent Similarity: 90.18%      Conservative: 3
Best Local Similarity: 87.50%      Mismatches: 10
Query Match:      83.31%      Indels:      1
DB:              7          Gaps:      1

US-10-733-563-109 (1-336) x US-11-054-515-1991 (1-244)
QY      1 GATGTAGTGTGATGACCCAGTCTCCACTCTCTGCGCGTTACCTTGGACGAGCCCTCC 60
      60
Db      133 AspValValMetThrGlnSerProLeuSerLeuProValThrLeuGlyGlnProAlaSer 152
      152
QY      61 ATCTCTTCAAGTCAAGTCAGAGCTCTTAGTAGTGTAGTGAAGACATTTTGAATTGG 120
      120
Db      153 IleSerCysArgSerSerGlnSerLeuValHisSerAspGlyAsnThrTyrLeuAsnTrp 172
      172
QY      121 TTTCAGCAGAGCCGAGCCAGTCTCCAGGCGCTCAAGCGCCTAATCTATCTGCTCTAACTGGAC 180
      180
Db      173 PheGlnGlnArgProGlyGlnSerProArgLeuIleTyrLysValSerAsnArgAsp 192
      192
QY      181 TCTGAGTCCCTGACAGGTTGACGGCGAGTGTGATCAGGACAGATTTTCACACTGAAAATC 240
      240
Db      193 PheGlyValProAspArgPheSerGlySerGlySerGlyThrTyrPheThrLeuLysIle 212
      212
QY      241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTGCTGGCAAGGTACACATTTCCG 300
      300
Db      213 SerArgValGluAlaGluAspValGlyValTyrCysMetGlnGlyThrHis---Arg 231
      231
QY      301 TACAGTTCCGACAGGACCCGACTGGAGATCAAG 336
      336
Db      232 IleThrPheGlyGlnGlyThrArgLeuGluLeuLys 243
      243
RESULT 13
US-11-056-825-2
; Sequence 2, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SGRP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13

```



```
Qy 181 TCTGGAGTCCCTGACAGGTTACCGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240
Db |||||
61 SerGlyValProAspArgPheSerGlySerGlyThrAspPheThrLeuLysIle 80
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGAGTTTATTATTCCTGGCAAGGTACACATTTCCG 300
Db |||||
81 SerArgValGluAlaGluAspValGlyValTyrCysLeuGlnValThrHisValPro 100
Qy 301 TACACGTTCCGACAGAGGACCGACTGGAGATCAAG 336
Db ::|||
101 PheThrPheGlyProGlyThrLysValAspIleLys 112
```

Search completed: January 28, 2006, 09:32:14  
Job time : 5.28829 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 172.928 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-110  
Perfect score: 1765  
Sequence: 1 ASTGKPSVFPLAPSKSTSG.....MHEALHNHYTKSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*  
9: geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	330	8	Adq89332 Human imm
2	1765	100.0	330	9	Aeb09605 Human IgG
3	1765	100.0	333	8	Adj95914 Human IgG
4	1765	100.0	333	8	Adq89336 Human imm
5	1765	100.0	333	9	Aeb09609 Human IgG
6	1765	100.0	356	8	Adj95974 Immunoglob
7	1765	100.0	444	3	AAY32263 Humanised
8	1765	100.0	448	8	Adp88447 Antibody
9	1765	100.0	448	8	Adp88431 Antibody
10	1765	100.0	462	9	Aeb08800 Anti-NOGO
11	1765	100.0	467	6	AdA47334 TRX1 heav
12	1765	100.0	467	6	AdA47336 TRX1 heav
13	1765	100.0	467	8	Adp88446 Antibody
14	1765	100.0	467	8	Adp88430 Antibody
15	1765	100.0	467	8	Adq87966 Heavy cha
16	1765	100.0	467	8	Adq87974 Heavy cha
17	1765	100.0	473	5	Abg70743 Mouse/hum
18	1765	100.0	475	8	Adl23051 Mouse/hum
19	1765	100.0	475	8	Adl23054 Humanised
20	1765	100.0	475	8	AdS88803 Humanised
21	1765	100.0	475	8	AdS88792 A mouse/h
22	1758	99.6	469	7	Adl23199 Human ant
23	1756	99.5	330	4	Aab04071 Zcytor 10
24	1756	99.5	330	5	Aam47856 Human Ig-

## ALIGNMENTS

RESULT 1  
ADQ89332  
ID ADQ89332 standard; protein; 330 AA.  
XX  
AC ADQ89332;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human immunoglobulin protein #44.  
XX  
KW Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;  
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
PN US2004I51721-A1.  
XX  
PD 05-AUG-2004.  
XX  
PF 10-DEC-2003; 2003US-00733563.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
PR 17-OCT-2002; 2002US-00272899.  
XX  
PA (OKEE/) O'KEEFE T.  
XX (PONA/) PONA P.  
PI O'Keefe T, Ponath P;  
XX WPI; 2004-580175/56.  
XX  
PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
PS Claim 1; SEQ ID NO 110; 128pp; English.  
XX  
CC The invention relates to humanised immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanised immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanised  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions

25 1756 99.5 330 5 AAE21960 Human dea  
26 1756 99.5 330 5 ABB81641 Human IGG  
27 1756 99.5 330 5 ABB05736 Human imm  
28 1756 99.5 330 6 ABE71856 Human IGG  
29 1756 99.5 330 6 ABE32915 Human imm  
30 1756 99.5 330 6 AAE32627 Human imm  
31 1756 99.5 330 6 ABR82103 Human DR6  
32 1756 99.5 330 6 AAO31102 Human A2-  
33 1756 99.5 330 6 ABR55836 Anti-Ang-  
34 1756 99.5 330 6 AAO30893 Human imm  
35 1756 99.5 330 7 ADF11389 Anti-OPGL  
36 1756 99.5 330 7 ADE97351 Human IGG  
37 1756 99.5 330 7 ADF83605 Cytokine  
38 1756 99.5 330 7 ADF75001 Human Ig  
39 1756 99.5 330 8 ADM41537 Anti-Inte  
40 1756 99.5 330 8 ADM68911 Human IGG  
41 1756 99.5 330 8 ADR43460 Heavy cha  
42 1756 99.5 330 8 ADR31605 Human IGG  
43 1756 99.5 330 8 ADS87909 Anti-IFN-  
44 1756 99.5 330 8 ADN33230 IGG1-CH h  
45 1756 99.5 330 8 ADS94906 Anti-IFN-

CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV  
CC infection and atherosclerosis. This sequence represents a human  
CC immunoglobulin protein of the invention.

KW immunoglobulin leader molecule; immunoglobulin domain;  
KW immunoglobulin therapeutic molecule; monobody; cancer; immunoglobulin G;  
KW Igg; heavy chain constant region; FcRmut; human.

XX Homo sapiens.  
OS Synthetic.

PN US2004033561-A1.

XX 19-FEB-2004.

XX 17-OCT-2002; 2002US-00272899.

XX 19-OCT-2001; 2001US-0350166P.

PR 26-JUN-2002; 2002US-0392364P.

XX (MILL-) MILLENNIUM PHARM INC.

PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;

XX WPI; 2004-180050/17.  
DR N-PSDB; ADJ95913.

PT New isolated nucleic acid molecules having an immunoglobulin cassette  
PT construct, useful for producing immunoglobulin therapeutic molecules  
PT termed monobodies, used as a therapeutic group in cancer disorders.

XX Example 2; SEQ ID NO 10; 84pp; English.

XX The invention describes an isolated nucleic acid molecule comprising an  
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
CC comprises an immunoglobulin leader molecule operably linked to a stable  
CC immunoglobulin domain region. The methods and compositions of the present  
CC invention are useful for producing immunoglobulins, in particular  
CC immunoglobulin therapeutic molecules termed monobodies, used as a  
CC therapeutic group in cancer disorders. This is the amino acid sequence of  
CC the human immunoglobulin G (IgG) heavy chain constant region mutant  
CC FcRmut used in the creation of immunoglobulin DNA cassette constructs.

XX Sequence 333 AA;

Query Match 100.0%; Score 1765; DB 8; Length 333;  
Best Local Similarity 100.0%; Pred. No. 4.9e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 60  
Db 4 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 63

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELAGA 120

Db 64 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELAGA 123

Qy 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Db 124 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 183

Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Db 184 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 303

Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

Db 304 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 333

RESULT 4

ADQ89336

ID ADQ89336 standard; protein; 333 AA.

XX

AC

XX

DT

XX

DE

XX

KW

KW

KW

XX

OS

XX

PN

XX

XX

PD

XX

PF

XX

PR

PR

PR

XX

PA

PA

XX

PI

XX

DR

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Query Match 100.0%; Score 1765; DB 8; Length 333;

Best Local Similarity 100.0%; Pred. No. 4.9e-124;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 60

Db 4 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTEPAVLQSS 63

Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELAGA 120

Db 64 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELAGA 123

Qy 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

Db 124 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 183

Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Db 184 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 243

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 303

Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 330  
 |||||  
 Db 304 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 333  
 |||||

RESULT 5

AEBO9609

ID AEB09609 standard; protein; 333 AA.

XX AC AEB09609;

XX 08-SEP-2005 (first entry)

XX Human IgG1 constant region FcRmut SEQ ID NO 114.

XX antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
 KW antibody engineering; therapeutic; diagnosis; inflammation;  
 KW autoimmune disease; immune disorder; graft rejection; HIV infection;  
 KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
 KW light chain constant region.

XX Homo sapiens.

XX W02005060368-A2.

XX 07-JUL-2005.

XX 10-DEC-2003; 2003WO-US039599.

XX 10-DEC-2003; 2003WO-US039599.

XX (MILL-) MILLENNIUM PHARM INC.

XX O'keefe T, Ponath P;

XX WPI; 2005-488561/49.

XX N-PSDB; AEB09610.

XX New humanized immunoglobulin or its antigen binding portion having  
 PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
 PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
 PT diseases.

XX Disclosure; SEQ ID NO 114; 192pp; English.

XX The invention describes a humanized immunoglobulin (I) or its antigen  
 CC binding portion having binding specificity for CC-chemokine receptor 2  
 CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
 CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
 CC sequence, given in specification or its portion, and the light chain  
 CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
 CC in specification. Also described are: a humanized immunoglobulin heavy  
 CC chain, or its antigen binding fragment, having binding specificity for  
 CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
 CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
 CC immunoglobulin light chain, or its antigen binding fragment, having  
 CC binding specificity for CCR2 and comprising the amino acid sequence of  
 CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
 CC sequence, given in specification. The following are disclosed: isolated  
 CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a  
 CC construct comprising nucleic acid molecule encoding (I); and host cell  
 CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic  
 CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
 CC reducing inflammatory response, for use in the treatment of diseases  
 CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
 CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
 CC infection and monocytic-mediated disorders such as atherosclerosis. (I) Is  
 CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.  
 CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
 CC fluid), and for modulating binding function and/or leukocyte trafficking  
 CC modulated by CCR2. This is the amino acid sequence of human IgG1 constant

CC region FcRmut used in the creation of a humanized anti-CCR2-antibody.

XX Sequence 333 AA;

SO

Query Match 100.0%; Score 1765; DB 9; Length 333;  
 Beat Local Similarity 100.0%; Pred. No. 4.9e-124; Indels 0; Gaps 0;  
 Matches 330; Conservative 0; Mismatches 0;

Qy 1 ASTKGPSPVFPPLAPSSKSTSGTAAALGCLVKDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 60  
 Db 4 ASTKGPSPVFPPLAPSSKSTSGTAAALGCLVKDYPPPEVTVSWNSGALTSGVHTFPVAVLQSS 63  
 Qy 61 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEVPKSCDKTHTCPCPAPELAGA 120  
 Db 64 GLYSLSVSVTVPSSSLGTQTYICNVNHPKSNKTKVDKKEVPKSCDKTHTCPCPAPELAGA 123  
 Qy 121 PSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 180  
 Db 124 PSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 183  
 Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSSRDE 240  
 Db 184 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSSRDE 243  
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 300  
 Db 244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLKLTVDKSRW 303  
 Qy 301 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 330  
 Db 304 QQGNVFCSCVMHEALHNNHYTKSLSLSPGK 333

## RESULT 6

ADJ95974

ID ADJ95974 standard; protein; 356 AA.

XX AC ADJ95974;

XX 06-MAY-2004 (first entry)

XX Immunoglobulin DNA cassette polypeptide seqid 70.

XX cytostatic; antibody therapy; immunoglobulin cassette construct;  
 KW immunoglobulin leader molecule; immunoglobulin domain;  
 KW immunoglobulin therapeutic molecule; monobody; cancer.

XX OS Synthetic.

XX UN2004033561-A1.

XX 19-FEB-2004.

XX 17-OCT-2002; 2002US-00272899.

XX 19-OCT-2001; 2001US-0350166P.

XX 26-JUN-2002; 2002US-0392364P.

XX (MILL-) MILLENNIUM PHARM INC.

XX O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;

XX WPI; 2004-180050/17.

XX N-PSDB; ADJ95973.

XX New isolated nucleic acid molecules having an immunoglobulin cassette  
 PT construct, useful for producing immunoglobulin therapeutic molecules  
 PT termed monobodies, used as a therapeutic group in cancer disorders.

XX Disclosure; SEQ ID NO 70; 84pp; English.

XX The invention describes an isolated nucleic acid molecule comprising an  
 CC immunoglobulin cassette construct, wherein the immunoglobulin cassette



CC comprises an immunoglobulin leader molecule operably linked to a stable  
 CC immunoglobulin domain region. The methods and compositions of the present  
 CC invention are useful for producing immunoglobulins, in particular  
 CC immunoglobulin therapeutic molecules termed monobodies, used as a  
 CC therapeutic group in cancer disorders. This is the amino acid sequence of  
 CC an immunoglobulin DNA cassette construct.

XX SQ Sequence 356 AA;

Query Match 100.0%; Score 1765; DB 8; Length 356;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 DB |||||  
 27 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 86  
 |||||  
 QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 DB |||||  
 87 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 146  
 |||||  
 QY 121 PSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 180  
 DB |||||  
 147 PSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 206  
 |||||  
 QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB |||||  
 207 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 266  
 |||||  
 QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
 DB |||||  
 267 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 326  
 |||||  
 QY 301 QGQNVFSCSVMEALHNYTKQSLSPGK 330  
 DB |||||  
 327 QGQNVFSCSVMEALHNYTKQSLSPGK 356  
 |||||

# RESULT 7

AAV32263

XX ID AAV32263 standard; protein; 444 AA.

AC AAV32263;

XX 15-FEB-2000 (first entry)

DT Humanised anti-CD23 Mab C11 heavy chain.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;

XX monoclonal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy.

XX Homo sapiens.

OS Synthetic.

XX Key

XX Location/Qualifiers

XX 1..30

XX /note= "framework region 1"

XX Region

XX 31..35

XX /note= "CDR 1"

XX Region

XX 36..49

XX /note= "framework region 2"

XX Region

XX 50..68

XX /note= "CDR 2"

XX Region

XX 69..100

XX /note= "framework region 3"

XX Region

XX 101..103

FT Region /note= "CDR 3"

FT Region /note= "framework region 4"

FT Region /note= "constant region"

FT Region /note= "constant region"

FT Region /note= "constant region"

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FT Region 101..103  
 FT Region /note= "CDR 3"  
 FT Region 104..111  
 FT Region /note= "framework region 4"  
 FT Region 112..144  
 FT Region /note= "constant region"

XX WO9958679-A1.  
 XX 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-GB001434.  
 XX 09-MAY-1998; 98GB-00009839.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;  
 XX WPI; 2000-053101/04.  
 XX N-PSDB; AA234748.  
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 XX diabetes, multiple sclerosis and psoriasis.  
 XX Claim 9; Fig 4; 81pp; English.  
 XX This amino acid sequence represents the heavy chain of humanised anti-  
 XX CD23 (FCERII) monoclonal antibody C11, composed of a human framework  
 XX (H5IGKVII) and the heavy chain complementarity determining regions (see  
 XX AAY32257-59) of murine antibody C11. The DNA was constructed by splice  
 XX overlap PCR. The invention provides altered antibodies, such as chimeric  
 XX or humanised antibodies, which comprise sufficient of the amino acid  
 XX sequences of the C11 light and heavy chain complementarity determining  
 XX regions to render them capable of binding to the CD23 type II molecule  
 XX expressed on haematopoietic cells. The antibodies are used to block  
 XX soluble CD23 formation in human therapy, for the treatment of arthritis,  
 XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,  
 XX glomerulonephritis, inflammatory bowel disease, ulcerative colitis,  
 XX Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,  
 XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-  
 XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic  
 XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell  
 XX malignancies (claimed). They are also useful for studying interactions  
 XX between CD23 and various ligands and determining the binding agents

SQ Sequence 444 AA;  
 Query Match 100.0%; Score 1765; DB 3; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 7e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 DB |||||  
 115 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 174  
 |||||  
 QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
 DB |||||  
 175 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELAGA 234  
 |||||  
 QY 121 PSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 180  
 DB |||||  
 235 PSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREQYN 294  
 |||||  
 QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB |||||  
 295 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354  
 |||||  
 QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
 DB |||||  
 355 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 414  
 |||||

Qy 301 QQGNVFCSCVMHEALHNHYTKQSLSPGK 330  
 Db 415 QQGNVFCSCVMHEALHNHYTKQSLSPGK 444

RESULT 8  
 ADP88447  
 ID ADP88447 standard; protein; 448 AA.  
 AC ADP88447;  
 XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Antibody TRX1 heavy chain SEQ ID NO: 24.  
 XX  
 XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
 KW TRX1.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2004052398-A1.  
 XX  
 XX 24-JUN-2004.  
 XX  
 XX 09-DEC-2003; 2003WO-US039165.  
 XX  
 XX 09-DEC-2002; 2002US-0431839P.  
 XX  
 XX (TOLE-) TOLERRX INC.  
 XX  
 XX Windsor-Hines D, Rao P, Ringler DJ;  
 XX WPI; 2004-468712/44.  
 XX  
 XX Treating a primate to induce tolerance to at least one antigen comprises  
 PT administering at least one anti-CD4 antibody or its fragment in an  
 PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
 PT CD8+ T cells.  
 XX  
 XX Disclosure; SEQ ID NO 24; 113pp; English.  
 XX  
 XX The present invention relates to a process of treating a primate to  
 CC induce tolerance to at least one antigen, which comprises administering  
 CC to the primate at least one anti-CD4 antibody or its fragment in an  
 CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
 CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
 CC the primate when the antigen is present in the primate. The method is  
 CC useful in treating a primate to induce tolerance to at least one foreign  
 CC antigen to prevent transplant rejection. The present sequence is an  
 CC antibody fragment used in the exemplification of the invention.  
 XX  
 XX Sequence 448 AA;  
 SQ

Query Match 100.0%; Score 1765; DB 8; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 7e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 Db 119 ASTKGPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178

Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELAGA 120  
 Db 179 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELAGA 238

Qy 121 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
 Db 239 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298

Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQRPQVYITLPPSRDE 240  
 Db 299 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKQRPQVYITLPPSRDE 358

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
 Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 418

Qy 301 QQGNVFCSCVMHEALHNHYTKQSLSPGK 330  
 Db 419 QQGNVFCSCVMHEALHNHYTKQSLSPGK 448

RESULT 9  
 ADP88431  
 ID ADP88431 standard; protein; 448 AA.  
 XX  
 AC ADP88431;  
 XX  
 XX 09-SEP-2004 (first entry)  
 XX  
 XX Antibody TRX1 heavy chain SEQ ID NO: 8.  
 XX  
 XX immunosuppressive; transplant rejection; antigen tolerance; antibody;  
 KW TRX1.  
 XX  
 XX Unidentified.  
 XX  
 XX WO2004052398-A1.  
 XX  
 XX 24-JUN-2004.  
 XX  
 XX 09-DEC-2003; 2003WO-US039165.  
 XX  
 XX 09-DEC-2002; 2002US-0431839P.  
 XX  
 XX (TOLE-) TOLERRX INC.  
 XX  
 XX Windsor-Hines D, Rao P, Ringler DJ;  
 XX WPI; 2004-468712/44.  
 XX  
 XX Treating a primate to induce tolerance to at least one antigen comprises  
 PT administering at least one anti-CD4 antibody or its fragment in an  
 PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
 PT CD8+ T cells.  
 XX  
 XX Disclosure; SEQ ID NO 8; 113pp; English.  
 XX  
 XX The present invention relates to a process of treating a primate to  
 CC induce tolerance to at least one antigen, which comprises administering  
 CC to the primate at least one anti-CD4 antibody or its fragment in an  
 CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
 CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
 CC the primate when the antigen is present in the primate. The method is  
 CC useful in treating a primate to induce tolerance to at least one foreign  
 CC antigen to prevent transplant rejection. The present sequence is an  
 CC antibody fragment used in the exemplification of the invention.  
 XX  
 XX Sequence 448 AA;  
 SQ

Query Match 100.0%; Score 1765; DB 8; Length 448;  
 Best Local Similarity 100.0%; Pred. No. 7e-124;  
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 Db 119 ASTKGPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178

Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELAGA 120  
 Db 179 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTCCPCPAPELAGA 238

Qy 121 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
 Db 239 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298

QY 191 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE 358  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 418  
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 448  
RESULT 10  
ID AEB08800 standard; protein; 462 AA.  
XX  
XX AEB08800;  
XX  
XX 08-SEP-2005 (first entry)  
XX  
XX Anti-NOGO-antibody heavy chain SEQ ID NO 88.  
XX  
XX cerebroprotective; vasotropic; neuroprotective; vulnerary; nootropic;  
KW antiparkinsonian; anticonvulsant; neuroleptic; antibody engineering;  
KW pharmaceutical; cerebrovascular ischemia; cardiovascular disease;  
KW neurological disease; brain injury; injury; spinal cord injury;  
KW Alzheimers disease; degeneration; dementia; neuropathy;  
KW parkinsons disease; Huntingtons chorea; genetic disorder;  
KW multiple sclerosis; immune disorder; Creutzfeldt Jakob disease;  
KW infection; schizophrenia; psychiatric disorder; motor neurone disease;  
KW cns-gen.; muscular-gen.  
XX  
XX Synthetic.  
XX  
XX WO2005061544-A2.  
XX  
XX 07-JUL-2005.  
XX  
XX 20-DEC-2004; 2004WO-GB005325.  
XX  
XX 22-DEC-2003; 2003GB-00029684.  
XX  
XX 22-DEC-2003; 2003GB-00029711.  
XX  
XX (GLAXO) GLAXO GROUP LTD.  
XX  
XX Ellis JH, Bon-Duval A, Grundy RI, Hussain F, Mcadam R;  
PI Plumpton C, Prinjha RK, Wilson PA;  
XX  
XX WPI; 2005-479448/48.  
XX  
XX N-PSDB; AEB08802.  
XX  
XX New antibody or its functional fragment that binds with and neutralizes  
PT human neurite outgrowth useful for treating or prophylaxis of stroke and  
PT other neurological disease e.g. traumatic brain injury, spinal cord  
PT injury, Alzheimer's disease.  
XX  
XX Example 8; SEQ ID NO 88; 143pp; English.  
XX  
XX The invention describes an antibody (A1) or its functional fragment, that  
CC binds with and neutralizes human neurite outgrowth (NOGO). Also described  
CC are: providing a first vector encoding a heavy chain of the antibody;  
CC providing a second vector encoding a light chain of the antibody; co-  
CC transfecting a mammalian host cell with the first and second vectors;  
CC culturing the host cell in culture media (preferably serum free) under  
CC conditions permissive to the secretion of the antibody from the host cell  
CC into the culture media; and recovering (and optionally purifying) the  
CC secreted antibody; and promoting axonal sprouting involving contacting a  
CC human axon with an anti-NOGO antibody. The antibody is useful in the  
CC preparation of a medicament for treating or prophylaxis of stroke and  
CC other neurological disease/disorders (e.g. traumatic brain injury, spinal  
CC cord injury, Alzheimer's disease, frontotemporal dementias (tauopathies),  
CC peripheral neuropathy, Parkinson's disease, Huntington's disease and

CC multiple sclerosis); Creutzfeldt-jakob disease (CJD), Schizophrenia,  
CC amyotrophic lateral sclerosis (ALS), inclusion body myositis. The  
CC antibody inhibits neurodegeneration and/or promotes functional recovery  
CC in a human patient suffering, or at risk of developing, stroke or other  
CC neurological diseases/disorder. This is the amino acid sequence of an  
CC anti-NOGO-antibody heavy chain created in the invention.  
XX  
XX Sequence 462 AA;  
Query Match 100.0%; Score 1765; DB 9; Length 462;  
Best Local Similarity 100.0%; Pred. No. 7.3e-124; Indels 0; Gaps 0;  
Matches 330; Conservative 0; Mismatches 0;  
QY 1 ASTKGPSVFPLAPSSKSTGTAALGCLIVKYDFFPEFVTVSNWSGALTSGVHTFPAVLQSS 60  
Db 133 ASTKGPSVFPLAPSSKSTGTAALGCLIVKYDFFPEFVTVSNWSGALTSGVHTFPAVLQSS 192  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 193 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 252  
QY 121 PSVFLPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 180  
Db 253 PSVFLPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 312  
QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE 240  
Db 313 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE 372  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 432  
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 433 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 462  
RESULT 11  
ID ADA47334 standard; protein; 467 AA.  
XX  
XX ADA47334;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX TRX1 heavy chain encoding DNA #SEQ ID 7.  
XX  
XX Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;  
KW graft rejection; autoimmune disease; humanised.  
XX  
XX Homo sapiens.  
XX  
XX WO2002102853-A2.  
XX  
XX 27-DEC-2002.  
XX  
XX 14-JUN-2002; 2002WO-GB002796.  
XX  
XX 14-JUN-2001; 2001GB-00014517.  
PR 20-SEP-2001; 2001GB-00022724.  
PR 19-OCT-2001; 2001US-0345194P.  
PR 18-APR-2002; 2002US-0373470P.  
PR 18-APR-2002; 2002US-0373471P.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
PA (TOLE-) TOLERRX INC.  
XX  
XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
PI Ringler D, Cobbold S, Winsor-Hines D;  
XX  
XX WPI; 2003-175228/17.

DR N-PSDB; ADA47336.  
XX Treating a primate to induce tolerance to at least one antigen, useful  
PT for inhibiting graft rejection or treating an autoimmune disease,  
PT comprises administering a TRX1 antibody to reduce the amount of CD4+  
PT CD25+ cells produced.  
XX  
XX  
PS Claim 26; Fig 1D; 131pp; English.  
XX  
CC The invention relates to a method for treating a primate to induce  
CC tolerance to at least one antigen. The method of the invention comprises  
CC administering at least one compound which when in a primary mixed  
CC lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells  
CC produced. The preferred compound is a humanised antibody or its fragment,  
CC that does not bind to the FC receptor, and includes CDRs that are free of  
CC a glycosylation site. The method of the invention is useful for inducing  
CC tolerance to at least one antigen, specifically for inhibiting,  
CC ameliorating or reducing an immune response to an antigen. The antibody  
CC is useful for manufacturing a medicament for inducing tolerance to an  
CC antigen (possibly in the form of a vaccine), for inhibiting an immune  
CC response, for inhibiting the rejection of a graft (such as an organ) in a  
CC human patient, and for treating an autoimmune disease. The current  
CC sequence represents the TRX1 heavy chain.  
XX  
SQ Sequence 467 AA;  
  
Query Match 100.0%; Score 1765; DB 6; Length 467;  
Best Local Similarity 100.0%; Pred. No. 7.4e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Db |||||  
Qy 138 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 197  
Db |||||  
Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db |||||  
Qy 198 GLYSLSSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257  
Db |||||  
Qy 121 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180  
Db |||||  
Qy 258 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 317  
Db |||||  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
Db |||||  
Qy 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377  
Db |||||  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
Db |||||  
Qy 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 437  
Db |||||  
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330  
Db |||||  
Qy 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467  
Db |||||  
  
RESULT 12  
ADA47336  
ID ADA47336 standard; protein; 467 AA.  
XX  
XX ADA47336;  
AC  
DT 20-NOV-2003 (first entry)  
XX  
DE TRX1 heavy chain #SEQ ID 9.  
XX  
XX Antibody; TRX1; immunosuppressive; immunomodulator; vaccine; antigen;  
KW graft rejection; autoimmune disease; humanised.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
PT /label= leader peptide

Region 50..54 /label= CDR  
Region 69..85 /label= CDR  
Region 118..126 /label= CDR  
XX  
FN WO2002102853-A2.  
XX  
XX 27-DEC-2002.  
XX  
XX 14-JUN-2002; 2002WO-GB002796.  
XX  
XX 14-JUN-2001; 2001GB-00014517.  
XX 20-SEP-2001; 2001GB-00022724.  
XX 19-OCT-2001; 2001US-0345194P.  
XX 18-APR-2002; 2002US-0373470P.  
XX 18-APR-2002; 2002US-0373471P.  
XX (ISIS-) ISIS INNOVATION LTD.  
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX (TOLE-) TOLERRX INC.  
XX  
XX Frewin M, Waldmann H, Gorman S, Hale G, Rao P, Kornaga T;  
XX Ringler D, Cobbold S, Winsor-Hines D;  
XX  
XX WPI; 2003-175228/17.  
XX  
XX Treating a primate to induce tolerance to at least one antigen, useful  
XX for inhibiting graft rejection or treating an autoimmune disease,  
XX comprises administering a TRX1 antibody to reduce the amount of CD4+  
XX CD25+ cells produced.  
XX  
XX Claim 27; Fig 1F; 131pp; English.  
XX  
XX The invention relates to a method for treating a primate to induce  
XX tolerance to at least one antigen. The method of the invention comprises  
XX administering at least one compound which when in a primary mixed  
XX lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells  
XX produced. The preferred compound is a humanised antibody or its fragment,  
XX that does not bind to the FC receptor, and includes CDRs that are free of  
XX a glycosylation site. The method of the invention is useful for inducing  
XX tolerance to at least one antigen, specifically for inhibiting,  
XX ameliorating or reducing an immune response to an antigen. The antibody  
XX is useful for manufacturing a medicament for inducing tolerance to an  
XX antigen (possibly in the form of a vaccine), for inhibiting an immune  
XX response, for inhibiting the rejection of a graft (such as an organ) in a  
XX human patient, and for treating an autoimmune disease. The current  
XX sequence represents the TRX1 heavy chain amino acid sequence.  
XX  
SQ Sequence 467 AA;  
  
Query Match 100.0%; Score 1765; DB 6; Length 467;  
Best Local Similarity 100.0%; Pred. No. 7.4e-124;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Db |||||  
Qy 138 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 197  
Db |||||  
Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db |||||  
Qy 198 GLYSLSSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 257  
Db |||||  
Qy 121 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180  
Db |||||  
Qy 258 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 317  
Db |||||  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
Db |||||  
Qy 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377  
Db |||||  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
Db |||||

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Db 378 LTKNQVSLTCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 13
ADP88446
ID ADP88446 standard; protein; 467 AA.
XX
AC ADP88446;
XX
DT 09-SEP-2004 (first entry)
XX
DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 23.
XX
KW immunosuppressive; transplant rejection; antigen tolerance; antibody;
TRX1.
XX
OS Unidentified.
XX
PN WO2004052398-A1.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US039165.
XX
PR 09-DEC-2002; 2002US-0431839P.
XX
PA (TOLE-) TOLERRX INC.
XX
PI Windsor-Hines D, Rao P, Ringler DJ;
XX
DR WPI; 2004-468712/44.
XX
DR N-PSDB; ADP88444, ADP88445.
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX
PS Disclosure; SEQ ID NO 23; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 1765; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.4e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 197
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 198 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 257
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 258 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 317
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Qy 191 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
Db 318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 14
ADP88430
ID ADP88430 standard; protein; 467 AA.
XX
AC ADP88430;
XX
DT 09-SEP-2004 (first entry)
XX
DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 7.
XX
KW immunosuppressive; transplant rejection; antigen tolerance; antibody;
TRX1.
XX
OS Unidentified.
XX
PN WO2004052398-A1.
XX
PD 24-JUN-2004.
XX
PF 09-DEC-2003; 2003WO-US039165.
XX
PR 09-DEC-2002; 2002US-0431839P.
XX
PA (TOLE-) TOLERRX INC.
XX
PI Windsor-Hines D, Rao P, Ringler DJ;
XX
DR WPI; 2004-468712/44.
XX
DR N-PSDB; ADP88429, ADP88428.
XX
PT Treating a primate to induce tolerance to at least one antigen comprises
PT administering at least one anti-CD4 antibody or its fragment in an
PT initial dose of at least 40 mg/kg and at least one compound that inhibits
PT CD8+ T cells.
XX
PS Disclosure; SEQ ID NO 7; 113pp; English.
XX
CC The present invention relates to a process of treating a primate to
CC induce tolerance to at least one antigen, which comprises administering
CC to the primate at least one anti-CD4 antibody or its fragment in an
CC initial dose of at least 40 mg/kg and at least one compound that inhibits
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC the primate when the antigen is present in the primate. The method is
CC useful in treating a primate to induce tolerance to at least one foreign
CC antigen to prevent transplant rejection. The present sequence is an
CC antibody fragment used in the exemplification of the invention.
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 1765; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 7.4e-124; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAAAGCLVKGYPSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 197
Qy 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 120
Db 198 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPCPAPELAGA 257
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 33.69377 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-110  
Perfect score: 1765  
Sequence: 1 ASTKGPSVFPLAPSKSTSG.....MHEALHNYTKSLSPGK 330  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	99.5	330	1 GHU	Ig gamma-1 chain C
2	1619.5	91.8	377	2 A23511	Ig gamma-3 chain C
3	1617.5	91.6	377	2 A0764	Ig gamma-3 chain C
4	1608	91.1	326	1 G2HU	Ig gamma-2 chain C
5	1579.5	89.5	327	1 G4HU	Ig gamma-4 chain C
6	1259	71.3	328	2 I47159	Ig gamma 2a chain
7	1253	71.0	328	2 I47160	Ig gamma 2b chain
8	1252.5	71.0	374	2 S69339	Ig heavy chain V r
9	1249	70.8	255	4 S31866	Ig gamma-1 chain C
10	1243	70.4	234	2 PT0207	Ig gamma chain C r
11	1235	70.0	328	2 I47158	Ig gamma 1 chain c
12	1231	69.7	328	2 I47161	Ig gamma 3 chain c
13	1219.5	69.1	323	1 GHRB	Ig gamma chain C r
14	1201.5	68.1	329	1 G2GP	Ig gamma-2 chain C
15	1195.5	67.7	472	2 S31459	Ig gamma-1 chain -
16	1176.5	66.7	470	2 S22080	Ig heavy chain pre
17	1157.5	65.6	308	2 C30554	Ig heavy chain C r
18	1156	65.5	444	2 PC4436	monoclonal antibod
19	1154	65.4	326	2 PS0017	Ig gamma-1 chain C
20	1144	64.8	324	1 G3MS	Ig gamma-1 chain C
21	1140	64.6	289	1 G3HWT	Ig gamma-1 chain C
22	1139	64.5	393	1 GLMSW	Ig gamma-3 heavy c
23	1135.5	64.3	333	2 PS0018	Ig gamma-1 chain C
24	1130	64.0	329	1 G3MSC	Ig gamma-2b chain
25	1119	63.4	398	1 G3MSM	Ig gamma-3 chain C
26	1115	63.2	330	1 G2MSA	Ig gamma-2a chain
27	1115	63.2	469	2 S37483	Ig gamma-2a chain
28	1114.5	63.1	329	2 S00847	Ig gamma-2c chain
29	1114	63.1	322	2 PS0019	Ig gamma-2a chain

RESULT 1  
GHU

Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370  
A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, ;  
A:Note: Lys-330 is removed after translation  
R:Haris, L.J.  
submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obara, M.; Nikaide, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C.

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A:Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,'

A:Cross-references: UNIPARC:UPI000017378E

A:Note: This sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A:Cross-references: UNIPARC:UPI000017378P  
A:Note: this sequence has the Gln(17) and Gln(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOI; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Cross-references: UNIPARC:UPI0000173790  
A:Note: this sequence has the Gln(3) and Gln(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM2>  
F;137-206/Domain: immunoglobulin homology <IM3>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental  
F;103/disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 99.5%; Score 1756; DB 1; Length 330;  
Best Local Similarity 99.4%; Pred. No. 9.8e-114; Indels 0; Gaps 0;  
Matches 328; Conservative 0; Mismatches 2;  
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSTKVDKVV----- 98  
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSTKVDKVV----- 98  
Qy 99 -----EPKSCDKHTHTCPPCPAPELLAGPSVFLPPPKPDT 133  
Db 121 DTPPPCPKPEPKSCDTPPPCPKPEPKSCDTPPPCPKPEPKPDT 180  
Qy 134 LMTSRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLIH 193  
Db 181 LMTSRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLIH 240  
Qy 194 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 253  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 300  
Qy 254 GYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVME 313  
Db 301 GYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVME 360  
Qy 314 ALHNHYTQKSLSLSPGK 330  
Db 361 ALHNRYTQKSLSLSPGK 377  
RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C:Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA

|||||  
Db 301 QQGNVFCSVWHEALHNHYTQKSLSLSPGK 330  
RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA2726  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM>  
Query Match 91.8%; Score 1619.5; DB 2; Length 377;  
Best Local Similarity 81.4%; Pred. No. 2.9e-104;  
Matches 307; Conservative 10; Mismatches 13; Indels 47; Gaps 1;  
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Db 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSTKVDKVV----- 98  
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSTKVDKVV----- 98  
Qy 99 -----EPKSCDKHTHTCPPCPAPELLAGPSVFLPPPKPDT 133  
Db 121 DTPPPCPKPEPKSCDTPPPCPKPEPKSCDTPPPCPKPEPKPDT 180  
Qy 134 LMTSRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLIH 193  
Db 181 LMTSRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLIH 240  
Qy 194 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 253  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVK 300  
Qy 254 GYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVME 313  
Db 301 GYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVME 360  
Qy 314 ALHNHYTQKSLSLSPGK 330  
Db 361 ALHNRYTQKSLSLSPGK 377  
RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C:Accession: A60764  
R;Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA

A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPROT:Q8NAY9; UNIPARC:UPI0000176F0B  
C;Superfamily: immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMW>

```
Query Match          91.6%; Score 1617.5; DB 2; Length 377;
Best Local Similarity 81.4%; Pred. No. 4e-104;
Matches 307; Conservative 10; Mismatches 13; Indels 47; Gaps 1;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVSWNSGALTSGVHTFPAVLQSS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 1 ASTKGPSVFPLAPCSRSTSGGTAALGLCLVQDYFFPPVTVSWNSGALTSGVHTFPAVLQSS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKDKV----- 98
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKDKVRLKTPGLDTHTCPCPEPKSC 120
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 99 ----- 1;
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

DB 121 DTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKSCDTPPC 133
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 134 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLH 193
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 181 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLH 240
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 194 QDWLNGKEYKCKVSNKALPAPIETISKAKQPREPQVYITLPPSRDELTKNQVSLTCLVK 253
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 241 QDWLNGKEYKCKVSNKALPAPIETISKAKQPREPQVYITLPPSRDELTKNQVSLTCLVK 300
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 254 GFYPDSIAVEHSGCPENNYKTPPVLDSDGSFPLYSLYKLTVDKSRWQQGNVFPSCSVNHE 313
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 301 GFYPDSIAVEHSGCPENNYKTPPVLDSDGSFPLYSLYKLTVDKSRWQQGNVFPSCSVNHE 360
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 314 ALHNHYTQKSLSLSPGK 330
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 361 ALHNRYTQKSLSLSPGK 377
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
```

## RESULT 4

G2HU

Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma chain com  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>  
A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:932  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Cross-references: UNIPARC:UPI0000173791  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
A;Cross-references: UNIPARC:UPI0000173794  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la;  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;127-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F;102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match          91.1%; Score 1608; DB 1; Length 326;
Best Local Similarity 91.5%; Pred. No. 1.5e-103;
Matches 302; Conservative 12; Mismatches 12; Indels 4; Gaps 2;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVQDYFFPPVTVSWNSGALTSGVHTFPAVLQSS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 1 ASTKGPSVFPLAPCSRSTSGGTAALGLCLVQDYFFPPVTVSWNSGALTSGVHTFPAVLQSS 60
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKDKVPEKSCDKTHTCPCPAPELAGA 120
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 61 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTPKDKVPEKSCDKTHTCPCPAPELAGA 116
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 121 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 117 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 176
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKQPREPQVYITLPPSRDE 240
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 177 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETISKAKQPREPQVYITLPPSRDE 236
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 241 LTKNQVSLTCLVKGFYPSDIAVEHSGCPENNYKTPPVLDSDGSFPLYSLYKLTVDKSRW 300
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 237 LTKNQVSLTCLVKGFYPSDIAVEHSGCPENNYKTPPVLDSDGSFPLYSLYKLTVDKSRW 296
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:

QY 301 QQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 330
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
DB 297 QQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 326
   |||||.....:|||||.....:|||||.....:|||||.....:|||||.....:
```

RESULT 5

G4HU

Ig gamma-4 chain C region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
 C/Accession: A90933; A90249; A02150  
 R:Ellison, J.; Buxbaum, J.; Hood, L.  
 DNA 1, 11-18, 1981  
 A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A/Reference number: A90933; MUID:8315104; PMID:6299662  
 A/Accession: A90933  
 A/Molecule type: DNA  
 A/Residues: 1-327 <ELL>  
 A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190  
 A/Note: the sequence was determined from the germline gene  
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
 A/Reference number: A90249; MUID:70207560; PMID:4192699  
 A/Accession: A90249  
 A/Molecule type: protein  
 A/Residues: 1-30,81-326 <PIN>  
 A/Cross-references: UNIPARC:UPI00000173795; UNIPARC:UPI00000173796  
 C/Genetics:  
 A/Genes: IGHG4  
 A/Map position: 14q32.33-14q32.33  
 A/Introns: 99/1; 111/1; 221/1  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:93-110/Region: hinge  
 F:134-203/Domain: immunoglobulin homology <IM2>  
 F:240-307/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
 F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.5%; Score 1579.5; DB 1; Length 327;  
 Best Local Similarity 90.3%; Pred. No. 1.4e-101;  
 Matches 298; Conservative 12; Mismatches 17; Indels 3; Gaps 1;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
 Db 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 180  
 Db 118 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 177

Qy 181 STYRVSVLTCLVKGFPYSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240  
 Db 178 STYRVSVLTCLVKGFPYSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 237

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
 Db 238 MTNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 297

Qy 301 QQGNVFSCSVNHEALHNNHYTKSLSPGK 330  
 Db 298 QEGNVFSCSVNHEALHNNHYTKSLSLGK 327

RESULT 6  
 Ig gamma 2a chain constant region - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C/Accession: I47159  
 R:Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3563-3573, 1994  
 A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
 A/Reference number: I47158; MUID:95015845; PMID:7930579  
 A/Accession: I47159  
 A/Status: preliminary; translated from GB/EMBL/DBDJ  
 A/Molecule type: mRNA  
 A/Residues: 1-328 <KAC>  
 A/Cross-references: UNIPARC:UPI00000115524; EMBL:U03779; NID:9433123; PIDN:AAAS2217.1; PII  
 C/Genetics:  
 A/Genes: IGG2a  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 1259; DB 2; Length 328;  
 Best Local Similarity 70.2%; Pred. No. 1.6e-79;  
 Matches 233; Conservative 42; Mismatches 51; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 AKPTAPSVYPLAPCSRDTSGPNVALGLASSYPPEPTVTWNSGALSSGVHTFPFSLVQPS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
 Db 61 GLYSLSSVWTVTPASSLSKSYTCNVNHPATTTKVDKRVGTYKT---KPCCICPACESFG- 116

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 180  
 Db 117 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREQYN 176

Qy 181 STYRVSVLTCLVKGFPYSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240  
 Db 177 STYRVSVLTCLVKGFPYSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 236

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 298  
 Db 237 LSRKSVISLTCLVGFYPPDDIDVEWQNGQPEPEGNVHTTPPQQDVGDTGYLYSKFSVDKA 296

Qy 299 RWOQGNVFSCSVNHEALHNNHYTKSLSPGK 330  
 Db 297 SWQGGGIFQCAVMHEALHNNHYTKSLSPGK 328

RESULT 7  
 Ig gamma 2b chain constant region - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C/Accession: I47160  
 R:Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3563-3573, 1994  
 A>Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
 A/Reference number: I47158; MUID:95015845; PMID:7930579  
 A/Accession: I47160  
 A/Status: preliminary; translated from GB/EMBL/DBDJ  
 A/Molecule type: mRNA  
 A/Residues: 1-328 <KAC>  
 A/Cross-references: UNIPARC:UPI00000115525; EMBL:U03780; NID:9433125; PIDN:AAAS2218.1; PII  
 C/Genetics:  
 A/Genes: IGG2b  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 1253; DB 2; Length 328;  
 Best Local Similarity 69.9%; Pred. No. 4.2e-79;  
 Matches 232; Conservative 41; Mismatches 53; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 AKPTAPLVYPLAPCGRDTSGPNVALGLASSYPPEPTVTWNSGALTSGVHTFPFSLVQPS 60

Qy 61 GLYSLSSVWTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120



Db 181 PENNYKTTTPVLDSGDFLYSLKTVDSKRWQGNVFCSCVMHEALHNHYTKS 234

RESULT 11  
147158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a swine IgG library  
A:Reference number: 147158; MUID:95015845; PMID:7930579  
A:Accession: I47158  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G433121; PIDN:AAAS2216.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
C:Genetics:  
A:Gene: Igg1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 1235; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 7.4e-78;  
Matches 231; Conservative 39; Mismatches 56; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFLPAPSKSTSGGTAALGCLVDKYPPEVTVSNWNSGALTSGVHTFPVAVLQSS 60  
Db 1 APTKAPSVYFLAPCGRDTSGPNVALGCLASSYFPPEVTVTNWNSGALTSGVHTFPVAVLQSS 60  
Qy 61 GLYSLSWVTVPPSSSLGTQTYICNNHKPSNTKVKVPEKSCDKTHTCCPCPAPELAGA 120  
Db 61 GLYSLSWVTVPPASSLSKSYTCNNVHPATTKVKDKRV---GIHQPTQCTPCPCCEVAG- 116  
Qy 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVEVHNNAKTKPREQYN 180  
Db 117 PSVFIFFPKPKDLMISQTEVTCVVDVSKHEAEVQFSWYVDGVEVHTAETRPKEQFN 176  
Qy 181 STYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 177 STYRVSVLPIQHQMKGKFKCKVNNVLDLPAPITRTISKAIGQSRPQVYITLPPPAEE 236  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSPFLYSLKLTVDKS 298  
Db 237 LRSKSVTLTCLVIGFYPPDIHVEWKSNGQPEPEGNVYRTTPPQDVGDTFFLYSKLAVDKA 296  
Qy 299 RWQGNVFCSCVMHEALHNHYTKSLSLSPGK 330  
Db 297 RWDHGDTEFCAMVHEALHNHYTKSISKTQK 328

Query Match 69.7%; Score 1231; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 7.4e-78;  
Matches 231; Conservative 39; Mismatches 56; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFLPAPSKSTSGGTAALGCLVDKYPPEVTVSNWNSGALTSGVHTFPVAVLQSS 60  
Db 1 APTKAPSVYFLAPCGRDTSGPNVALGCLASSYFPPEVTVTNWNSGALTSGVHTFPVAVLQSS 60  
Qy 61 GLYSLSWVTVPPSSSLGTQTYICNNHKPSNTKVKVPEKSCDKTHTCCPCPAPELAGA 120  
Db 61 GLYSLSWVTVPPASSLSKSYTCNNVHPATTKVKDKRV---GIHQPTQCTPCPCCEVAG- 116  
Qy 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVEVHNNAKTKPREQYN 180  
Db 117 PSVFIFFPKPKDLMISQTEVTCVVDVSKHEAEVQFSWYVDGVEVHTAETRPKEQFN 176  
Qy 181 STYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 177 STYRVSVLPIQHQMKGKFKCKVNNVLDLPAPITRTISKAIGQSRPQVYITLPPPAEE 236  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSPFLYSLKLTVDKS 298  
Db 237 LRSKSVTLTCLVIGFYPPDIHVEWKSNGQPEPEGNVYRTTPPQDVGDTFFLYSKLAVDKA 296  
Qy 299 RWQGNVFCSCVMHEALHNHYTKSLSLSPGK 330  
Db 297 RWDHGDTEFCAMVHEALHNHYTKSISKTQK 328

RESULT 12  
147161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a swine IgG library  
A:Reference number: 147161; MUID:95015845; PMID:7930579  
A:Accession: I47161  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:G433127; PIDN:AAAS2219.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
C:Genetics:  
A:Gene: IgG3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 1231; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 7.4e-78;  
Matches 231; Conservative 39; Mismatches 56; Indels 6; Gaps 3;

Best Local Similarity 69.3%; Pred. No. 1.4e-77;  
Matches 230; Conservative 40; Mismatches 56; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFLPAPSKSTSGGTAALGCLVDKYPPEVTVSNWNSGALTSGVHTFPVAVLQSS 60  
Db 1 APTKAPSVYFLAPCGRDTSGPNVALGCLASSYFPPEVTVTNWNSGALTSGVHTFPVAVLQSS 60  
Qy 61 GLYSLSWVTVPPSSSLGTQTYICNNHKPSNTKVKVPEKSCDKTHTCCPCPAPELAGA 120  
Db 61 GLYSLSWVTVPPASSLSKSYTCNNVHPATTKVKDKRVGKT---KPPCPCPCCEVAG- 116  
Qy 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHDEPKVFNWYVDGVEVHNNAKTKPREQYN 180  
Db 117 PSVFIFFPKPKDLMISQTEVTCVVDVSKHEAEVQFSWYVDGVEVHTAETRPKEQFN 176  
Qy 181 STYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 177 STYRVSVLPIQHQMKGKFKCKVNNVLDLPAPITRTISKAIGQSRPQVYITLPPPAEE 236  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPVLDSDGSPFLYSLKLTVDKS 298  
Db 237 LRSKSVTLTCLVIGFYPPDIHVEWKSNGQPEPEGNVYRTTPPQDVGDTFFLYSKLAVDKA 296  
Qy 299 RWQGNVFCSCVMHEALHNHYTKSLSLSPGK 330  
Db 297 RWDHGDTEFCAMVHEALHNHYTKSISKTQK 328

RESULT 13  
GHRB  
Ig gamma chain C region - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
C:Accession: A91749; A90290; A93928; A94416; A02161  
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
Immunogenetics 18, 387-397, 1983  
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype  
A:Reference number: A91749; MUID:84030930; PMID:6133520  
A:Accession: A91749  
A:Molecule type: mRNA  
A:Residues: 1-323 <BER>  
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D  
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
R:Pratt, D.M.; Mole, L.E.  
Biochem. J. 151, 337-349, 1975  
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G  
A:Reference number: A90290; MUID:76135469; PMID:1243651  
A:Accession: A90290  
A:Molecule type: protein  
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>  
A:Cross-references: UNIPARC:UPI00001737AB  
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
A:Reference number: A93928; MUID:83299917; PMID:6193512  
A:Accession: A93928  
A:Molecule type: mRNA  
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AA31289.1; PID:133-202/Domain: immunoglobulin homology <IMM>  
A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
Biochem. J. 116, 249-259, 1970  
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C  
A:Reference number: A90245; MUID:70110015; PMID:5461106  
A:Accession: A90245  
A:Molecule type: protein  
A:Residues: 132-143, 'E', 145-161 <FRU>  
A:Cross-references: UNIPARC:UPI00001737AC  
R:Hill, R.D.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, 1970  
A:Reference number: A94416  
A:Accession: A94416  
A:Molecule type: protein



A;Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q',  
A;Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE  
A;Note: this has the e15 allotypic marker, 185-Ala  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:130-199/Domain: immunoglobulin homology <IM2>  
F:136-303/Domain: immunoglobulin homology <IM3>  
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.1%; Score 1219.5; DB 1; Length 323;  
Best Local Similarity 69.4%; Pred. No. 8.4e-77;  
Matches 227; Conservative 34; Mismatches 59; Indels 7; Gaps 2;

Qy 4 KGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNGLTSGVHTFPAVLQSSGLY 63  
Db 4 KAPSVFPLAPCGDTPSTVTLGCLVKGLYPEPTVWSNGLTNGVTRFPSVRQSSGLY 63

Qy 64 SLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHCTCPCPAPELAGAPSV 123  
Db 64 SLSSVTVTPSSS---QPVTQNVAPATNTKVDKTVAPSTCSK----PTCPPELLGGPSV 116

Qy 124 FLPPPKDPTLMISRTPEVTCVVDVSHEDPEKFNWYDGVVEVHNATKPREQYNSTY 183  
Db 117 FIFPPKPKDPTLMISRTPEVTCVVDVSDDEPEQVPTWYINNEQVTRAPPLREQQPNSTI 176

Qy 184 RVSVSLTVLHODWLNGEKYCKVSNKALPAPIETISKAKGPREPQVYTLPPSRDELTK 243  
Db 177 RVSTLPTLTHODWLNGEKFKCKVHNKALPAPIETISKAGQPLEPKVYTWGPPREELSS 236

Qy 244 NQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQOG 303  
Db 237 RVSLSLTCLMNGFYPSDISEVEKNGKAEDNTKTPAVLDSGSFPLYNKLVSPTSEWQRG 296

Qy 304 NVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 297 DVFTCSVNHEALHNHYTQKSISRSPGK 323

RESULT 14  
GzGP  
Ig gamma-2 chain C region - guinea pig  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004  
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R;Trischmann, T.M.  
submitted to the Atlas, April 1975  
A;Reference number: A94553  
A;Accession: A94553  
A;Molecule type: protein  
A;Residues: 1-3 <TRI>  
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E  
B;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A;Reference number: A90352; MUID:71058471; PMID:5538606  
A;Accession: A90352  
A;Molecule type: protein  
A;Residues: 4-68 <BIR>  
A;Cross-references: UNIPARC:UPI000017379F  
R;Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
A;Reference number: A90359; MUID:71058486; PMID:5538616  
A;Accession: A90359  
A;Molecule type: protein  
A;Residues: 69-133;312-329 <TUR>  
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1  
R;Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665  
A;Accession: A90384  
A;Molecule type: protein  
A;Residues: 134-256 <TRA>  
A;Cross-references: UNIPARC:UPI00001737A2  
R;Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A;Reference number: A90385; MUID:75036073; PMID:4609467  
A;Accession: A90385  
A;Molecule type: protein  
A;Residues: 227-311 <TR2>  
A;Cross-references: UNIPARC:UPI00001737A3  
R;Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A;Reference number: A90354; MUID:71058474; PMID:4922544  
A;Contents: annotation; disulfide bonds  
A;Note: Cys-16 is involved in a heavy-light chain bond  
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:135-204/Domain: immunoglobulin homology <IM1>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 1201.5; DB 1; Length 329;  
Best Local Similarity 69.7%; Pred. No. 1.5e-75;  
Matches 232; Conservative 28; Mismatches 64; Indels 9; Gaps 4;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNGLTSGVHTFPAVLQSS 60  
Db 2 ARTTAPSVFPLAASCVDTSMTLGLCLVKGYFPEPTVKNWNSGALTSGVHTFPAVLQ-S 60

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTH--TCPPCPAPELA 118  
Db 61 GLYSLTSMVTPSSSQAT----CNVAHPASSTKVDKTVPEIRTPZPBCTCPKCPPENL 116

Qy 119 GAPSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEKFNWYDGVVEVHNATKPREEQ 178  
Db 117 GGPSVFIPPPKPKDPTLMISLTPTVTCVVDVSDDEPEQVPTWYDNKPVGNATKPRVEQ 176

Qy 179 YNSTYRVSVSLTVLHODWLNGEKYCKVSNKALPAPIETISKAKGPREPQVYTLPPSR 238  
Db 177 YNTTFRVESVLPQHQDWLNGEKFKCKVHNKALPAPIETISKAGQPRMDDVTLPPSR 236

Qy 239 DELTKNQVSLTCLVKGFYPSDIAVEESNGQP--ENNYKTTPPVLDSDGSFPLYSKLTVD 296  
Db 237 DELSKSKSVTCLLIINFPPADIHVEMASNRVPVSEKEYKNTPTPIEDADGGSFPLYSKLTVD 296

Qy 297 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPG 329  
Db 297 KSAWDQGTVTYTCVSNHEALHNHYTQKISRSPG 329

RESULT 15  
S31459

Ig gamma-1 chain - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C;Accession: S31459  
R;Patric, S.; Nau, P.  
submitted to the EMBL Data Library, December 1992  
A;Reference number: S31459  
A;Accession: S31459  
A;Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-472 <PAT>  
C:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 1195.5; DB 2; Length 472;  
Best Local Similarity 67.2%; Pred. No. 6e-75;  
Matches 223; Conservative 38; Mismatches 68; Indels 3; Gaps 2;

Qy	1	ASTKGPSVFLAPSSKSTSGGTAALGCLVADYPPPEPTVSWNSGALTSGVHTFPVILQSS	60
Db	142	ASTTPPKVYPLTSCGDTSSSIVTLGCLVSSYMPPEPTVWNSGALTSGVHTFPVILQSS	201
Qy	61	GLYSLSSVVTVPSSSLGTQTYICNVNKKPSNTKVDKVPKSCDKTHTCPCPAPELAGA	120
Db	202	GLYSLSSVVTVPASTSGAQTFCNVVHPASSTKVDKRVPGCPDCKHC-RCPPPELPGG	260
Qy	121	PSVPLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVHNATKPREQYN	180
Db	261	PSVFIFPPPKKDTLTISGTPEVTCVVDVGGDDPEVQFSWFVDNVEVTRTARTKPREQFN	320
Qy	181	STYRWVSVLTVLHQDLNGKEYCKVSNKALPAIEKTIKAKGQPREPQVYTLPPSRDE	240
Db	321	STFRVVSALPIQHQDWGKGKFKCKVHNEALPAFIVRTISRTKGQAREPQVYVLAPQSE	380
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLPDSGGSFFLYSKLTVDKS	298
Db	381	LSKSTLSVTCLVTGYPDYIAVEWQKNGQPESEDKYGTTSQLDADGSGYFLYSRLRYDKN	440
Qy	299	RWQGNVFCSVMEHALNHYTKSLSPGK	330
Db	441	SWQEGDTYACVVMHEALNHYTKSLSPGK	472

Search completed: January 28, 2006, 09:45:39  
Job time : 34.6937 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 174.91 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNHYTKSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	99.5	330	1	IGHG1 HUMAN
2	1756	99.5	465	2	Q6MX6 HUMAN
3	1756	99.5	469	2	Q569F4 HUMAN
4	1756	99.5	469	2	Q727P5 HUMAN
5	1756	99.5	470	2	Q7Z5W1 HUMAN
6	1756	99.5	470	2	Q6FJA4 HUMAN
7	1756	99.5	475	2	Q5BFB5 HUMAN
8	1756	99.5	475	2	Q6GMW7 HUMAN
9	1756	99.5	476	2	Q6GMX1 HUMAN
10	1753	99.3	466	2	Q6IN78 HUMAN
11	1753	99.3	472	2	Q6N089 HUMAN
12	1752	99.3	473	2	Q6P055 HUMAN
13	1752	99.3	475	2	Q6MZ06 HUMAN
14	1752	99.3	480	2	Q6N094 HUMAN
15	1752	99.3	481	2	Q6N097 HUMAN
16	1752	99.3	482	2	Q7Z351 HUMAN
17	1749	99.1	466	2	Q6N096 HUMAN
18	1747	99.0	348	2	Q6PYX1 HUMAN
19	1747	99.0	478	2	Q6PI81 HUMAN
20	1747	99.0	480	2	Q6PJF1 HUMAN
21	1745	98.9	475	2	Q6N095 HUMAN
22	1745	98.9	544	2	Q6PJ95 HUMAN
23	1737	98.4	473	2	Q6MZV7 HUMAN
24	1687	95.6	475	2	Q3RE17 PONPY
25	1619.5	91.8	518	2	Q6N030 HUMAN
26	1619.5	91.8	519	2	Q5EBM2 HUMAN
27	1615.5	91.5	521	2	Q6N4Y9 HUMAN
28	1608	91.1	326	1	IGHG2 HUMAN
29	1608	91.1	417	2	Q6N093 HUMAN
30	1604.5	90.9	509	2	Q6NF17 HUMAN
31	1603	90.8	465	2	Q6P6C4 HUMAN

32	1594	90.3	470	2	Q68CN4 HUMAN	Q68cn4 homo sapien
33	1593	90.3	464	2	Q6MZU6 HUMAN	Q6mzu6 homo sapien
34	1579.5	89.5	327	1	IGHG4 HUMAN	P01861 homo sapien
35	1579.5	89.5	473	2	Q8TC63 HUMAN	Q8tc63 homo sapien
36	1570.5	89.0	476	2	Q8MZK7 HUMAN	Q8mzx7 homo sapien
37	1513.5	85.8	354	2	Q86TT2 HUMAN	Q86tt2 homo sapien
38	1255.5	71.1	337	2	Q95M34 HORSE	Q95m34 equus cabal
39	1253	71.0	679	2	Q96PQ8 HUMAN	Q96pq8 homo sapien
40	1237.5	70.1	487	2	Q65ZL2 9MURI	Q65zl2 mus sp. fv/
41	1219.5	69.1	323	1	GC RABIT	P01870 oryctolagus
42	1201.5	68.1	329	1	IGHG2 CAVPO	P01862 cavia porce
43	1157	65.6	463	2	Q99LC4 MOUSE	Q99lc4 mus musculu
44	1156	65.5	458	2	Q65ZQ1 HUMAN	Q65zq1 homo sapien
45	1154	65.4	326	1	GC1 RAT	P20759 rattus norv

#### ALIGNMENTS

RESULT 1  
IGHG1 HUMAN STANDARD; PRT; 330 AA.  
AC P01857; 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DB IG gamma-1 chain C region.  
GN Name=IGHG1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP PROTEIN SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponsingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.

RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RN Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Draker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GIM (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; J00228; AAC8527.1; ALT\_INIT; Genomic DNA.  
 DR PIR; A93433; GHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
 DR PDB; 1AQK; X-ray; H=1-103.  
 DR PDB; 1D5B; X-ray; B/H=1-101.  
 DR PDB; 1D5I; X-ray; H=1-101.  
 DR PDB; 1D6V; X-ray; H=1-101.  
 DR PDB; 1DN2; X-ray; A/B=120-326.  
 DR PDB; 1E4K; X-ray; A/B=106-330.  
 DR PDB; 1FC1; X-ray; A/B=106-329.  
 DR PDB; 1FC2; X-ray; D=106-329.  
 DR PDB; 1FC3; X-ray; A=121-326.  
 DR PDB; 1H2H; X-ray; H/K=1-330.  
 DR PDB; 1I72; X-ray; B/D=1-103.  
 DR PDB; 1I1S; X-ray; A/B=107-330.  
 DR PDB; 1I1X; X-ray; A/B=107-330.  
 DR PDB; 1L6X; X-ray; A=120-326.  
 DR PDB; 1Q0X; X-ray; A/B=119-330.  
 DR PDB; 1T83; X-ray; A/B=107-330.  
 DR PDB; 2RCS; X-ray; H=1-103.  
 DR HGNC; HGNC:5525; IGHL1.  
 DR MIM; 147100; .  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; P:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; C1-set; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW immunoglobulin C region; Immunoglobulin domain.  
 FT REGION 1 98 CH1.

FT	REGION	99	110	Hinge.
FT	REGION	111	223	CH2.
FT	REGION	224	330	CH3.
FT	CARBOHYD	180	180	N-linked (GlcNAc. . .).
FT	DISULFID	27	83	Interchain (with light chain).
FT	DISULFID	103	103	Interchain (with heavy chain).
FT	DISULFID	109	109	Interchain (with heavy chain).
FT	DISULFID	112	112	Interchain (with heavy chain).
FT	DISULFID	144	204	Interchain (with heavy chain).
FT	DISULFID	250	308	Interchain (with heavy chain).
FT	VARIANT	97	97	K -> R (in GIM(3) marker).
FT	VARIANT	239	239	/FTid=VAR_003886.
FT	VARIANT	241	241	D -> E (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTid=VAR_003887.
FT	VARIANT	241	241	L -> M (in GIM(non-1) marker).
FT	VARIANT	241	241	/FTid=VAR_003888.
FT	NON TER	1	1	
FT	STRAND	23	24	
FT	STRAND	26	33	
FT	STRAND	38	38	
FT	STRAND	41	41	
FT	STRAND	42	45	
FT	TURN	48	49	
FT	STRAND	50	52	
FT	STRAND	57	58	
FT	TURN	59	61	
FT	STRAND	62	71	
FT	HELEX	73	75	
FT	TURN	76	78	
FT	STRAND	82	87	
FT	TURN	88	91	
FT	STRAND	92	97	
FT	TURN	102	103	
FT	STRAND	122	126	
FT	HELEX	130	134	
FT	TURN	136	137	
FT	STRAND	141	149	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	167	
FT	STRAND	171	172	
FT	STRAND	176	177	
FT	TURN	179	180	
FT	STRAND	183	190	
FT	HELEX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELEX	238	242	
FT	STRAND	245	256	
FT	STRAND	261	266	
FT	TURN	267	268	
FT	STRAND	269	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELEX	297	301	
FT	TURN	302	303	
FT	STRAND	306	311	
FT	TURN	313	314	
FT	HELEX	316	318	
FT	STRAND	319	324	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;

Query Match 99.5%; Score 1756; DB 1; Length 330;  
 Best Local Similarity 99.4%; Pred. No. 5.8e-120;  
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSPFLAPSSKSTSGTAAALGLVKDYPPETVTSWNSGALTSVHTFPVAVLQSS 60

Db 1 ASTKGPSVFPPLAPSCKSTSGGTAALGCLVKDYFPPEVTVVSNWGALTSVHTFPVAVLQSS 60  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPPELAGA 120  
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPPELAGG 120  
QY 121 PSVFLFPPKPKDGLMIKRTPEVTVVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEOYN 180  
Db 121 PSVFLFPPKPKDGLMIKRTPEVTVVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEOYN 180  
QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISAKGQPREPQVYVTLPPSRDE 240  
Db 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISAKGQPREPQVYVTLPPSRDE 240  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
QY 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330  
Db 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330

## RESULT 2

Q6GMX6 HUMAN  
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.  
AC Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]

## NUCLEOTIDE SEQUENCE.

TISSUE=Primary B-Cells;  
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences;"  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]

## NUCLEOTIDE SEQUENCE.

TISSUE=Primary B-Cells;  
RC Strausberg R.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG\_v.

Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_Like; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; B3A9B7D0FDB1386E CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 465;

Best Local Similarity 99.4%; Pred. No. 9.1e-120;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSCKSTSGGTAALGCLVKDYFPPEVTVVSNWGALTSVHTFPVAVLQSS 60

Db 136 ASTKGPSVFPPLAPSCKSTSGGTAALGCLVKDYFPPEVTVVSNWGALTSVHTFPVAVLQSS 195

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPPELAGA 120

Db 196 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCPCPAPPELAGG 255

QY 121 PSVFLFPPKPKDGLMIKRTPEVTVVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEOYN 180

Db 256 PSVFLFPPKPKDGLMIKRTPEVTVVVDVSHEDPEVKFNWTVDGVGVHNAKTKPREEOYN 315

QY 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISAKGQPREPQVYVTLPPSRDE 240

Db 316 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISAKGQPREPQVYVTLPPSRDE 375

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300

Db 376 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 435

QY 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330

Db 436 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 465

## RESULT 3

Q569F4 HUMAN  
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q569F4  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]

## NUCLEOTIDE SEQUENCE.

TISSUE=Lymph;  
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```

RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 9.2e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 140 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKHTCCPCPAPELAGA 120
Db 200 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKHTCCPCPAPELGG 259
Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 260 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 319
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 320 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 379
Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 439
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 440 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 469

RESULT 4
Q727P5 HUMAN
ID Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSSP; P01857; IHZH.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 469;
Best Local Similarity 99.4%; Pred. No. 9.2e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 140 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKHTCCPCPAPELAGA 120
Db 200 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSPNTKVDKVEPKSCDKHTCCPCPAPELGG 259
Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 260 PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 319
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 320 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 379
Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSKLTVDKSRW 439
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 440 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 469

RESULT 5
Q725W1 HUMAN
ID Q725W1 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -; mRNA.  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 470;  
Best Local Similarity 99.4%; Pred. No. 9.2e-120;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 60  
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 200

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLAGA 120  
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLGG 260

QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRREQYN 180  
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRREQYN 320

QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
DB 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300  
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 440

QY 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
DB 441 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 470

RESULT 6  
Q6PJA4 HUMAN PRELIMINARY; PRT; 470 AA.  
AC Q6PJA4;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018747; AAH18747.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR SMR; Q6PJA4; 20-470.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 470;  
Best Local Similarity 99.4%; Pred. No. 9.2e-120;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 60  
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 200

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLAGA 120  
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLGG 260

QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRREQYN 180  
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRREQYN 320

QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
DB 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300  
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 440

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Qy 301 OQGNVFCVNMHEALHNHYTKQSLSPGK 330
Db 441 OQGNVFCVNMHEALHNHYTKQSLSPGK 470

RESULT 7
QSEPF5_HUMAN
ID QSEPF5_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEPF5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Bellard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125."
EMBL: AY894992; AAWB2028.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN
FT SEQUENCE 475 AA; 52362 MW; 1367D400DC7B2859 CRC64;

Query Match 19 Potential.
Best Local Similarity 99.5%; Score 1756; DB 2; Length 475;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGLVVDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPPLAPSSKSTSGGTAALGLVVDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCPAPELAGA 120
Db 206 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCPAPELAGG 265

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 326 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 385

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 386 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 445

Qy 301 OQGNVFCVNMHEALHNHYTKQSLSPGK 330
Db 446 OQGNVFCVNMHEALHNHYTKQSLSPGK 475

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RESULT 8
Q6GMW7_HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL: BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 99.5%; Score 1756; DB 2; Length 475;
Best Local Similarity 99.4%; Pred. No. 9.3e-120;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGLVVDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPPLAPSSKSTSGGTAALGLVVDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 205

Qy 61 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCPAPELAGA 120
Db 206 GLYSLSSVWTVPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKTHTCPPCPAPELAGG 265

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325

```



QY 191 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAGQRPQVYTLPPSRDE 240  
 |||||  
 Db 326 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAGQRPQVYTLPPSRDE 385  
 |||||  
 QY 241 LTKNQVSLTCLVKGFPYSDIAVWESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSRW 300  
 |||||  
 Db 386 LTKNQVSLTCLVKGFPYSDIAVWESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSRW 445  
 |||||  
 QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330  
 |||||  
 Db 446 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 475  
 |||||  
 RESULT 9  
 Q6GMX1\_HUMAN  
 ID Q6GMX1\_HUMAN PRELIMINARY; PRT; 476 AA.  
 AC Q6GMX1  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073773; AAH7373.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.V.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 5286 MW; 622AABA5C62DDE9D CRC64;

Query Match

99.5%; Score 1756; DB 2; Length 476;

Best Local Similarity 99.4%; Pred. No. 9.3e-120;  
 Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFLPAPSSKSTGGTAAAGCLVADKDYFPEPVTVSNWNGALTSGVHTFPVAVLOSS 60  
 |||||  
 Db 147 ASTKGPSVFLPAPSSKSTGGTAAAGCLVADKDYFPEPVTVSNWNGALTSGVHTFPVAVLOSS 206  
 |||||  
 QY 61 GLYSLSVVTVSSSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPPELAGA 120  
 |||||  
 Db 207 GLYSLSVVTVSSSSSLGTQTYICNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPPELAGG 266  
 |||||  
 QY 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHDEPKVKNWYVDGVFVNNAKTKPREEOVN 180  
 |||||  
 Db 267 PSVFLPPPKDPTLMISRTPEVTCVVDVSHDEPKVKNWYVDGVFVNNAKTKPREEOVN 326  
 |||||  
 QY 181 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAGQRPQVYTLPPSRDE 240  
 |||||  
 Db 327 STYRVSVLTVLHODWLNKGKCVSNKALPAPIEKTISKAGQRPQVYTLPPSRDE 386  
 |||||  
 QY 241 LTKNQVSLTCLVKGFPYSDIAVWESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSRW 300  
 |||||  
 Db 387 LTKNQVSLTCLVKGFPYSDIAVWESNGQPNNTKTPPVLDSDGSPFLYSKLTVDKSRW 446  
 |||||  
 QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330  
 |||||  
 Db 447 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 476  
 |||||

## RESULT 10

Q6IN78\_HUMAN  
 ID Q6IN78\_HUMAN PRELIMINARY; PRT; 466 AA.  
 AC Q6IN78;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DE IGHI protein.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RC NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC072419; AAH72419.1; -; mRNA.  
 DR HSSP; P01861; 1ADQ.

DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCEDE81076E CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 466;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-119;  
 Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 60  
 |||||  
 Db 137 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 196  
 |||||

Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120  
 |||||  
 Db 197 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 256  
 |||||

Qy 121 PSVPLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
 |||||  
 Db 257 PSVPLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 316  
 |||||

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
 |||||  
 Db 317 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 376  
 |||||

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
 |||||  
 Db 377 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 436  
 |||||

Qy 301 OQGNVFCVSNVHEALHNHYTKSLSPGK 330  
 |||||  
 Db 437 OQGNVFCVSNVHEALHNHYTKSLSPGK 466  
 |||||

RESULT 11  
 Q6N089\_HUMAN PRELIMINARY; PRT; 472 AA.  
 AC Q6N089;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Rectum tumor;  
 RG The German cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640627; CA845781.1; -; mRNA.  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGc1; 3.

DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 99.3%; Score 1753; DB 2; Length 472;  
 Best Local Similarity 99.1%; Pred. No. 1.5e-119;  
 Matches 327; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 60  
 |||||  
 Db 143 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 202  
 |||||

Qy 61 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120  
 |||||  
 Db 203 GLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 262  
 |||||

Qy 121 PSVPLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
 |||||  
 Db 263 PSVPLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 322  
 |||||

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
 |||||  
 Db 323 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 382  
 |||||

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
 |||||  
 Db 383 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 442  
 |||||

Qy 301 OQGNVFCVSNVHEALHNHYTKSLSPGK 330  
 |||||  
 Db 443 OQGNVFCVSNVHEALHNHYTKSLSPGK 472  
 |||||

RESULT 12  
 Q6P055\_HUMAN PRELIMINARY; PRT; 473 AA.  
 AC Q6P055;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]



```
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          99.3%; Score 1752; DB 2; Length 473;
Best Local Similarity 99.1%; Pred. No. 1.8e-119;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAVLQSS 60
Db 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAVLQSS 203
QY 61 GLYSLSSVTVTPSSSLGQTICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLGG 120
Db 204 GLYSLSSVTVTPSSSLGQTICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLGG 263
QY 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 264 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 323
QY 181 STYRVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 240
Db 324 STYRVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 383
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 443
QY 301 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 330
Db 444 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 473

RESULT 13
Q6MZQ6 HUMAN
ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFP686G11190.
GN Name=DKFP686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CRE45972.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6MZQ6; 20-475.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          99.3%; Score 1752; DB 2; Length 475;
Best Local Similarity 99.1%; Pred. No. 1.8e-119;
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAVLQSS 60
Db 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSVNSGALTSGVHTFPAVLQSS 205
QY 61 GLYSLSSVTVTPSSSLGQTICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLAGA 120
Db 206 GLYSLSSVTVTPSSSLGQTICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPELLGG 265
QY 121 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 266 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 325
QY 181 STYRVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 240
Db 326 STYRVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRDE 385
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 445
QY 301 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 330
Db 446 QQGNVFCVSMVHEALHNHYTQKSLSLSPGK 475

RESULT 14
Q6N094 HUMAN
ID Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFP686G001196.
GN Name=DKFP686G001196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAB45776.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
```

DR SMART; SM00407; IGel; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 2252473D3D35AEC18 CRC64;  
  
Query Match 99.3%; Score 1752; DB 2; Length 480;  
Best Local Similarity 99.1%; Pred. No. 1.8e-119;  
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60  
Db 151 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 210  
  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 211 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGG 270  
  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRBEOYN 180  
Db 271 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRBEOYN 330  
  
Qy 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240  
Db 331 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 390  
  
Qy 241 LTRKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 391 LTRKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 450  
  
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 451 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 480

RESULT 15  
Q6N097\_HUMAN PRELIMINARY; PRT; 481 AA.  
AC Q6N097;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFP686H20196.  
GN Name=DKFP686H20196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,  
RA Pobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the ENBL/GenBank/DBJ databases.  
DR EMBL; BX640619; CAB45773.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGel; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 99.3%; Score 1752; DB 2; Length 481;  
Best Local Similarity 99.1%; Pred. No. 1.9e-119;  
Matches 327; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60  
Db 152 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 211  
  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 212 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGG 271  
  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRBEOYN 180  
Db 272 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPRBEOYN 331  
  
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Db 332 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 391  
  
Qy 241 LTRKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 392 LTRKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 451  
  
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 452 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 481

Search completed: January 28, 2006, 09:44:19  
Job time : 175.91 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 48.586 seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTGSPVFLAPSKSTSG.....MREALHNHYTKSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgm2\_6/ptodata/1/iaa/5 COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/H COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/PCRTUS COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/RE COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	99.5	371	1	US-08-236-311-7
2	1756	99.5	371	2	US-08-457-918-7
3	1756	99.5	371	2	US-10-157-408-7
4	1756	99.5	446	2	US-08-397-411-7
5	1756	99.5	449	1	US-08-458-516-13
6	1756	99.5	467	2	US-08-030-175-41
7	1756	99.5	467	2	US-08-030-175-42
8	1756	99.5	470	2	US-10-104-047-3730
9	1756	99.5	476	1	US-08-378-939-10
10	1756	99.5	547	2	US-09-746-359A-54
11	1756	99.5	567	2	US-09-825-561A-16
12	1756	99.5	571	2	US-09-746-359A-53
13	1756	99.5	951	2	US-09-313-942-9
14	1756	99.5	951	2	US-10-282-162-9
15	1752	99.3	462	2	US-09-289-942A-7
16	1752	99.3	475	2	US-09-740-002-27
17	1752	99.3	476	2	US-08-487-550-4
18	1752	99.3	476	2	US-08-487-550-12
19	1752	99.3	476	2	US-09-526-088-4
20	1752	99.3	476	2	US-09-526-098-12
21	1752	99.3	476	2	US-09-383-916-4
22	1752	99.3	476	2	US-09-383-916-12
23	1752	99.3	476	2	US-09-758-173-4
24	1752	99.3	476	2	US-09-758-173-12
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26	1752	99.3	476	2	US-09-576-424-12
27	1752	99.3	478	2	US-08-487-550-8

28	1752	99.3	478	2	US-09-526-098-8
29	1752	99.3	478	2	US-09-383-916-8
30	1752	99.3	478	2	US-09-758-173-8
31	1752	99.3	478	2	US-09-576-424-8
32	1751	99.2	459	1	US-08-157-101A-7
33	1751	99.2	470	2	US-09-238-741-4
34	1750	99.2	330	2	US-09-301-593-22
35	1750	99.2	451	1	US-08-887-352B-14
36	1750	99.2	451	1	US-08-887-352B-16
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45	1750	99.2	451	2	US-09-296-005-16

ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-236-311-7

Query Match 99.5%; Score 1756; DB 1; Length 371;  
Best Local Similarity 99.4%; Pred. No. 6e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60  
Db 42 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101  
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 102 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELGG 161  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
Db 162 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 221  
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Db 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 281  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 341  
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

## RESULT 2

US-08-457-918-7  
; Sequence 7, Application US/08457918  
; Patent No. 6117655

; GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J.

; APPLICANT: Gregory, Timothy J.

; TITLE OF INVENTION: Adhesion Variants

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 1-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/236311

; FILING DATE: 02-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/936190

; FILING DATE: 26-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/842777

; FILING DATE: 18-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/250785

; FILING DATE: 28-SEP-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/104329

; FILING DATE: 02-OCT-1987

; ATTORNEY/AGENT INFORMATION:

; NAME: Kubinec, Jeffrey S.

; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0444P1C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-8228

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 371 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-457-918-7

## Query Match

Best Local Similarity 99.5%; Score 1756; DB 2; Length 371;

Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60  
Db 42 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 101  
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 102 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKTHTCPPCPAPELGG 161  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180  
Db 162 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 221  
Qy 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 281  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
Db 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 341  
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

## RESULT 3

US-10-157-408-7

; Sequence 7, Application US/10157408

; Patent No. 6710169

; GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J.

; APPLICANT: Gregory, Timothy J.

; TITLE OF INVENTION: Adhesion Variants

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/157,408

; FILING DATE: 28-MAY-2002

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 1-JUN-1995

; APPLICATION NUMBER: 08/236311

; FILING DATE: 02-MAY-1994

; APPLICATION NUMBER: 07/936190

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 99.5%; Score 1756; DB 2; Length 371;  
Best Local Similarity 99.4%; Pred. No. 6e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
DB 42 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 101  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120  
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGG 161  
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DB 162 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 221  
QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240  
DB 222 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 281  
QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
DB 282 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 341  
QY 301 QQGNVFCVSMHEALHNHYTOKSLSPGK 330  
DB 342 QQGNVFCVSMHEALHNHYTOKSLSPGK 371

RESULT 4  
US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 446 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 99.5%; Score 1756; DB 2; Length 446;  
Best Local Similarity 99.4%; Pred. No. 7.9e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
DB 117 ASTKGPSVFLPAPSSKSTGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176  
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120  
DB 177 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPELAGG 236  
QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180  
DB 237 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 296  
QY 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 240  
DB 297 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDE 356  
QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300  
DB 357 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 416  
QY 301 QQGNVFCVSMHEALHNHYTOKSLSPGK 330  
DB 417 QQGNVFCVSMHEALHNHYTOKSLSPGK 446

RESULT 5  
US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-13

Query Match 99.5%; Score 1756; DB 1; Length 449;  
Best Local Similarity 99.4%; Pred. No. 7.9e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGSPVFLAPSSKSTSGTAAALCLVXDYFPEPTVSNVSGALTSVGHVTFPAVLQSS 60  
DB 120 ASTKGSPVFLAPSSKSTSGTAAALCLVXDYFPEPTVSNVSGALTSVGHVTFPAVLQSS 179  
QY 61 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKHTCCPCPAPELAGA 120  
DB 180 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKHTCCPCPAPELAGG 239  
QY 121 PSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNKTKPREQYN 180  
DB 240 PSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNKTKPREQYN 299  
QY 181 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKQPREPQVYTLPPSRDE 240  
DB 300 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKQPREPQVYTLPPSRDE 359  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 419  
QY 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330  
DB 420 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 449

RESULT 6  
US-08-030-175-41  
Sequence 41, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.  
COUNTRY: U.S.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: WordPerfect 5.0 (Dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-41

Query Match 99.5%; Score 1756; DB 2; Length 467;  
Best Local Similarity 99.4%; Pred. No. 8.4e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGSPVFLAPSSKSTSGTAAALCLVXDYFPEPTVSNVSGALTSVGHVTFPAVLQSS 60  
DB 138 ASTKGSPVFLAPSSKSTSGTAAALCLVXDYFPEPTVSNVSGALTSVGHVTFPAVLQSS 197  
QY 61 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKHTCCPCPAPELAGA 120  
DB 198 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKHTCCPCPAPELAGG 257  
QY 121 PSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNKTKPREQYN 180  
DB 258 PSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYVDGVEVHNKTKPREQYN 317  
QY 181 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKQPREPQVYTLPPSRDE 240  
DB 318 STRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKQPREPQVYTLPPSRDE 377  
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 437  
QY 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330  
DB 438 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 467

RESULT 7  
US-08-030-175-42  
Sequence 42, Application US/08030175  
Patent No. 6767996  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D.  
APPLICANT: Clark, Michael R.  
APPLICANT: Cobbold, Stephen P.  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
STREET: 555 13TH ST., NW Suite 701 East  
CITY: Washington  
STATE: D. C.

```
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Doc Text)
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1993
; APPLICATION NUMBER: US/08/030,175
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-175-42

Query Match 99.5%; Score 1756; DB 2; Length 467;
Best Local Similarity 99.4%; Pred. No. 8.4e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVVWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVVWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 257
Qy 121 PSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180
Db 258 PSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 317
Qy 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 240
Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 8
US-10-104-047-3730
; Sequence 3730, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cdna
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3730

; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Doc Text)
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1993
; APPLICATION NUMBER: US/08/030,175
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-175-42

Query Match 99.5%; Score 1756; DB 2; Length 467;
Best Local Similarity 99.4%; Pred. No. 8.4e-157;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVVWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVVWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELLAG 257
Qy 121 PSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 180
Db 258 PSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREEQYN 317
Qy 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 240
Db 318 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 9
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876361
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
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;  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 99.5%; Score 1756; DB 1; Length 476;  
Best Local Similarity 99.4%; Pred. No. 8.7e-157;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 147 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 206

Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 207 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 266

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 180  
Db 267 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 326

Qy 181 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 327 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 386

Qy 241 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 387 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 446

Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 447 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 10  
US-09-746-359A-54  
; Sequence 54, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Egan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekhar, Yasmin A.  
; APPLICANT: No. 6610286ak, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746.359A  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 54  
; LENGTH: 547  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-746-359A-54

Query Match 99.5%; Score 1756; DB 2; Length 547;  
Best Local Similarity 99.4%; Pred. No. 1.1e-156;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 218 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 277

Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 278 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 337

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 180  
Db 338 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 397

Qy 181 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 398 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 457

Qy 241 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 458 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 517

Qy 301 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 330  
Db 518 QOQNVFSCVMHEALHNHYTQKSLSLSPGK 547

RESULT 11  
US-09-825-561A-16  
; Sequence 16, Application US/09825561A  
; Patent No. 677539  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. 677539ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825.561A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: soluble zalpha11r/IgGgamma1 polypeptide  
US-09-825-561A-16

Query Match 99.5%; Score 1756; DB 2; Length 567;  
Best Local Similarity 99.4%; Pred. No. 1.1e-156;  
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
Db 238 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 297

Qy 61 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 298 GLYSLSVSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPELAGG 357

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 180  
Db 358 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKTPREQYN 417

Qy 181 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 418 STRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 477

Qy 241 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 478 LTKNQVSLTCLVKGFYPSDIAVESNGQPENNYKTTTPPVLDSDGSPFLYSKLTVDKSRW 537



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; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-9

Query Match      99.5%; Score 1756; DB 2; Length 951;
Best Local Similarity 99.4%; Pred. No. 2.4e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 622 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 681
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 682 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGG 741
QY 121 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 742 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 801
QY 181 STYRVSVTLVHODWLNKGKVKVSNKALPAPIEKTIISKAKGQPRFPQVYTLPPSRDE 240
Db 802 STYRVSVTLVHODWLNKGKVKVSNKALPAPIEKTIISKAKGQPRFPQVYTLPPSRDE 861
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 921
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 922 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 951

RESULT 14
US-10-282-162-9
; Sequence 9, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-9

Query Match      99.5%; Score 1756; DB 2; Length 951;
Best Local Similarity 99.4%; Pred. No. 2.4e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 538 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 567

RESULT 12
US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-53

Query Match      99.5%; Score 1756; DB 2; Length 571;
Best Local Similarity 99.4%; Pred. No. 1.1e-156;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 242 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 301
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 302 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGG 361
QY 121 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 362 PSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 421
QY 181 STYRVSVTLVHODWLNKGKVKVSNKALPAPIEKTIISKAKGQPRFPQVYTLPPSRDE 240
Db 422 STYRVSVTLVHODWLNKGKVKVSNKALPAPIEKTIISKAKGQPRFPQVYTLPPSRDE 481
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 300
Db 482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRW 541
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 542 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 571

RESULT 13
US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 140.721 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765

Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYTQKSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1765	100.0	330	4	US-10-733-563-110
2	1765	100.0	333	4	US-10-272-899A-10
3	1765	100.0	333	4	US-10-733-563-114
4	1765	100.0	356	4	US-10-272-899A-70
5	1765	100.0	448	4	US-10-171-452A-42
6	1765	100.0	448	4	US-10-171-452A-54
7	1765	100.0	448	4	US-10-353-708-42
8	1765	100.0	448	4	US-10-353-708-54
9	1765	100.0	448	4	US-10-731-984-8
10	1765	100.0	448	4	US-10-731-984-24
11	1765	100.0	467	4	US-10-171-452A-53
12	1765	100.0	467	4	US-10-353-708-53
13	1765	100.0	467	4	US-10-731-984-7
14	1765	100.0	467	4	US-10-731-984-23
15	1759	99.7	473	4	US-10-467-253-13
16	1758	99.6	469	4	US-10-404-724-72
17	1756	99.5	330	3	US-09-995-898A-15
18	1756	99.5	330	3	US-09-892-949-38
19	1756	99.5	330	4	US-10-047-542-20
20	1756	99.5	330	4	US-10-269-805-68
21	1756	99.5	330	4	US-10-310-719-8
22	1756	99.5	330	4	US-10-112-582-1
23	1756	99.5	330	4	US-10-320-231A-81
24	1756	99.5	330	4	US-10-363-902A-6
25	1756	99.5	330	4	US-10-408-901-2
26	1756	99.5	330	4	US-10-420-034A-15
27	1756	99.5	330	4	US-10-257-907-5

28	1756	99.5	330	4	US-10-656-769-2	Sequence 2, Appli
29	1756	99.5	330	4	US-10-772-531-38	Sequence 38, Appli
30	1756	99.5	330	4	US-10-479-326-1	Sequence 1, Appli
31	1756	99.5	330	5	US-10-815-449-8	Sequence 8, Appli
32	1756	99.5	330	5	US-10-684-957-2	Sequence 2, Appli
33	1756	99.5	330	5	US-10-886-838-6	Sequence 6, Appli
34	1756	99.5	330	5	US-10-822-300-7	Sequence 3, Appli
35	1756	99.5	330	5	US-10-822-300-7	Sequence 7, Appli
36	1756	99.5	330	5	US-10-687-118-3	Sequence 3, Appli
37	1756	99.5	330	5	US-10-687-118-7	Sequence 7, Appli
38	1756	99.5	330	5	US-10-901-735-2	Sequence 2, Appli
39	1756	99.5	330	5	US-10-698-907-22	Sequence 22, Appli
40	1756	99.5	330	5	US-10-928-305-7	Sequence 7, Appli
41	1756	99.5	330	5	US-10-480-109-5	Sequence 5, Appli
42	1756	99.5	330	5	US-10-891-658-2	Sequence 2, Appli
43	1756	99.5	330	5	US-10-867-506-81	Sequence 81, Appli
44	1756	99.5	330	5	US-10-937-596-31	Sequence 31, Appli
45	1756	99.5	330	5	US-10-893-576-45	Sequence 45, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-733-563-110  
; Sequence 110, Application US/10733563  
; Publication No. US20040151721A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Ponath, Paul  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 10448-213001  
; CURRENT APPLICATION NUMBER: US/10/733,563  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: US 10/272,899  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: US 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human IgG1-FcRmut protein  
US-10-733-563-110

Query Match						100.0%; Score 1765; DB 4; Length 330;
Best Local Similarity						100.0%; Pred. No. 1.3e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA
Db	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA	1	ASTKGPSVFPLAPSSKSTSGGTAA
Qy	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN
Db	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN	61	GLYSLSSVTVTPSSSLGTQTYICNVN
Qy	121	PSVFLPPPKDITLMISRTPEVTCVV	121	PSVFLPPPKDITLMISRTPEVTCVV	121	PSVFLPPPKDITLMISRTPEVTCVV
Db	121	PSVFLPPPKDITLMISRTPEVTCVV	121	PSVFLPPPKDITLMISRTPEVTCVV	121	PSVFLPPPKDITLMISRTPEVTCVV
Qy	181	STYRWVSVLTVLHODLNGKEYCKV	181	STYRWVSVLTVLHODLNGKEYCKV	181	STYRWVSVLTVLHODLNGKEYCKV
Db	181	STYRWVSVLTVLHODLNGKEYCKV	181	STYRWVSVLTVLHODLNGKEYCKV	181	STYRWVSVLTVLHODLNGKEYCKV
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEW	241	LTKNQVSLTCLVKGFYPSDIAVEW	241	LTKNQVSLTCLVKGFYPSDIAVEW
Db	241	LTKNQVSLTCLVKGFYPSDIAVEW	241	LTKNQVSLTCLVKGFYPSDIAVEW	241	LTKNQVSLTCLVKGFYPSDIAVEW

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Db      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Qy      301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db      301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
US-10-272-899A-10
; Sequence 10, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MEI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-272-899A-10

Query Match      100.0%; Score 1765; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db      4 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 63
Qy      61 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPCPAPELAGA 120
Db      64 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPCPAPELAGA 123
Qy      121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRREQYN 180
Db      124 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRREQYN 183
Qy      181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db      184 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 243
Qy      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db      244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 303
Qy      301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db      304 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 333

RESULT 3
US-10-733-563-114
; Sequence 114, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
```

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; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-733-563-114

Query Match      100.0%; Score 1765; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db      4 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 63
Qy      61 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPCPAPELAGA 120
Db      64 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVPEKSCDKHTCTCPCPAPELAGA 123
Qy      121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRREQYN 180
Db      124 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRREQYN 183
Qy      181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Db      184 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 243
Qy      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 300
Db      244 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRW 303
Qy      301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db      304 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 333

RESULT 4
US-10-272-899A-70
; Sequence 70, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
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; LENGTH: 356
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette protein sequence
US-10-272-899A-70

Query Match      100.0%; Score 1765; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 27 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 86
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 87 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 146
QY 121 PSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 147 PSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 206
QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITLPPSRDE 240
Db 207 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITLPPSRDE 266
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 267 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 326
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 327 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 356

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```

RESULT 5
US-10-171-452A-42
; Sequence 42, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobboid, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 42
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-42

```

```

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.9e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 120
Db 179 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELAGA 238
QY 121 PSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 239 PSVFLPPPKPDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 298
QY 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITLPPSRDE 240
Db 299 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITLPPSRDE 358
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFPLYSKLTVDKSRW 418
QY 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 6
US-10-171-452A-54
; Sequence 54, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobboid, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10/171,452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-54

Query Match      100.0%; Score 1765; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.9e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

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Db 119 ASTKGPSVFPPLAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238  
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 358  
Qy 241 LTRKNQVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 359 LTRKNQVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 418  
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 419 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 448

RESULT 7  
US-10-353-708-42  
; Sequence 42, Application US/10353708  
; Publication No. US20030219403A1  
; GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobbold, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen  
; FILE REFERENCE: 695458-73  
; CURRENT APPLICATION NUMBER: US/10/353,708  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US10/171,452  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 60  
; SEQ ID NO 42  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain of humanized antibody  
US-10-353-708-42

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238

Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298  
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Db 299 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 358  
Qy 241 LTRKNQVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 359 LTRKNQVSLTCLVKGFPYSDIAVESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 418  
Qy 301 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
Db 419 QOQNVFSCSVNHEALHNHYTQKSLSLSPGK 448

RESULT 8  
US-10-353-708-54  
; Sequence 54, Application US/10353708  
; Publication No. US20030219403A1  
; GENERAL INFORMATION:  
; APPLICANT: Frewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobbold, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen  
; FILE REFERENCE: 695458-73  
; CURRENT APPLICATION NUMBER: US/10/353,708  
; PRIOR FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US10/171,452  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 60  
; SEQ ID NO 54  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Heavy chain of humanized antibody  
US-10-353-708-54

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60  
Db 119 ASTKGPSVFPPLAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 178  
Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120  
Db 179 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 238  
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180  
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 298

Qy 181 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 448

## RESULT 9

US-10-731-984-8  
; Sequence 8, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TLN-022  
; CURRENT APPLICATION NUMBER: US/10/731,984  
; PRIOR FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-8

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADYFPEPPTVSNVSGALTSVHTFPAVLOSS 60  
Db 119 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADYFPEPPTVSNVSGALTSVHTFPAVLOSS 178  
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPAPELAGA 120  
Db 179 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPAPELAGA 238  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEQYN 180  
Db 239 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEQYN 298  
Qy 181 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 448

## RESULT 10

US-10-731-984-24  
; Sequence 24, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia

; APPLICANT: RINGLER, Douglas J.  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TLN-022  
; CURRENT APPLICATION NUMBER: US/10/731,984  
; PRIOR FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-24

Query Match 100.0%; Score 1765; DB 4; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.9e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADYFPEPPTVSNVSGALTSVHTFPAVLOSS 60  
Db 119 ASTKGPSVFPLAPSSKSTSGGTAAAGCLVADYFPEPPTVSNVSGALTSVHTFPAVLOSS 178  
Qy 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPAPELAGA 120  
Db 179 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPAPELAGA 238  
Qy 121 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEQYN 180  
Db 239 PSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNATKPREEQYN 298  
Qy 181 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 240  
Db 299 STYRVSVLTCLVHODWLNKGYCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRDE 358  
Qy 241 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 300  
Db 359 LTKNQVSLTCLVKGPYSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSKLTVDKSRW 418  
Qy 301 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 330  
Db 419 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 448

## RESULT 11

US-10-171-452A-53  
; Sequence 53, Application US/10171452A  
; Publication No. US20030108518A1  
; GENERAL INFORMATION:  
; APPLICANT: Prewin, Mark  
; APPLICANT: Waldmann, Herman  
; APPLICANT: Gorman, Scott  
; APPLICANT: Hale, Geoff  
; APPLICANT: Rao, Patricia  
; APPLICANT: Kornaga, Tadeusz  
; APPLICANT: Ringler, Douglas  
; APPLICANT: Cobboid, Stephen  
; APPLICANT: Winsor-Hines, Dawn  
; TITLE OF INVENTION: TX1 Antibody and Uses Therefor  
; FILE REFERENCE: 695458-59  
; CURRENT APPLICATION NUMBER: US/10/171,452A  
; PRIOR FILING DATE: 2003-02-10  
; PRIOR APPLICATION NUMBER: US60/373,471  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/373,470  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: US60/345,194  
; PRIOR FILING DATE: 2002-10-19  
; PRIOR APPLICATION NUMBER: GB0122724.8  
; PRIOR FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: GB0114517.6



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; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPISRDE 240
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPISRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 467

RESULT 12
US-10-353-708-53
; Sequence 53, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobboid, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-53

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPISRDE 240
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPISRDE 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCVSMHEALHNHYTQKSLSLSPGK 467

RESULT 13
US-10-731-984-7
; Sequence 7, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-731-984-7

Query Match      100.0%; Score 1765; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 60
Db 138 ASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTFAVLQSS 197
Qy 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 120
Db 198 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKHTCTCPCPAPELAGA 257
Qy 121 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
Db 258 PSVFLPPPKPDTLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317
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Qy 181 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
Db 318 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 377  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 378 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNHYTKQSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNHYTKQSLSPGK 467

## RESULT 14

US-10-731-984-23  
; Sequence 23, Application US/10731984  
; Publication No. US20040175381A1  
; GENERAL INFORMATION:  
; APPLICANT: WINDSOR-HINES, Dawn  
; APPLICANT: RAO, Patricia  
; APPLICANT: RINGLER, Douglas J.  
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES  
; FILE REFERENCE: TLM-022  
; CURRENT APPLICATION NUMBER: US/10/731.984  
; CURRENT FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: 60/431839  
; PRIOR FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric Sequence  
US-10-731-984-23

Query Match 100.0%; Score 1765; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 2e-128;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Db 138 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCTPCPAPELAGA 120  
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCTPCPAPELAGA 257  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317  
Qy 181 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
Db 318 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 377  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 378 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 437  
Qy 301 QQGNVFCSCVMHEALHNHYTKQSLSPGK 330  
Db 438 QQGNVFCSCVMHEALHNHYTKQSLSPGK 467

## RESULT 15

US-10-467-253-13  
; Sequence 13, Application US/10467253  
; Publication No. US20040170627A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham plc

; APPLICANT: Irving, Elaine A  
; APPLICANT: Vinson, Mary  
; TITLE OF INVENTION: Novel Method of Treatment  
; FILE REFERENCE: SAL/P32763  
; CURRENT APPLICATION NUMBER: US/10/467.253  
; CURRENT FILING DATE: 2003-08-05  
; PRIOR APPLICATION NUMBER: GB 0103174.9  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 473  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: mouse/human  
; OTHER INFORMATION: chimeric anti-MAG antibody heavy chain  
US-10-467-253-13

Query Match 99.7%; Score 1759; DB 4; Length 473;  
Best Local Similarity 99.7%; Pred. No. 5.9e-128;  
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Db 144 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203  
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCTPCPAPELAGA 120  
Db 204 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCTPCPAPELAGA 263  
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180  
Db 264 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 323  
Qy 181 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240  
Db 324 STYRVSVLTCLVHQLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 383  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 300  
Db 384 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPPVLDSDGSPFLYSLKLTVDKSRW 443  
Qy 301 QQGNVFCSCVMHEALHNHYTKQSLSPGK 330  
Db 444 QQGNVFCSCVMHEALHNHYTKQSLSPGK 473

Search completed: January 28, 2006, 10:11:23

Job time : 141.721 secs

**THIS PAGE BLANK (USPTO)**

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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 19.8198 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-110

Perfect score: 1765  
Sequence: 1 ASTKGPSVFPLAPSSKSTSG.....MHEALHNHYTKSLSPGK 330

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	100.0	448	7 US-11-158-505-8	Sequence 8, Appli
2	1765	100.0	448	7 US-11-158-505-24	Sequence 24, Appl
3	1765	100.0	467	7 US-11-158-505-5	Sequence 5, Appli
4	1765	100.0	467	7 US-11-158-505-7	Sequence 7, Appli
5	1765	100.0	467	7 US-11-158-505-21	Sequence 21, Appl
6	1765	100.0	467	7 US-11-158-505-23	Sequence 23, Appl
7	1756	99.5	330	6 US-10-886-383-6	Sequence 6, Appli
8	1756	99.5	330	7 US-10-493-909-20	Sequence 20, Appl
9	1756	99.5	330	7 US-11-022-289-11	Sequence 11, Appli
10	1756	99.5	330	7 US-11-075-351-1	Sequence 1, Appli
11	1756	99.5	330	7 US-11-165-141-15	Sequence 15, Appl
12	1756	99.5	330	7 US-11-102-621-3	Sequence 3, Appli
13	1756	99.5	330	7 US-11-102-621-7	Sequence 7, Appli
14	1756	99.5	335	7 US-11-024-251-35	Sequence 35, Appl
15	1756	99.5	444	7 US-11-172-320-6	Sequence 6, Appli
16	1756	99.5	444	7 US-11-173-969-6	Sequence 6, Appli
17	1756	99.5	451	7 US-11-158-505-33	Sequence 33, Appl
18	1756	99.5	551	7 US-11-022-289-7	Sequence 7, Appli
19	1756	99.5	551	7 US-11-022-289-8	Sequence 8, Appli
20	1756	99.5	557	7 US-11-022-289-4	Sequence 4, Appli
21	1756	99.5	557	7 US-11-022-289-5	Sequence 5, Appli
22	1756	99.5	557	7 US-11-022-289-6	Sequence 6, Appli
23	1754	99.4	592	6 US-10-016-686-4	Sequence 4, Appli
24	1753	99.3	330	7 US-11-102-621-71	Sequence 71, Appl
25	1753	99.3	446	7 US-11-102-621-121	Sequence 121, App

26	1753	99.3	447	7 US-11-102-621-132	Sequence 132, Appl
27	1752	99.3	476	7 US-11-139-499-4	Sequence 4, Appli
28	1752	99.3	476	7 US-11-139-499-12	Sequence 12, Appl
29	1752	99.3	478	7 US-11-139-499-8	Sequence 8, Appli
30	1751	99.2	330	7 US-11-102-621-70	Sequence 70, Appl
31	1750	99.2	330	7 US-11-022-289-1	Sequence 1, Appli
32	1750	99.2	330	7 US-11-102-621-67	Sequence 67, Appl
33	1750	99.2	330	7 US-11-102-621-68	Sequence 68, Appl
34	1750	99.2	330	7 US-11-102-621-69	Sequence 69, Appl
35	1750	99.2	446	7 US-11-102-621-119	Sequence 119, Appl
36	1750	99.2	446	7 US-11-102-621-120	Sequence 120, Appl
37	1750	99.2	447	7 US-11-102-621-130	Sequence 130, Appl
38	1750	99.2	447	7 US-11-102-621-131	Sequence 131, Appl
39	1750	99.2	449	7 US-11-154-337-17	Sequence 17, Appl
40	1750	99.2	451	6 US-10-923-327-7	Sequence 7, Appli
41	1750	99.2	451	6 US-10-923-327-9	Sequence 9, Appli
42	1750	99.2	451	6 US-10-923-327-11	Sequence 11, Appl
43	1750	99.2	452	7 US-11-120-338-14	Sequence 14, Appl
44	1750	99.2	452	7 US-11-107-028-32	Sequence 32, Appl
45	1750	99.2	452	7 US-11-106-820-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1  
US-11-158-505-8  
; Sequence 8, Application US/11158505  
; Publication No. US20060002921A1  
; GENERAL INFORMATION:  
; APPLICANT: WINSOR-HINES, DAWN  
; APPLICANT: RAO, PATRICIA  
; APPLICANT: RINGLER, DOUGLAS J  
; APPLICANT: POWATH, PAUL  
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE  
; FILE OF INVENTION: INDUCTION IN PRIMATES  
; FILE REFERENCE: TLN-031  
; CURRENT APPLICATION NUMBER: US/11/158,505  
; PRIOR FILING DATE: 2005-06-21  
; PRIOR APPLICATION NUMBER: 60/582,181  
; PRIOR FILING DATE: 2004-06-22  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1  
; OTHER INFORMATION: antibody heavy chain construct  
US-11-158-505-8

Query Match 100.0%; Score 1765; DB 7; Length 448;  
Best Local Similarity 100.0%; Pred. No. 2.4e-133;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSVGVHTEPAVLQSS	60
Db	119	ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYPPEPTVSWNSGALTSVGVHTEPAVLQSS	178
Qy	61	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTTCCPCAPAPELAGA	120
Db	179	GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNPKVDKVPKSCDKTHTTCCPCAPAPELAGA	238
Qy	121	PSVFLPPPKDPTLMISRTPEVTCVVDVSHDEVEKFNVTVDGVGVHNAKTKPREEQYN	180
Db	239	PSVFLPPPKDPTLMISRTPEVTCVVDVSHDEVEKFNVTVDGVGVHNAKTKPREEQYN	298
Qy	181	STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVYTLPPSRDE	240
Db	299	STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYVYTLPPSRDE	358
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW	300

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Db 359 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 418
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 2
US-11-158-505-24
; Sequence 24, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-24

Query Match 100.0%; Score 1765; DB 7; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.4e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 119 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPAPELAGA 120
Db 179 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPAPELAGA 238
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 239 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 298
Qy 181 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240
Db 299 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 358
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 359 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 418
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 419 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 3
US-11-158-505-5
; Sequence 5, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
```

```
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-5

Query Match 100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPAPELAGA 120
Db 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPPAPELAGA 257
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 180
Db 258 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 317
Qy 181 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 240
Db 318 STYRVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 377
Qy 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-11-158-505-7
; Sequence 7, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-7
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Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 5
US-11-158-505-21
; Sequence 21, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-21

Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 6
US-11-158-505-23
; Sequence 23, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-23

Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 257

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
DB 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 317

QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 7
US-10-886-383-6
; Sequence 6, Application US/10886383
; Publication No. US20060005571A1
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QY 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 318 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 377

QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

RESULT 6
US-11-158-505-23
; Sequence 23, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-23

Query Match      100.0%; Score 1765; DB 7; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 120
DB 198 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGA 257

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QY 241 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 437

QY 301 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYTKQSLSPGK 467

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; Sequence 6, Application US/10886383
; Publication No. US20060005571A1
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; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; FILE OF INVENTION: thereof
; REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886.383
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-886-383-6

Query Match          99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180
Db 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

RESULT 9
US-11-022-289-11
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022.289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-022-289-11

Query Match          99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180
Db 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

US-10-909-909-20
; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; TITLE OF INVENTION: AND PATHOGEN-MEDIATED DISEASES
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493.909
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-493-909-20

Query Match          99.5%; Score 1756; DB 6; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180
Db 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

RESULT 9
US-11-022-289-11
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022.289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-022-289-11

Query Match          99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180
Db 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

US-11-022-289-11
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Query Match          99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSVWTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELAGG 120

Qy 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180
Db 121 PSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREPQYN 180

Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRDE 240

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

US-11-022-289-11
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RESULT 10
US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 11
US-11-165-141-15
; Sequence 15, Application US/111165141
; Publication No. US20050266485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/11/165,141
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/09/995,898
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
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; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-141-15

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 12
US-11-102-621-3
; Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsuruhita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF ECRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-3

Query Match      99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHKTPCPAPPELAGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
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Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 13
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsuruhita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PeRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05982.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 14
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsuruhita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PeRN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05982.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 99.5%; Score 1756; DB 7; Length 330;
Best Local Similarity 99.4%; Pred. No. 8.7e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Db 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
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```
US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IgG Secreted Constant Domain
US-11-024-251-35

Query Match 99.5%; Score 1756; DB 7; Length 335;
Best Local Similarity 99.4%; Pred. No. 8.8e-133;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 65
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA 120
Db 66 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGG 125
Qy 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 180
Db 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKNNYVDGVEVHNATKPREQYN 185
Qy 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240
Db 186 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 245
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
Db 246 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 305
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db 306 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 335

RESULT 15
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
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; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

Query Match          99.5%; Score 1756; DB 7; Length 444;
Best Local Similarity 99.4%; Pred. No. 1.2e-132;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 174

Qy 61 GLYSLSVVTVFPSSSLGQTYYICNVNHPKSNTKVDKVEPKSCDKHTCTPCPAPDELAGA 120
Db 175 GLYSLSVVTVFPSSSLGQTYYICNVNHPKSNTKVDKVEPKSCDKHTCTPCPAPDELGG 234

Qy 121 PSVFLFPPPKPDTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 235 PSVFLFPPPKPDTLNISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 294

Qy 181 STYRVVSVLTVQLHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
Db 295 STYRVVSVLTVQLHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 414

Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 415 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 444
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Search completed: January 28, 2006, 10:12:15  
Job time : 20.8198 secs

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GenCore version 5.1.6  
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OM nucleic - protein search using frame\_plus\_n2p model

Run on: January 28, 2006, 08:12:21 ; Search time 154.595 Seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797

Sequence: 1 gctccaccagggcccatc.....tctccctgtctccgggtaaa 990

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2 1/USPTO spool p/US10733563/runat 27012006 180005 4773/app\_query fasta 1.2716  
-DB-A Geneseq -QFWT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USR=US10733563 @CGN 1 1 624 @runat 27012006 180005 4773 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	98.2	333	8	Adj95914 Human IgG
2	1765	98.2	333	8	Adq89336 Human Imm
3	1765	98.2	333	9	Aeb09609 Human IgG
4	1765	98.2	356	8	Adj95974 Immunoglo
5	1765	98.2	444	3	Aay32263 Humanised
6	1765	98.2	448	8	Adp88447 Antibody
7	1765	98.2	448	8	Adp88431 Antibody
8	1765	98.2	467	6	Ada47334 TRX1 heav
9	1765	98.2	467	6	Ada47336 TRX1 heav

10	1765	98.2	467	8	ADP88446	ADP88446 Antibody
11	1765	98.2	467	8	ADP88430	ADP88430 Antibody
12	1765	98.2	467	8	ADQ87966	Adq87966 Heavy cha
13	1765	98.2	467	8	ADQ87974	Adq87974 Heavy cha
14	1765	98.2	473	5	ABG70743	ABG70743 Mouse/hum
15	1765	98.2	475	8	ADL23051	ADL23051 Mouse/hum
16	1765	98.2	475	8	ADL23054	ADL23054 Humanised
17	1765	98.2	475	8	ADS88803	ADS88803 Humanised
18	1765	98.2	475	8	ADS88792	Ad88792 A mouse/h
19	1760	97.9	330	8	ADQ89332	Adq89332 Human Imm
20	1760	97.9	330	9	AEB09605	Aeb09605 Human IgG
21	1760	97.9	462	9	AEB08800	Aeb08800 Anti-NOGO
22	1758	97.8	469	7	ADL23199	ADL23199 Human ant
23	1756	97.7	332	8	ADL35095	ADL35095 Human IgG
24	1756	97.7	332	9	ADW07455	Adw07455 Human IgG
25	1756	97.7	333	8	ADJ95912	Adj95912 Human IgG
26	1756	97.7	333	8	ADL22761	Adl22761 Human ant
27	1756	97.7	335	9	AEC22665	Aec22665 Secreted
28	1756	97.7	351	2	AAR43685	Aar43685 Human Kap
29	1756	97.7	356	8	ADJ95976	Adj95976 Immunoglo
30	1756	97.7	371	1	AAP91918	Aap91918 Sequence
31	1756	97.7	444	6	AAE35327	Aae35327 Humanised
32	1756	97.7	444	6	AAE34876	Aae34876 BIWA4/8 a
33	1756	97.7	444	8	ADL15443	ADL15443 Humanised
34	1756	97.7	444	8	ADO0851	Ado0851 Humanised
35	1756	97.7	444	9	AEB29789	Aeb29789 Humanized
36	1756	97.7	444	9	AEB29780	Aeb29780 Humanized
37	1756	97.7	445	6	AAO31101	Aao31101 Human A2-
38	1756	97.7	445	7	ADF11421	Adf11421 2811 anti
39	1756	97.7	445	7	ADF11429	Adf11429 18B2 anti
40	1756	97.7	445	9	ADY74778	Ady74778 Rat anti-
41	1756	97.7	447	2	AAV31669	Aav31669 Human IgG
42	1756	97.7	447	8	ADQ31274	Adq31274 Humanised
43	1756	97.7	447	8	ADQ31271	Adq31271 Murine 11
44	1756	97.7	447	8	ADQ31276	Adq31276 Humanised
45	1756	97.7	447	8	ADS87928	Ads87928 Anti-IFN-

ALIGNMENTS

RESULT 1

ADJ95914

ID ADJ95914 standard; protein; 333 AA.

XX AC ADJ95914;

XX AC ADJ95914;

DT 06-MAY-2004 (first entry)

XX DB Human IgG heavy chain constant region FCRmut.

XX KW cytostatic; antibody therapy; immunoglobulin cassette construct;

XX KW immunoglobulin leader molecule; immunoglobulin domain;

XX KW immunoglobulin therapeutic molecule; monobody; cancer; immunoglobulin G;

XX KW IgG; heavy chain constant region; FCRmut; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN US2004033561-A1.

XX PD 19-FEB-2004.

XX PF 17-OCT-2002; 2002US-00272899.

XX PR 19-OCT-2001; 2001US-0350166P.

XX PR 26-JUN-2002; 2002US-0392364P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA;

XX WPI; 2004-180050/17.

XX DR N-PSDB; ADJ95913.

XX DR

XX New isolated nucleic acid molecules having an immunoglobulin cassette  
PT construct, useful for producing immunoglobulin therapeutic molecules  
PT termed monobodies, used as a therapeutic group in cancer disorders.

XX Example 2; SEQ ID NO 10; 84pp; English.

XX The invention describes an isolated nucleic acid molecule comprising an  
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
CC comprises an immunoglobulin leader molecule operably linked to a stable  
CC immunoglobulin domain region. The methods and compositions of the present  
CC invention are useful for producing immunoglobulins, in particular  
CC immunoglobulin therapeutic molecules termed monobodies, used as a  
CC therapeutic group in cancer disorders. This is the amino acid sequence of  
CC the human immunoglobulin G (IgG) heavy chain constant region mutant  
CC FCKmut used in the creation of immunoglobulin DNA cassette constructs.

XX SQ Sequence 333 AA;

Alignment Scores:  
Pred. No.: 5.89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADJ95914 (1-333)

Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCGCACCTCTCCCAAGAGCACCTCTGGG 60  
Db 4 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
Qy 61 GGCAACGCGCCCTGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTG 120  
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
Qy 121 TGGAACTCAGCGCGCTGACGCGGGGTGACACCTTCCCGGTGCTGCTACAGTCTCA 180  
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 63  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCGCACCTTGGGACCCAGAC 240  
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
Qy 241 TACATCTGCAACGTGAATCAACAGCCGACCAACCAAGGTGGACAAGAGTTGAGCCC 300  
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103  
Qy 301 AAATCTTGTCACAAACTCACAATGCCACCGTCCCGACCTGAACTCGCGGGGCA 360  
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAGGACACCTCTCATGATCTCCCGGACCCCT 420  
Db 124 ProSerValPheLeuPheProProLysPheLysAspThrLeuMetIleSerArgThrPro 143  
Qy 421 GAGTCTACATCGGTGGTGGAGCGTGAAGCCAGCAAGACCTGAGGTCAAGTTCACCTGG 480  
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163  
Qy 481 TAGCTGACGCGGTGGAGTGCATAATGCCAAGCAAGCCCGCGGAGGACGACATACAC 540  
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluInTyrAsn 183  
Qy 541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 184 SerThrTyrArgValValSerValValThrValValLeuHisGlnAspTrpLeuAsnGlyLys 203  
Qy 601 GAGTACAAAGTGTGCTCCCAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAG 660  
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223

Qy 661 AAGCCAAAGGCGAGCCCGAGACACAGGTGTACACCTGCTCCCGCCATCCCGGATCAG 720  
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGlu 243  
Qy 721 CTGACCAAGAACACAGGTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780  
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
Qy 781 GCCCTGAGTGGAGAGCAATGGGAGCCCGAGAACAACTACAGACACGCTCCCGTG 840  
Db 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 283  
Qy 841 CTGACTCCGACGCTCTTCTCTCTACAGCAAGCTCACCTGGGACAGACAGGTGG 900  
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303  
Qy 901 CAGCAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACACCTACACG 960  
Db 304 GlnGlnGlyAsnValPheSerCysSerValMethIleGluAlaLeuHisAsnHisTyrThr 323  
Qy 961 CAGAAGAGCTCTCTCTGCTCTCCGGGTAAA 990  
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333  
RESULT 2  
ADQ89336  
ID ADQ89336 standard; protein; 333 AA.  
XX  
AC ADQ89336;  
DT 21-OCT-2004 (first entry)  
XX  
DE Human immunoglobulin protein #46.  
XX  
KW Human; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;  
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;  
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;  
KW anti-HIV; virucide; antiarteriosclerotic.  
XX  
OS Homo sapiens.  
XX  
PN US2004151721-A1.  
XX  
PD 05-AUG-2004.  
XX  
PF 10-DEC-2003; 2003US-00733563.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
PR 17-OCT-2002; 2002US-00272899.  
XX  
PA (OKEE/) O'KEEFE T.  
PA (PONA/) PONATH P.  
PI  
PI O'keefe T, Ponath P;  
XX  
XX WPI; 2004-580175/56.  
DR  
XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,  
PT useful for diagnosing and/or treating inflammatory or autoimmune  
PT diseases, and HIV infection.  
XX  
XX Disclosure; SEQ ID NO 114; 128pp; English.  
XX  
CC The invention relates to humanized immunoglobulin heavy and light chains  
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an  
CC immunoglobulin or its antigen binding fragment comprising the chains. The  
CC humanized immunoglobulin or its antigen binding fragment preferably  
CC comprises two heavy chains and two light chains. The humanized  
CC immunoglobulin and its heavy and light chains are useful for the  
CC diagnosis, prevention and/or treatment of diseases or conditions  
CC associated with aberrant expression or activity of the CCR2 polypeptide,  
CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV

CC infection and atherosclerosis. This sequence represents a human  
XX immunoglobulin protein of the invention.

SQ Sequence 333 AA;

Alignment Scores:

Pred. No.: 5,89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADQ89336 (1-333)

QY 1 GCCTCCACAAAGGCGCCATCGCTCTTCCCTGGCAGCCCTCTCTCCAGAGCACCTCTCTGGG 60  
DB 4 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
QY 61 GGCACAGCGCGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGTGC 120  
DB 24 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
QY 121 TGGAACTCAGCGCGCTCAGCAGCGCGGTGACACCTTCCCGGCTGTCTACAGTCTCA 180  
DB 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63  
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGCAGCCAGACC 240  
DB 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
QY 241 TACATCTCAAGTGAATCAAGCCCGAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
DB 84 TyrIleCysAsnValAsnHisLysProSerAenthThrLysValAspLysValGluPro 103  
QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGAGCAGCTGAACCTCGCGGGCA 360  
DB 104 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 123  
QY 361 CCCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 124 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 143  
QY 421 GAGTCAATCGGTGGTGGAGCTGAGCCAGCAGACCTGAGGTCAAGTTCACTGCG 480  
DB 144 GluValThrCysValValAlaAspValSerHisGluAspProGluValLysPheAsnTrp 163  
QY 481 TACGTGAGCGGTGGAGTGCATATCCCAAGACAAAGCCCGGAGGAGCAGTACAC 540  
DB 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 183  
QY 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203  
QY 601 GAGTCAAGTCAAGGTCTCCAAAGACCCCTCCAGCCCGCCATCGAGAAACCATCTCC 660  
DB 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 223  
QY 661 AAAGCCAAAGGCGCGCGGAGACCAAGTGTACACCTGCGCCCGCCATCCCGGATGAG 720  
DB 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243  
QY 721 CTGACCAAGAACAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780  
DB 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
QY 781 GCCGTGAGTGGGAGAGCAATGGGAGCGCGGAGAACAACTACAAGACCAACCCCTCCCGT 840  
DB 264 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 283  
QY 841 CTGACCTCCGAGCGGTCTCTTCTCTTACAGCAAGTCAACCGTGGACAGAGCGGTGG 900

DB 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303  
QY 901 CAGCAGGCGGAAAGTCTTCTCATGCTCCGCTGATGATGATGATGATGATGATGATGATG 960  
DB 304 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323  
QY 961 CAGAAGAGCCTCTCCCT 990  
DB 324 GlnLysSerLeuSerLeuSerProGlyLys 333

RESULT 3

AEBO9609

ID AEB09609 standard; protein; 333 AA.

XX

AC AEB09609;

XX

DT 08-SEP-2005 (first entry)

XX

DE Human IgG1 constant region FcRmut SEQ ID NO 114.

XX

KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;  
KW antibody engineering; therapeutic; diagnosis; inflammation;  
KW autoimmune diseases; immune disorder; graft rejection; HIV infection;  
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;  
KW light chain constant region.

OS Homo sapiens.

XX

PN WO2005060368-A2.

XX

PD 07-JUL-2005.

XX

PF 10-DEC-2003; 2003WO-US039599.

XX

PR 10-DEC-2003; 2003WO-US039599.

XX

PA (MILL-) MILLENNIUM PHARM INC.

PI Okeefe T, Ponath P;

XX

DR WPI; 2005-488561/49.

XX

DR N-PSDB; AEB09610.

XX

PT New humanized immunoglobulin or its antigen binding portion having  
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain  
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune  
PT diseases.

PS

XX Disclosure; SEQ ID NO 114; 192pp; English.

XX

CC The invention describes a humanized immunoglobulin (I) or its antigen  
CC binding portion having binding specificity for CC-chemokine receptor 2  
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain  
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)  
CC sequence, given in specification or its portion, and the light chain  
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given  
CC in specification. Also described are: a humanized immunoglobulin heavy  
CC chain, or its antigen binding fragment, having binding specificity for  
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the  
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized  
CC immunoglobulin light chain, or its antigen binding fragment, having  
CC binding specificity for CCR2 and comprising the amino acid sequence of  
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)  
CC sequence, given in specification. The following are disclosed: isolated  
CC nucleic acid molecules comprising nucleic acid sequence encoding (i); a  
CC construct comprising nucleic acid molecule encoding (i); and host cell  
CC comprising the nucleic acid molecule. (i) Is useful as a therapeutic  
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus  
CC reducing inflammatory response, for use in the treatment of diseases  
CC associated with leukocyte infiltration of tissue, e.g. in the treatment  
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV  
CC infection and monocyte-mediated disorders such as atherosclerosis. (i) Is  
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.

CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel  
CC fluid), and for modulating binding function and/or leukocyte trafficking  
CC modulated by CCR2. This is the amino acid sequence of human I9G1 constant  
CC region FcRmut used in the creation of a humanized anti-CCR2-antibody.  
XX  
SQ Sequence 333 AA;

Alignment Scores:  
Pred. No.: 5.89e-113 Length: 333  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 9 Gaps: 0

US-10-733-563-111 (1-990) x ABB09609 (1-333)

Qy 1 GCCTCCACCAAGCGCCCATCGTCTTCCCTGGCAGCCCTCTCCAGAGCAGCCTCTGGG 60  
Db 4 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23  
Qy 61 GGCACAGCGCCCTGGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43  
Qy 121 TGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTCTCAGTCTCTCA 180  
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 63  
Qy 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTGGGACCCAGACC 240  
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83  
Qy 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103  
Qy 301 AAATCTGTGCAAAACTCACAATGCCAGCCCAAGCAACCAAGGAGTGGACAGCTGCGGGGCA 360  
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACCCCTCATGATCTCCCGGACCCCT 420  
Db 124 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 143  
Qy 421 GAGTCCATCAGCTGGTGGTGGAGCTGAGCCAGCAAGACCTTGAGGTCAAGTTCAACTGG 480  
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTyr 163  
Qy 481 TACGTGACGGCTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAC 540  
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 183  
Qy 541 AGCAGTACCGTGTGGTCTCAGCGTCTCAGCGTCTGCAACAGGAGTGTGCTCAAGTGGCAAG 600  
Db 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTyrPheLysGlnLys 203  
Qy 601 GAGTACAAGTGAAGGTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAACCACTCTCC 660  
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 223  
Qy 661 AAAGCCAAAGGCGCCCGGAGACCAACCAAGTGTACACCTGCGCCCTCCCGGAGTGA 720  
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243  
Qy 721 CTGACCAAGAACAGGTGAGCTGAGCTGCTGCTCAAGGCTTCTATCCAGGAGCATC 780  
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263  
Qy 781 GCCGTGAGTGGGAGAGCAATGGGAGCGGAGAACCACTACAAGACCAAGCCCTCCCGTG 840  
Db 264 AlaValGluTyrGluSerAsnGlyGlnProGluAsnGlyTyrLysThrThrProProVal 283

Qy 841 CTGCACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCCTGGGACAGAGCAGGTGG 900  
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTyr 303  
Qy 901 CAGCAGGGGAAACGCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGAT 960  
Db 304 GlnGlnGlyAsnValPheSerCysSerValMethisGluAlaLeuHisAsnHisTyrThr 323  
Qy 961 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990  
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333  
RESULT 4  
ADJ95974  
ID ADJ95974 standard; protein; 356 AA.  
XX  
AC ADJ95974;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Immunoglobulin DNA cassette polypeptide seqid 70.  
XX  
KW cytostatic; antibody therapy; immunoglobulin cassette construct;  
KW immunoglobulin leader molecule; immunoglobulin domain;  
KW immunoglobulin therapeutic molecule; monobody; cancer.  
XX  
OS Synthetic.  
XX  
PN US2004033561-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 17-OCT-2002; 2002US-00272899.  
XX  
PR 19-OCT-2001; 2001US-0350166P.  
PR 26-JUN-2002; 2002US-0392364P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI O'keefe TL, Healey JJ, Newman W, Ponath PD, Keyt BA,  
XX  
XX WPI; 2004-180050/17.  
DR N-PSDB; ADJ95973.  
XX  
PT New isolated nucleic acid molecules having an immunoglobulin cassette  
PT construct, useful for producing immunoglobulin therapeutic molecules  
PT termed monobodies, used as a therapeutic group in cancer disorders.  
XX  
PS Disclosure; SEQ ID NO 70; 84pp; English.  
XX  
CC The invention describes an isolated nucleic acid molecule comprising an  
CC immunoglobulin cassette construct, wherein the immunoglobulin cassette  
CC comprises an immunoglobulin leader molecule operably linked to a stable  
CC immunoglobulin domain region. The methods and compositions of the present  
CC invention are useful for producing immunoglobulins, in particular  
CC immunoglobulin therapeutic molecules termed monobodies, used as a  
CC therapeutic group in cancer disorders. This is the amino acid sequence of  
CC an immunoglobulin DNA cassette construct.  
XX  
SQ Sequence 356 AA;

Alignment Scores:  
Pred. No.: 5.96e-113 Length: 356  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADJ95974 (1-356)

Qy 1 GCCTCCACCAAGCGCCCATCGTCTTCCCTGGCAGCCCTCTCCAGAGCAGCCTCTGGG 60  
|||||

Db 27 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 46  
Qy 61 GGCACAGCGCGCTGGTGGTCAAGAGTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 47 GlyThrAlaLeuLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 66  
Qy 121 TGGAACTCAGCGCGCTGACAGCGGGGTGCACACTTCCCGGTGTCTACAGTCTCA 180  
Db 67 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 86  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGGTACCGTGGCTCCAGCAGCTGGGCAACCGACC 240  
Db 87 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 106  
Qy 241 TACATCTGCAAGTGAATCACAAGCCCAACACCAAGGTGGACAAAGTTGAGCCC 300  
Db 107 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 126  
Qy 301 AAATCTTGTCACAAACTCACAATGCCACCGTGGCCAGCACTGAATCGCGGGGCA 360  
Db 127 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 146  
Qy 361 CCGTCAGTCTCTCTTCCCGCCCAACCAACCAAGCAGCACTCATGATCTCCCGACCCCT 420  
Db 147 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 166  
Qy 421 GAGGTCAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
Db 167 GluValThrCysValValValValValValValValValValValValValValVal 186  
Qy 481 TACGTGAGCGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAC 540  
Db 187 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 206  
Qy 541 AGCAGTCCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 207 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTyrLeuAsnGlyLys 226  
Qy 601 GAGTACAGTCAAGGTCTCAACAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCC 660  
Db 227 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysGluLysThrIleSer 246  
Qy 661 AAAGCCAAAGCGAGCGCGGAGAACCAACAGGTGTACACCTGCGCCCATCCCGGATGAG 720  
Db 247 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 266  
Qy 721 CTGACCAAGACAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780  
Db 267 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 286  
Qy 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGGAGAACCAACTACAAGACCGCCCTCCCGTG 840  
Db 287 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAspTyrLysThrProProVal 306  
Qy 841 CTGACCTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGCAAGCAGGTGG 900  
Db 307 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTyr 326  
Qy 901 CAGCAGGGGAACGTCTTCTATGCTCGGTGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 327 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 346  
Qy 961 CAGAAGAGCTCTCCCTGCTCCCGGTAAA 990  
Db 347 GlnLysSerLeuSerLeuSerProGlyLys 356

RESULT 5  
AAV32263  
ID AAV32263 standard; protein; 444 AA.  
AC AAV32263;  
XX  
DT 15-FEB-2000 (first entry)

XX DE XX KW KW KW KW KW KW KW KW KW XX OS XX FH FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FT FN PD PP PR PA PI XX DR XX PT PT XX PS CC

Humanised anti-CD23 MAB C11 heavy chain.

CD23; FCRII; IgG receptor; monoclonal antibody; C11; mouse; human;  
monoclonal antibody; chimeric antibody; humanised antibody;  
complementarity determining region; CDR; autoimmune disease;  
inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
urticaria; nephrotic syndrome; glomerulonephritis;  
inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
therapy.

Homo sapiens.

Synthetic.

Key	Location/Qualifiers
Region 1	1..30
Region 1	/note= "framework region 1"
Region 1	31..35
Region 1	/note= "CDR 1"
Region 1	36..49
Region 1	/note= "framework region 2"
Region 1	50..68
Region 1	/note= "CDR 2"
Region 1	69..100
Region 1	/note= "framework region 3"
Region 1	101..103
Region 1	/note= "CDR 3"
Region 1	104..111
Region 1	/note= "framework region 4"
Region 1	112..444
Region 1	/note= "constant region"

W09958679-A1.

18-NOV-1999.

07-MAY-1999; 99WO-GB001434.

09-MAY-1998; 98GB-00009839.

(GLAX ) GLAXO GROUP LTD.

Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

WPI; 2000-053101/04.

N-PSDB; AA234748.

Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.

Claim 9; Fig 4; 81pp; English.

This amino acid sequence represents the heavy chain of humanised anti-CD23 (FCRII) monoclonal antibody C11, composed of a human framework (H5IGKV1) and the heavy chain complementarity determining regions (see AAY32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type 1 diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents

Sequence 444 AA;

Alignment Scores:		
Pred. No.:	6.19e-113	444
Score:	1765.00	330
Percent Similarity:	100.0%	
Best Local Similarity:	100.0%	
Query Match:	98.22%	
DB:	3	
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-733-563-111 (1-990) x AAY32263 (1-444)

Qy	1	GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGGACCCCTCTCTCCAAAGACACCTCTGGG	60
Db	115	AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly	134
Qy	61	GGCACAGCGGCCCTGGGTCTCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTGCG	120
Db	135	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	154
Qy	121	TGGAACTCAGCGCCCTGACACAGCGCGTGCACACTTCCCGGTGTCTTACAGTCTCTCA	180
Db	155	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	174
Qy	181	GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC	240
Db	175	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	194
Qy	241	TACATCTGCAACGTGAATCATCAAGCCGACGACACACCAAGGTGGACAAGAAAGTTGAGCC	300
Db	195	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro	214
Qy	301	AAATCTTGTCAAAACTCACACATGCCACCGTGCACGACCTGAACTCCGGGGGCA	360
Db	215	LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla	234
Qy	361	CCGTCAAGTCTTCTTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT	420
Db	235	ProSerValPheLeuPheProProlsProLysAspThrLeuMetLieserArgThrPro	254
Qy	421	GAGTCACATCGGTGGTGGAGCTGTGACGACACGAGACCCCTGAGGTCAAGTTCAACTGG	480
Db	255	GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp	274
Qy	481	TACGTGAGCGCGTGGAGGTGCATAACTCCAAAGACAAAGCCCGGAGGAGCAGATCAAC	540
Db	275	TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	294
Qy	541	AGCAGTACCTGTGGTCAAGCGTCTCTACCGTCTCTGCACCCAGGACTGGCTGAATGGCAAG	600
Db	295	SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	314
Qy	601	GAGTACAGTCCAGGCTCTCAACAAGACCCCTCCAGCCCCCATCGAGAAACCATCTCC	660
Db	315	GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer	334
Qy	661	AAAGCCAAAGCGGACGCCCGGAGAACCAAGGTGTATACCCCTCCCGCATCCCGGATGAG	720
Db	335	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	354
Qy	721	CTGACCAAGAACCGGTGAGCTGACCTGCTGCTGGTCAAGGGCTTCTATCCAGCGACATC	780
Db	355	LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle	374
Qy	781	GCCGTGAGTGGGAGAGCAATGGGCGACGGAGAAACAATCAAGACCAACGCTTCTATCCAGCGACATC	840
Db	375	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	394
Qy	841	CTGACCTCCGACGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG	900
Db	395	LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	414



139	GlyThrAlaLeuGlyCysLeuValIysAspTyrPheProGluProValThrValSer	155
121	TGGAACCTCAGGCGCCTGACCAGCGCGGTGCACACCTTCCCGCGCTGTCTCAGACGTCCTCA	180
159	TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	178
181	GGACTCTACTCCTCAGCAGCGTGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCAGACC	240
179	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	198
241	TACATCTCCAACGTCAATCACAAAGCCACAGCACCAAGGTGGACAGAAAGTTCGAGCC	300
199	TyrIleCysAsnValIAsnHisIysProSerAenThrLysValAspLysLysValGluPro	218
301	AAATCTTGTGCAMAACTCACACATGCCACCGTGCACAGACCTCGAACTCCGCGGGGCA	360
219	LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla	238
361	CCGTGAGTCTCCTCTTCCCGCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT	420
239	ProSerValPheLeuPheProProllysProIysAspThrLeuMetIleSerArgThrPro	258
421	GAGTTCACATCGGTGGTGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCACATGG	480
259	GluValThrCysValValValAspValSerHisGluAspProGluValIysPheAsnTrp	278
481	TACGTGAGCGCGTGGAGGTGCATATGTCGAAGCAAAAGCCGCGGAGGAGCAGGTACACAC	540
279	TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	298
541	AGCACGTACCGTGTGGTCAGCGTCTCTCACCGTCTCGCACACGAGACTGGCTGAATGGCAAG	600
299	SerThrTyrArgValValIserValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	318
601	GAGTACAAAGTCAGGTCTCCAAAGAGCCTCCAGAGCCCGCCCATCGAGAAACCATCTCC	660
319	GluTyrLysCysLysValIserAsnLysAlaLeuProAlaProIleGluLysThrIleSer	338
661	AAAGCCAAAGCGCAGCCCGGAGAACACAGGTGTACACCTGCCCGCCCATCCCGGATGAG	720
339	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	358
721	CTGACCAGAAACACAGGTGAGCTGACCTCGCTGGTCAAAGGCTTCTATCTCCAGCCACATC	780
359	LeuThrLysAsnGlnValIserLeuThrCysLeuValLysGlyPheTyrProSerAspIle	378
781	GCCGTGGAGTGGGAGAGCAATGGGCGAGCCGAGAAACAACACTACAAGACCAACGCTCCCGT	840
379	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	398
841	CTGAGCTCCGACGGCTCTCTTCTCTTACAGCAGCTCACCGTGGACAGAGCAGGTGG	900
399	LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	418
901	CAGCAGGGGAACGTCTTCTCATGCTCCGTGTGATGATGAGGCTCTGCACAAACCACTACAG	960
419	GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr	438
961	CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA	990
439	GlnLysSerLeuSerLeuSerProGluLys	448

## RESULT 7

ADP88431  
ID ADP88431 standard; protein; 448 AA.

AX  
AC ADP88431;

09-SEP-2004 (first entry)

XX DE Antibody TRX1 heavy chain SEQ ID NO: 8.

KW immunosuppressive; transplant rejection; antigen tolerance; antibody;

KW	TRX1.
XX	Unidentified.
OS	
XX	WO2004052398-A1.
PN	
XX	24-JUN-2004.
PD	
XX	
PF	09-DEC-2003; 2003WO-US039165.
XX	
PR	09-DEC-2002; 2002US-0431839P.
XX	
PA	(TOLE-) TOLERRX INC.
PI	
XX	Windsor-Hines D, Rao P, Ringler DJ;
XX	
DR	WPI; 2004-468712/44.
XX	
PT	Treating a primate to induce tolerance to at least one antigen comprises
XX	administering at least one anti-CD4 antibody or its fragment in an
PT	initial dose of at least 40 mg/kg and at least one compound that inhibits
PT	CD8+ T cells.
XX	
PS	Disclosure; SEQ ID NO 8; 113pp; English.
XX	
CC	The present invention relates to a process of treating a primate to
CC	induce tolerance to at least one antigen, which comprises administering
CC	to the primate at least one anti-CD4 antibody or its fragment in an
CC	initial dose of at least 40 mg/kg and at least one compound that inhibits
CC	CD8+ T cells, where the anti-CD4 antibody or its fragment is present in
CC	the primate when the antigen is present in the primate. The method is
CC	useful in treating a primate to induce tolerance to at least one foreign
CC	antigen to prevent transplant rejection. The present sequence is an
CC	antibody fragment used in the exemplification of the invention.
XX	
SQ	Sequence 448 AA;
Alignment Scores:	
Pred. No.:	6.2e-113 Length: 448
Score:	1765.00 Matches: 330
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	98.22% Indels: 0
DB:	8 Gaps: 0
US-10-733-563-111 (1-990) x ADP88431 (1-448)	
Qy	1 GCCTCCACCAAGGGCCCATCGGTCTTCCCCTGGCACCTCCTCCAAGAGCACCTCTGCGG 60
Db	119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
Qy	61 GGACACGGGCCCTGGCTGCCTGGTCGAAGACTACTTCCCGRACCCTGACGGTGTCG 120
Db	139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
Qy	121 TGGAACCTCAGGCGCCCTGACACGGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCCTCA 180
Db	159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
Qy	181 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACC 240
Db	179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198
Qy	241 TAGATCTGCAACGTGAATCAGACGCCCGCAACACCAAGGTGGACAGAAGTTGAGCCC 300
Db	199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 218
Qy	301 AATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGACACCTGAACCTGCGGGGGCA 360
Db	219 LysSerCysAspLysThrHisThrCysProProCysProAlaIaproGluLeuAlaGlyAla 238
Qy	361 CCGTCAGTCTTCTCTTCCCCCCCCAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420





QY 481 TACGTGACGGCGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGACGACGTACAAC 540  
Db TyValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
QY 541 AGCAGGTACCGTGTGGTCAGCGTCTCACCGTCTCGACACGAGGACTGGCTGAATGGCAAG 600  
Db SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTyrLeuAsnGlyLys 337  
QY 601 GAGTACAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCATCGAGAAAACCATCTCC 660  
Db GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357  
QY 661 AAGCCAAAGGCGACCCGAGACACACAGGTGTACACCTCGCCCTCCCGGATCAG 720  
Db LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGAACACGAGTCCAGCTCAGCTCCTCGTCAAAAGGCTTCTATCCAGCGACATC 780  
Db LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397  
QY 781 GCCGTGAGTGGGAGAGCAATGGGAGCGCGAGAACCACTACAAGACACACCCCTCCGCTG 840  
Db AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 417  
QY 841 CTGCACTCCGACGGCTCTCTCTCTCTACAGCAAGCTCACCGTGGCAAGACGAGTGG 900  
Db LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTyr 437  
QY 901 CAGCAGGGGAACTCTCTCTCATGCTCCGTGATGATGAGGCTCTGCAACCAACCATACAAG 960  
Db GlnGlnGlnValPheSerCysSerValMethisGluAlaLeuHisAsnHisTyrThr 457  
QY 961 CAGAAGAGCCCTCTCCCTGCTCCGGGTAAA 990  
Db GlnLysSerLeuSerLeuSerProGlyLys 467  
RESULT 10  
ADP88446  
ID ADP88446 standard; protein; 467 AA.  
XX  
AC ADP88446;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 23.  
DE immunosuppressive; transplant rejection; antigen tolerance; antibody;  
KW TRX1.  
XX  
XX Unidentified.  
XX  
XX WO2004052398-A1.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-US039165.  
XX  
XX 09-DEC-2002; 2002US-0431839P.  
XX  
XX (TOLE-) TOLERRX INC.  
XX  
XX Windsor-Hines D, Rao P, Ringler DJ;  
XX  
XX WPI; 2004-468712/44.  
DR  
DR N-PSDB; ADP88444, ADP88445.  
XX  
XX Treating a primate to induce tolerance to at least one antigen comprises  
PT administering at least one anti-CD4 antibody or its fragment in an  
PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
PT CD8+ T cells.  
XX  
XX Disclosure; SEQ ID NO 23; 113pp; English.  
PS

XX The present invention relates to a process of treating a primate to  
CC induce tolerance to at least one antigen, which comprises administering  
CC to the primate at least one anti-CD4 antibody or its fragment in an  
CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
CC the primate when the antigen is present in the primate. The method is  
CC useful in treating a primate to induce tolerance to at least one foreign  
CC antigen to prevent transplant rejection. The present sequence is an  
CC antibody fragment used in the exemplification of the invention.  
XX  
SQ Sequence 467 AA;  
Alignment Scores: 6.24e-113 Length: 467  
Pred. No.: 1765.00 Matches: 330  
Score: 100.00% Conservativeness: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 98.22% Indels: 0  
Query Match: 8 Gaps: 0  
DB: 0  
US-10-733-563-111 (1-990) x ADP88446 (1-467)  
QY 1 GCCTCCACCAAGGCGCCATCGCTCTCCCTGGCACCTCTCCCAAGAGCACCTCTGGG 60  
Db 138 AlAserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
QY 61 GGCAACAGCGCCCTGGGCTGCTGGTCAAGGACTTACTTCCCGCAACCGGTGACGTGCG 120  
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177  
QY 121 TGGNACTCAGCGCCCTGACGAGCGGCGTGCACACCTTCCCGGCTGCTCTACAGTCTCA 180  
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGAGCTTGGGCGCCACGACC 240  
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217  
QY 241 TACATCTGAACGTGAATCAAGCCCAAGCCCAAGCAACCAAGTGGCAAGAAGTTGAGCCC 300  
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
QY 301 AATCTTTGTGACAAACTCAGCATGCCACCGTCCCGCCAGCACCTGAACCTCGCGGGGCA 360  
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
QY 361 CCGTGAGTCT 420  
Db 258 ProSerValPheLeuPheProProLysProLysProLysAspThrLeuMetIleSerArgThrPro 277  
QY 421 GAGTCAATCGCTGGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCACATCGG 480  
Db 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
QY 481 TACGTGACGGCGTGGAGTGCATATGCCAAGACCAAGCCGCGGAGGAGGACGTACAAC 540  
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317  
QY 541 AGCAGGTACCGTGTGGTGGAGCTCTCACCGTCTCGACACGAGGACTGGCTGAATGGCAAG 600  
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTyrLeuAsnGlyLys 337  
QY 601 GAGTACAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCATCGAGAAAACCATCTCC 660  
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357  
QY 661 AAGCCAAAGGCGACCCGAGACACACAGGTGTACACCTCGCCCTCCCGGATCAG 720  
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377  
QY 721 CTGACCAAGAACACGAGTCCAGCTCAGCTCCTCGTCAAAAGGCTTCTATCCAGCGACATC 780

Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 397  
Qy 781 GCCGTGGAGTGGGAGCAATGGGAGCGGAGAGCAACTACAGACACGCTCCCGTG 840  
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyLysThrProVal 417  
Qy 841 CTGGACTCGAGCGGCTCTTCTCTCTACAGCAAGCTCAGGTGGACAGAGCGTGG 900  
Db 418 LeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 437  
Qy 901 CAGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACACCACTACACG 960  
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyThr 457  
Qy 961 CAGAAGAGCCTCTCCCTCTCTCCGGTAAA 990  
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 11  
ADP88430  
ID ADP88430 standard; protein; 467 AA.  
XX AC  
XX ADP88430;  
XX DT 09-SEP-2004 (first entry)  
XX DE Antibody TRX1 heavy chain with leader sequence SEQ ID NO: 7.  
XX KW immunosuppressive; transplant rejection; antigen tolerance; antibody;  
XX KW TRX1.  
XX OS Unidentified.  
XX PN WO2004052398-A1.  
XX PD 24-JUN-2004.

XX PF 09-DEC-2003; 2003WO-US039165.  
XX PR 09-DEC-2002; 2002US-0431839P.  
XX PA (TOLE-) TOLERRX INC.  
XX PI Windsor-Hines D, Rao P, Ringler DJ;  
XX DR WPI; 2004-468712/44.  
XX DR N-PSDB; ADP88429, ADP88428.  
XX FT Treating a primate to induce tolerance to at least one antigen comprises  
PT administering at least one anti-CD4 antibody or its fragment in an  
PT initial dose of at least 40 mg/kg and at least one compound that inhibits  
PT CD8+ T cells.

XX PS Disclosure; SEQ ID NO 7; 113pp; English.  
XX CC The present invention relates to a process of treating a primate to  
CC induce tolerance to at least one antigen, which comprises administering  
CC to the primate at least one anti-CD4 antibody or its fragment in an  
CC initial dose of at least 40 mg/kg and at least one compound that inhibits  
CC CD8+ T cells, where the anti-CD4 antibody or its fragment is present in  
CC the primate when the antigen is present in the primate. The method is  
CC useful in treating a primate to induce tolerance to at least one foreign  
CC antigen to prevent transplant rejection. The present sequence is an  
CC antibody fragment used in the exemplification of the invention.  
XX SQ Sequence 467 AA;

Alignment Scores:  
Pred. No.: 6.24e-113 Length: 467  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0

DB: 8 Gaps: 0  
US-10-733-563-111 (1-990) x ADP88430 (1-467)  
Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCCGACCGCTCTCCAGAGCACCTCTGGG 60  
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157  
Qy 61 GGCACAGCGCGCTCGTCAAGGACTACTTCCCGAACCGGTGACGGTGTGCG 120  
Db 158 GlyThrAlaLeuLeuGlyCysLeuValLysAspTyPheProGluProValThrValSer 177  
Qy 121 TGGAACTCAGCGCGCTGACCCAGCGGCTGCACACTTCCCGGCTGCTCCTACAGTCTCA 180  
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 198 GlyLeuTySerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 217  
Qy 241 TACATCTGCAACGTGAATCAAGCCAGCAACCAAGTGGCAAGAAAGTTGAGGCC 300  
Db 218 TyrlleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237  
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACCTGAATCCGCGGGGCA 360  
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257  
Qy 361 CCGTCAGTCTCTCTTCCCCCCCCCAAGCAGACACCTCATGATCTCCCGGACCCCT 420  
Db 258 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 277  
Qy 421 GAGGTACATGCTGCTGTGGAGTGTAGCCACCAAGACCTCTAGGTCAAGTTCAACTGG 480  
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297  
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGCAAGCCGCGGAGGAGCAGTACAAAC 540  
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 317  
Qy 541 AGCAGTACCGTGTGCTCAGGTCTCTACCGTCTGTGCACAGGACTGGCTGAATGGCAAG 600  
Db 318 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337  
Qy 601 GAGTACAAGTGCAAGGTCTCCAAACAAAGCCCTCCAGCGCCCTCATCGAGAAACCATCTCC 660  
Db 338 GluTyLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrLysSer 357  
Qy 661 AAAGCCAAAGGCGAGCGCCGAGAACACAGGTGTACACCTGTGCCCTCCCGGATGAG 720  
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyThrLeuProProSerArgAspGlu 377  
Qy 721 CTGACCAAGAACAGGTGAGCTGACCTGCTGTGTCAAGGCTTCTATCCAGCGACATC 780  
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 397  
Qy 781 GCCGTGGAGTGGGAGAGCAATGGGAGCGGAGAGCAACTACAGACACCCCTCCCGTG 840  
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyLysThrProVal 417  
Qy 841 CTGGACTCCGAGCGGCTCTTCTCTCTACAGCAAGCTCAGGTGGACAGAGCGTGG 900  
Db 418 LeuAspSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 437  
Qy 901 CAGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACACCACTACACG 960  
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyThr 457  
Qy 961 CAGAAGAGCCTCTCCCTCTCTCCGGTAAA 990  
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467







```
Db      178 TrpAnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
Qy      181 GGACTTACTCCCTCAGCAGCGTGGTGAACCTGCCCTCCACAGCTTGGGACCCAGAC 240
Db      198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
Qy      241 TACATCTGCACGCGTAATCACAAGCCCAAGCAACCAAGTGGACAGAAAGTTGAGCCC 300
Db      218 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 237
Qy      301 AAATCTTGTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db      238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
Qy      361 CCGTCAGTCTTCTCTTCCCCCCCCAAAACCAAGACACCTCATGATCTCCCGGACCCCT 420
Db      258 ProSerValPheLeuPheProProLysPheProLysAepThrLeuMetIleSerArgThrPro 277
Qy      421 GAGGTCAATCGTGGTGGTGGAGTGGAGCCAGCAAGACCTGAGTCAAGTTCAGTGG 480
Db      278 GluValThrCysValValValAspValSerHisGluAepProGluValLysPheAenTrp 297
Qy      481 TACGTGCACGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGACGACTACAAC 540
Db      298 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGluGlnTyrAen 317
Qy      541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db      318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAepTrpLeuAenGlyLys 337
Qy      601 GAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGCCGCCATCGAAGAAACCATCTCC 660
Db      338 GluTyrLysCysLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 357
Qy      661 AAAGCCAAAGGAGCGAGCCGAGAACCAAGTGTACACCCCTGCCCTCCCGGATGAG 720
Db      358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
Qy      721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      378 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
Qy      781 GCGGTGAGTGGGAGAGCATGGCCGAGCCGAGAACCAACTACAGACCAAGCCCTCCG 840
Db      398 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyrLysThrThrProProVal 417
Qy      841 CTGACTCCGACGCGCTCTTCTCTCTCTTACAGCAAGCTCACCGTGGCAAGCAGCGTGG 900
Db      418 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
Qy      901 CAGCAGGGGAAACGCTTCTCTATGCTATGCTGATGATGATGATGATGATGATGATGATGAT 960
Db      438 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyrThr 457
Qy      961 CAGAGAGCCCTCTCCCTGCTCTCCGGTAAA 990
Db      458 GlnLysSerLeuSerLeuSerProGlyLys 467
```

## RESULT 14

ABG70743

ID ABG70743 standard; protein; 473 AA.

XX

AC ABG70743;

XX

DT 02-DEC-2002 (first entry)

XX

DE Mouse/human chimeric anti-MAG antibody heavy chain protein.

XX

KW Stroke; neurological disease; neurodegeneration; brain injury;

KW spinal cord injury; chronic disease; Alzheimer's disease; tauopathy;

KW fronto-temporal dementia; peripheral neuropathy; Parkinson's disease;

KW Huntington's disease; multiple sclerosis; mouse; human; anti-MAG;

KW antibody; heavy chain.

XX Mus sp.

OS Homo sapiens.

OS Synthetic.

OS Chimeric.

XX

PN WO200262383-A2.

XX

XX 15-AUG-2002.

XX

XX 08-FEB-2002; 2002WO-GB000551.

XX

XX 08-FEB-2001; 2001GB-00003174.

XX

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX

XX Irving EA, Vinson M;

XX

XX WPI; 2002-698554/75.

XX

PT Treating or preventing stroke and neurological diseases, e.g. Alzheimer's disease, multiple sclerosis or Parkinson's disease, comprises administering a myelin-associated glycoprotein (MAG) antagonist or anti-MAG antibody.

PT

XX Disclosure; Fig 5; 41pp; English.

XX

CC The present invention relates to a new method of treating or preventing stroke and other neurological diseases in a human. The method involves administering a myelin-associated glycoprotein (MAG) antagonist or anti-MAG antibody, including altered antibodies or their functional fragment. The MAG antagonist or anti-MAG antibody, including altered antibodies or their functional fragments are useful in preparing a medicament for treating or preventing stroke and other neurological diseases, or for inhibiting neurodegeneration and/or promoting functional recovery in a human patient suffering or at risk of developing stroke or other neurological disease, such as stroke, traumatic brain injury and spinal cord injury, chronic diseases including Alzheimer's disease, fronto-temporal dementia (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease and multiple sclerosis. The present amino acid sequence represents the mouse/human chimeric anti-MAG antibody heavy chain protein

XX

SQ Sequence 473 AA;

## Alignment Scores:

Pred. No.:	6.25e-113	Length:	473
Score:	1765.00	Matches:	330
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.22%	Indels:	0
DB:	5	Gaps:	0

US-10-733-563-111 (1-990) x ABG70743 (1-473)

Qy 1 GCCTCCACCAAGGCCCATCGTCTTCCCTCGCACCTCTCCCAAGAGCAGCTCTGGG 60

Db 144 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 163

Qy 61 GGCACAGCGCCCTGGGCTCGCTGGTCAAGGACTACTTCCCGCAACCGGTGAGGTGTCG 120

Db 164 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 183

Qy 121 TGGAACTCAGCGCCCTGACCGCGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 180

Db 184 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 203

Qy 181 GGACTTACTCTCCCTACGACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240

Db 204 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 223

Qy 241 TACATCTGCAACGTGAATCATCAAGCCCGAGCAACCAAGGTGGCAAGAAAGTTGAGCCC 300



```
Db 224 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 243
Qy 301 AAATCTTGTCGACAAACTCACACATGCCACCGTCCCGACGACCTGAACTGCGGGGCA 360
Db 244 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuAlaGlyAla 263
Qy 361 CGGTGAGTCTTCTCTTCCCAAAACCAAGGACACCTCATGATCTCCGGACCCCT 420
Db 264 ProSerValPheLeuPheProProlsProlsAspThrLeuMetIleSerArgThrPro 283
Qy 421 GAGTTCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 284 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 303
Qy 481 TACGTGAGCGGTGGAGTGCATATGCAAGACAAAGCCGCGGAGCAGGACGATACAC 540
Db 304 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 323
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 324 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 343
Qy 601 GAGTCAAGTCAAGTCTCCAAAGCCCTCCCGACGCGCCCATCGAGAAACCATCTCC 660
Db 344 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 363
Qy 661 AAAGCAAGGCGACCCCGAGAACACAGGTGTACCCCTGCGCCCATCCCGGATCAG 720
Db 364 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProSerArgAspGlu 383
Qy 721 CTGACCAAGAACAGGTGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 384 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 403
Qy 781 GCCGTGGTGGAGAGCAATGGGAGCGCGGAGAACTACAGACACGCTCCCGTGG 840
Db 404 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 423
Qy 841 CTGGAATCCGACGGTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 424 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 443
Qy 901 CAGCAGGGGAACGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 444 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 463
Qy 961 CAGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 464 GlnLysSerLeuSerLeuSerProGlyLys 473
```

## RESULT 15

ADL23051  
ID ADL23051 standard; protein; 475 AA.

XX AC  
XX AC  
XX AC

DT 20-MAY-2004 (first entry)

XX Mouse/human chimeric anti-MAG antibody heavy chain #1.

DE antibody; MAG; myelin associated glycoprotein; heavy chain; CDR; stroke;  
XX neurodegenerative disorder; gene therapy; vaccine; human; mouse.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

FN WO2004014953-A2.

XX 19-FEB-2004.

PD 05-AUG-2003; 2003WO-EP008749.

XX 06-AUG-2002; 2002GB-00018229.  
PR 06-AUG-2002; 2002GB-00018230.  
PR 06-AUG-2002; 2002GB-00018232.  
PR 06-AUG-2002; 2002GB-00018234.  
XX (GLAXO) GLAXO GROUP LTD.  
PA Ellis JH, Germaeschewski V;  
XX WPI; 2004-180641/17.

XX New altered antibody that binds to and neutralizes myelin associated glycoprotein (MAG), useful for preparing a composition for treating or preventing stroke or other neurodegenerative disorders e.g., Alzheimer's disease.

XX Example 2; Fig 1; 67pp; English.

XX The present invention relates to a new altered antibody or its functional fragment, which binds to and neutralizes myelin associated glycoprotein (MAG) and comprises a light chain variable domain (VL) comprising complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The antibody is useful for preparing a composition for treating or preventing stroke or other neurodegenerative disorders in a human, e.g., traumatic brain injury, Alzheimer's disease, dementia, peripheral neuropathy, Parkinson's disease, Huntington's disease and multiple sclerosis. The present sequence is a human/mouse chimeric anti-MAG antibody heavy chain.

XX Sequence 475 AA;

## Alignment Scores:

Pred. No.: 5,26e-113 Length: 475  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-111 (1-990) x ADL23051 (1-475)

Qy 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCTCTCTCCAGAGCACCTCTGGG 60  
Db 146 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165  
Qy 61 GGCACAGCGGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120  
Db 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
Qy 121 TGGAACTCAGCGCGCTGGCAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCTCA 180  
Db 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
Qy 181 GGACTTACTCTCTCAGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240  
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
Qy 241 TACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTGGAGCAAGAAAGTTGAGCCC 300  
Db 226 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 245  
Qy 301 AAATCTTGTCGACAAACTCACACATGCCACCGTCCCGACGACCTGAACTGCGGGGCA 360  
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 265  
Qy 361 CCGTCAGTCTTCT 420  
Db 266 ProSerValPheLeuPheProProlsProlsAspThrLeuMetIleSerArgThrPro 285  
Qy 421 GAGTTCATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
Db 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305

QY	481	TACGTGGACGGCGTGGAGGTGCTAATGTC	540
DB	306	TyrValAspGlyValGluValHisAsnAlaIysThrLysProArgGluGluGlnTyrAsn	325
QY	541	AGCAGTACCGTGTGGTTCAGCGTCTCCACCGTCTCTGCACAGGACTGGCTGAATGGCAAG	600
DB	326	SerThrTyrArgValIysSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	345
QY	601	GAGTACCAAGTGCAGAGTCTCCAAACAAGCGCTCCAGCGCCCATCGAGAAAACCATCTCC	660
DB	346	GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer	365
QY	661	AAAGCAAAGGSCAGCCCGCAGAACACAGGTGTACACCTCCGCCCATCCCGGATGAG	720
DB	366	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	385
QY	721	CTGACCAAGAACCGGTGAGCTGACCTGCTGGTCAAAGGGTTCTATCCCAAGCAATC	780
DB	386	LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle	405
QY	781	GCCTGGAGTGGAGAGCAATGGCGAGCGGAGAACACTACAAAGCACCGCTCCCGT	840
DB	406	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	425
QY	841	CTGGACTCCGACGGGTCTCTTCTCTTACACGAAGCTCACCGTGGCAAGAGCAGGTGG	900
DB	426	LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp	445
QY	901	CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCGATGAGGCTCTGCACAACCACTACACG	960
DB	446	GlnGlnGlyAsnValIpheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr	465
QY	961	CAGAAGACCTCTCCCTGTCTCCGGGTAAA	990
DB	466	GlnLysSerLeuSerLeuSerProGlyLys	475

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GenCore version 5.1.6  
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-Q=/cgn2\_1/USPTO spool p/US10733563/runat\_27012006.180006.4797/app\_query.fasta\_1.2716  
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1 83 @runat\_27012006.180006.4797 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUEURY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1751	97.4	330	1 GHU	Ig gamma-1 chain C
2	1619.5	90.1	377	2 A23511	Ig gamma-3 chain C
3	1617.5	90.0	377	2 A60764	Ig gamma-3 chain C
4	1603	89.2	326	1 G2HU	Ig gamma-2 chain C
5	1579.5	87.9	327	1 G4HU	Ig gamma-4 chain C
6	1259	70.1	328	2 I47159	Ig gamma 2a chain
7	1256.5	69.9	374	2 S69339	Ig heavy chain v r
8	1253	69.7	328	2 I47160	Ig gamma 2b chain
9	1249	69.5	255	4 S31866	Ig gamma-1 chain C
10	1243	69.2	234	2 P70207	Ig gamma chain C r
11	1235	68.7	328	2 I47158	Ig gamma 1 chain c
12	1231	68.5	328	2 I47161	Ig gamma 1 chain c
13	1219.5	67.9	323	1 GHRB	Ig gamma chain C r
14	1201.5	66.9	329	1 G2GP	Ig gamma-2 chain C

15	1195.5	66.5	472	2 S31459	Ig gamma-1 chain -
16	1171.5	65.2	470	2 S22080	Ig heavy chain pre
17	1157.5	64.4	308	2 C30554	Ig heavy chain C r
18	1156	64.3	444	2 PC4436	monoclonal antibody
19	1149	63.9	326	2 PS0017	Ig gamma-1 chain C
20	1148.5	63.9	289	1 G3HUW1	Ig gamma-3 heavy c
21	1144	63.7	324	1 G1MS	Ig gamma-1 chain C
22	1139	63.4	393	1 G1MSM	Ig gamma-1 chain C
23	1135.5	63.2	333	2 PS0018	Ig gamma-2b chain
24	1130	62.9	329	1 G3MSC	Ig gamma-3 chain C
25	1119	62.3	398	1 G3MSM	Ig gamma-3 chain C
26	1115	62.0	469	2 S37483	Ig gamma-2a chain
27	1114.5	62.0	329	2 S00847	Ig gamma-2c chain
28	1112.5	61.9	335	1 G2MSAB	Ig gamma-2a chain
29	1110	61.8	330	1 G2MSA	Ig gamma-2a chain
30	1110	61.8	399	1 G2MSAM	Ig gamma-2a chain
31	1109	61.7	322	2 PS0019	Ig gamma-2a chain
32	1100	61.2	446	2 S40295	Ig gamma-2a chain
33	1092.5	60.8	327	2 S06611	Ig gamma-2 chain C
34	1078	60.0	405	1 G2MSBM	Ig gamma-2b chain
35	1063	59.2	475	2 S01321	Ig gamma-2b chain
36	1061	59.0	277	2 I47162	Ig gamma 4 chain c
37	1055.5	58.7	474	1 G2MS11	Ig gamma-2b chain
38	707	39.3	180	2 I46732	Ig gamma heavy C
39	672.5	37.4	548	2 S38864	Ig epsilon chain C
40	577.5	32.1	249	2 S69340	Ig heavy chain VHI
41	574.5	32.0	218	2 A36040	Ig heavy chain V-I
42	571	31.8	152	2 S14236	Ig gamma-1 chain C
43	560	31.2	549	2 S04845	Ig heavy chain pre
44	536	29.8	241	2 S69131	Ig heavy chain (DO
45	534	29.7	220	2 A49444	Ig gamma-1 heavy c

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 5

A>Note: Lys-330 is removed after translation

R:Haris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI0000013C6FE; EMBL:Z17370

R:Yakahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113:235-330 <TAK>

A:Cross-references: UNIPARC:UPI0000017378B; UNIPARC:UPI0000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>  
A:Cross-references: UNIPARC:UPI000017378D  
R:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,  
A:Cross-references: UNIPARC:UPI00017378E  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
Igen Primärstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A:Cross-references: UNIPARC:UPI00017378F  
A:Note: this sequence has the G1m(17) and G1m(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
A:Cross-references: UNIPARC:UPI000173790  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
  
Alignment Scores:  
Pred. No.: 9.74e-104 Length: 330  
Score: 1751.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.44% Indels: 0  
DB: 1 Gaps: 0  
  
US-10-733-563-111 (1-990) x GHU (1-330)  
1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGACCCCTCTCCAGAGCACCTCTGGG 60

Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20  
Qy 61 GGCACAGCGGCGCTCGCTGGTCAAGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
Qy 121 TGGAACTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTCTCTACAGTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGCCTGCTCCAGCAGCTTGGGCAACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
Qy 241 TACATCTGCACGTAATCAACGCCAGCAACCAAGGTGGCAAGAAAGTTGAGCCC 300  
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100  
Qy 301 AATCTTGTGACAAAACCTCACATGCCACCGTGCAGCACCTGAACTCGCGGGGCA 360  
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 120  
Qy 361 CCGTCAGTCTCTCTCTCCCGCAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140  
Qy 421 GAGGTCACTGCGTGTGTGGAGCTGAGCCAGCAACCGTGCAGGTCAAGTTCAACTGG 480  
Db 141 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
Qy 481 TACGTGACGGCGTGGAGGTGCATATATGCCAAGCAAAAGCCGCGGAGGACGACTACAAC 540  
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 180  
Qy 541 AGCAGGTACCGTGTGTGTGAGCTCCTCACCGTCTCGCACCGAGTCTGCTGAATGGCAAG 600  
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
Qy 601 GAGTACAGTGCAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAACCATCTCC 660  
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrLysSer 220  
Qy 661 AAGCCAAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTGCCTCCCGGAGTGTAG 720  
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
Qy 721 CTGACCAAGAACCAAGGTGACGCTGACCTGTGTGTCAAGGCTTCTATCCAGCGACATC 780  
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
Qy 781 GCCGTGAGTGGGAGAGCAATGGGACCGCGAGAACCAACTACAGACCAACCGCTCCCGTG 840  
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 280  
Qy 841 CTGACTCCAGCGGCTCTCTTCTCTTCTACAGCAAGCTCACCGTGGGACAGAGCAGGTGG 900  
Db 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
Qy 901 CAGCAGGGGAGCGTCTTCTCATGCTCGTGTGATGATGAGGCTCTGCAACCACTACACG 960  
Db 301 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 320  
Qy 961 CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330  
RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c  
A:Reference number: A23511; MUID:86148507; PMID:3081877  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272  
C:Genetics:  
A:Gene: IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>  
  
Alignment Scores:  
Pred. No.: 2,15e-95 Length: 377  
Score: 1619.50 Matches: 307  
Percent Similarity: 84.08% Conservative: 10  
Best Local Similarity: 81.43% Mismatches: 13  
Query Match: 90.12% Indels: 47  
DB: 2 Gaps: 1  
  
US-10-733-563-111 (1-990) x A23511 (1-377)  
  
Qy 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTGGCACCCTCTCCAAAGAGCACTCTGGG 60  
Db 1 AlaserThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20  
  
Qy 61 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
  
Qy 121 TGGAACTCAGCGCCCTGACACAGCGCGTGCACACCTTCCCGGTGCTCTCAGTCTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
  
Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCGCACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80  
  
Qy 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAAGATT----- 294  
Db 81 TyrThrCysAsnValAsnHisLysProSerAsnThrLysValAspLysArgValGluLeu 100  
  
Qy 294 ----- 294  
  
Db 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120  
Qy 294 ----- 294  
  
Db 121 AspThrProProProCysProArgCysProGluProLysSerCysAspThrProProPro 140  
Qy 295 -----GAGCCCAAACTTGTGTGACAAAACCTCACATGCGCCACCGTGCCCA 339  
Db 141 CysProArgCysProGluProLysSerCysAspThrProProProCysProArgCysPro 160  
  
Qy 340 GCACCTGAACCTCGGGGGGCGACCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGACAC 399  
Db 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr 180  
  
Qy 400 CTCATGATCTCCCGGACCCCTGAGGTACATGTCATGCGTGGTGGACGTGAGCCAGAC 459  
Db 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200  
  
Qy 460 CCTGAGGTCAAGTTCAACTGGTACCTGGACCGGTGGAGGTGCATAATGCCAACACAAG 519  
Db 201 ProGluValGlnPheLysTyrValAspGlyValGluValHisAsnAlaLysThrLys 220  
  
Qy 520 CCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCCCTCAGCGTCTCCTGAC 579  
Db 181 GGAAGTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGGCGACCCAGACC 240

Db 221 ProArgGluGluGlnTyrAsnSerThrPheArgValValSerValLeuThrValLeuHis 240  
Qy 580 CAGGACTGGCTGAATGGCAAGAGTACAAAGTGAAGGTCTCCAAAGAGCCCTCCAGCC 639  
Db 241 GlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeuProAla 260  
Qy 640 CCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAGAGTGTACACC 699  
Db 261 ProIleGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyrThr 280  
Qy 700 CTGCCCCCATCCCGGATGAGTACCAAGAACCAAGAGTGCAGCTCAGCTGCTGGTCAAA 759  
Db 281 LeuProProSerArgGluMetThrLysAsnGlnValSerLeuThrCysLeuValLys 300  
Qy 760 GGCTTCTATCCACGACATCGCGTGGAGTGGAGAGCAATGGCAGCCGAGAACCAAC 819  
Db 301 GlyPheTyrProSerAspIleAlaValGluTrpLysSerGlyGlnProGluAsnAsn 320  
Qy 820 TACAAGACACGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTTCTACAGCAAGCTC 879  
Db 321 TyrAsnThrThrProProMetLeuAspSerAspGlySerPheLeuTyrSerLysLeu 340  
Qy 880 ACCGTGGACAGACAGGTGGCAGCGGGGAACTCTTCTCTCATGCTCCGTGATGATGAG 939  
Db 341 ThrValAspLysSerArgTrpGlnGlnGlyAsnIlePheSerCysSerValMetHisGlu 360  
  
Qy 940 GCTCTGCACCAACTACACGACAGAGCTCTCCCTGTCTCCGGGTAAA 990  
Db 361 AlaLeuHisAsnArgPheThrGlnLysSerLeuSerProGlyLys 377  
  
RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 31-Dec-2004  
C:Accession: A60764  
R:Huck, S.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
A:Reference number: A60764; MUID:90007613; PMID:2571587  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
C:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI00000176F0B  
C:Superfamily: immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>  
  
Alignment Scores:  
Pred. No.: 2,88e-95 Length: 377  
Score: 1617.50 Matches: 307  
Percent Similarity: 84.08% Conservative: 10  
Best Local Similarity: 81.43% Mismatches: 13  
Query Match: 90.01% Indels: 47  
DB: 2 Gaps: 1  
  
US-10-733-563-111 (1-990) x A60764 (1-377)  
  
Qy 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTGGCACCCTCTCCAAAGAGCACTCTGGG 60  
Db 1 AlaserThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGly 20  
  
Qy 61 GGCACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120  
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
  
Qy 121 TGGAACTCAGCGCCCTGACACAGCGCGTGCACACCTTCCCGGTGCTCTCAGTCTCTCA 180  
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Qy 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCGCACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80  
  
Qy 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAAGATT----- 294  
Db 81 TyrThrCysAsnValAsnHisLysProSerAsnThrLysValAspLysArgValGluLeu 100  
  
Qy 294 ----- 294  
  
Db 101 LysThrProLeuGlyAspThrThrHisThrCysProArgCysProGluProLysSerCys 120  
Qy 294 ----- 294  
  
Db 121 AspThrProProProCysProArgCysProGluProLysSerCysAspThrProProPro 140  
Qy 295 -----GAGCCCAAACTTGTGTGACAAAACCTCACATGCGCCACCGTGCCCA 339  
Db 141 CysProArgCysProGluProLysSerCysAspThrProProProCysProArgCysPro 160  
  
Qy 340 GCACCTGAACCTCGGGGGGCGACCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGACAC 399  
Db 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr 180  
  
Qy 400 CTCATGATCTCCCGGACCCCTGAGGTACATGTCATGCGTGGTGGACGTGAGCCAGAC 459  
Db 181 LeuMetIleSerArgThrProGluValThrCysValValValAspValSerHisGluAsp 200  
  
Qy 460 CCTGAGGTCAAGTTCAACTGGTACCTGGACCGGTGGAGGTGCATAATGCCAACACAAG 519  
Db 201 ProGluValGlnPheLysTyrValAspGlyValGluValHisAsnAlaLysThrLys 220  
  
Qy 520 CCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCCCTCAGCGTCTCCTGAC 579  
Db 181 GGAAGTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGGCGACCCAGACC 240

Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
Qy 241 TACATCTGCACGCTGAATCATCAAGCCGACGACACACCAAGGTGGACAGAAAGTT----- 294  
Db 81 TyrThrCysAenValAenHisLysProSerAenThrLysValAspLysArgValGluLeu 100  
Qy 294 ----- 294  
Db 101 LysThrProLeuGlyAspThrHisThrCysProArgCysProGluProLysSerCys 120  
Qy 294 ----- 294  
Db 121 AspThrProProCysProArgCysProGluProLysSerCysAspThrProProPro 140  
Qy 295 -----GAGCCCAATCTGTGACAAAACCTCACATGCCACCGTGGCCCA 339  
Db 141 CysProArgCysProGluProLysSerCysAspThrProProCysProArgCysPro 160  
Qy 340 GCACCTGAACCTCGCGGGGACCGCTCAGTCTCTCTTCCCCCAAAACCCCAAGGACAC 399  
Db 161 AlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLysProLysAspThr 180  
Qy 400 CTCATGATCTCCCGAGACCCCTGAGGTCAATGCGTGGTGGAGCGTGGAGCCAGCAAGAC 459  
Db 181 LeuMetIleSerArgThrProGluValThrCysValValAspValSerHisGluAsp 200  
Qy 460 CCTGAGGTCAAGTTCAACTGTGAGCGCGGTGGAGGTGCATATATGCCAAGCAAAAG 519  
Db 201 ProGluValGlnPheLysTrpTyrValAspGlyValGluValHisAsnAlaLysThrLys 220  
Qy 520 CCGCGGGAGGAGCAGTCAACAGCAGCTPACCGTGGTTCAGCGTCCCTCACCGCTCCGAC 579  
Db 221 ProArgGluGluInTyraAsnSerThrPheArgValValSerValLeuThrValLeuHis 240  
Qy 580 CAGGACTGGCTGAATGGCAAGGAGTCAAGGTGCAAGGTCTCCAAACAAGCCCTCCAGCC 639  
Db 241 GlnAspTrpLeuAenGlyLysGluTyrLysCysLysValSerAenLysAlaLeuProAla 260  
Qy 640 CCCATCGAGAAACATCTCAAGCCAAAGGGAGCCCGGAGAACCCACAGGTGTACACC 699  
Db 261 ProileGluLysThrIleSerLysThrLysGlyGlnProArgGluProGlnValTyThr 280  
Qy 700 CTGCCCCCATCCCGGGATGAGTGCACCAAGACCAAGTCCAGCTGCTCGTGGTCAAA 759  
Db 281 LeuProSerArgGluGluMetThrLysAenGlnValSerLeuThrCysLeuValLys 300  
Qy 760 GCCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGCGAGCCGAGACAAC 819  
Db 301 GlyPheTyrProSerAspIleAlaValGluTrpGluSerSerGlyGlnProGluAenAsn 320  
Qy 820 TACAAGACCGCTCCCGTGTGAGTCCGACGCTCCCTCTCTCTCTCTACAGCAAGCTC 879  
Db 321 TyrAenThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSerArgLeu 340  
Qy 880 ACCGTGGAACAAGACAGGTGCACAGCGGAGACGTCTCTCATGCTCGTGCATGCATGAG 939  
Db 341 ThrValAspLysSerArgTrpGlnGluLysAenValPheSerCysSerValMetHisGlu 360  
Qy 940 GCTCTGCACACCACTACACGACAGAAGACCTCTCCCTGTCTCCGGGTAAA 990  
Db 361 AlaLeuHisAenArgPheThrGlnLysSerLeuSerLeuSerProGlyLys 377  
RESULT 4  
G2HU  
Ig gamma-2 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
C/Accession: A93906; A92809; A90752; A93132; A02148  
R/Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A/Reference number: A93906; MUID:82197621; PMID:6804948  
A/Accession: A93906

A/Molecule type: DNA  
A/Residues: 1-326 <ELL>  
A/Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32:  
A/Note: Lys-326 is probably removed posttranslationally  
R/Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fi  
A/Reference number: A92809; MUID:81007873; PMID:6774012  
A/Contents: myeloma protein T11  
A/Accession: A92809  
A/Molecule type: protein  
A/Residues: 1-19,'Q','21-57','Z','59','A','61-193','D','195-325 <WAN>  
A/Cross-references: UNIPARC:UPI0000173791  
A/Note: Trp-156 is at or near the complement-binding site  
R/Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A/Title: The amino acid sequences of the three heavy chain constant region domains of a t  
A/Reference number: A90752; MUID:80001357; PMID:113060  
A/Contents: myeloma protein Zie  
A/Accession: A90752  
A/Molecule type: protein  
A/Residues: 1-24,'E','26-57','EV','60-85;132-171,'ZZZ','175','B','177-193','D','195-196','Q','198-;  
A/Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A/Note: this sequence has since been revised  
R/Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A/Reference number: A93132; MUID:80114419; PMID:118920  
A/Contents: Zie  
A/Accession: A93132  
A/Molecule type: protein  
A/Residues: 238-275 <HOF>  
A/Cross-references: UNIPARC:UPI0000173794  
R/Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A/Reference number: A94591  
A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R/Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A/Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A/Reference number: A90253; MUID:72033500; PMID:4940472  
A/Contents: annotation; myeloma protein Sa, disulfide bonds  
R/Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A/Title: Structural studies of immunoglobulin G.  
A/Reference number: A93157; MUID:69064124; PMID:5782707  
A/Contents: annotation; Sa, disulfide bonds  
C/Genetics:  
A/Gene: GDB:IGHG2  
A/Cross-references: GDB:119338; OMIM:147110  
A/Map position: 14q32.33-14q32.33  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F/20-85/Domain: immunoglobulin homology <IM1>  
F/133-202/Domain: immunoglobulin homology <IM2>  
F/239-306/Domain: immunoglobulin homology <IM3>  
F/14/Disulfide bonds: interchain (to light chain) #status experimental  
F/27-83,140-200,246-304/Disulfide bonds: #status experimental  
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 2,42e-94 Length: 326  
Score: 1603.00 Matches: 302  
Percent Similarity: 95.15% Conservative: 12  
Best Local Similarity: 91.52% Mismatches: 12  
Query Match: 89.20% Indels: 4  
DB: 1 Gaps: 2

US-10-733-563-111 (1-990) x G2HU (1-326)

```
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGG 60
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20
QY 61 GGCACAGGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCAGGTGACGTGTG 120
Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCTGACACAGCGCGTGCACACTTCCCGGCTGCTCAGTCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerAsnPheGlyThrGlnThr 80
QY 241 TACATCTGCAAGCTGAATCACAAGCCCGAACAACACAGGTGGACAAGAAAGTTGAGCCC 300
Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysThrValGluArg 100
QY 301 AAATCTGTGCACAAACTCACACATGCCCGTCCCGTCCAGACCTGAACCTCCGGGGGCA 360
Db 101 LysCysCysValGlu-----CysProProCysProAlaProProValAlaGly--- 116
QY 361 CGGTCAAGTCTTCTCTCTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 117 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 136
QY 421 GAGTTCACATGCTGCTGCTGACGTGACGACGACGACGACGACGACGACGACGACGACG 480
Db 137 GluValThrCysValValValAspValSerHisGluAspProGluValGlnPheAsnTrp 156
QY 481 TACGTGGAGCGGTGAGTGCATATCCAGACAGAAAGCCCGGAGGACGAGTACACAC 540
Db 157 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnPheAsn 176
QY 541 AGCAGTACCGTGTGCTCAGCGTCTCTCCCGTCCGACAGGACTGCTGAATGGCAAG 600
Db 177 SerThrPheArgValValSerValLeuThrValValHisGlnAspTrpLeuAsnGlyLys 196
QY 601 GAGTACAAGTCAAGGTCTTCCAAAGACCTTCCAGCGCCCTCCAGAGAAACCAATCTCC 660
Db 197 GluTyrLysCysLysValSerAsnLysGlyLeuProAlaProIleGluLysThrIleSer 216
QY 661 AAAGCCAAAGGCGCCCGGAGAACCAACAGGTGTACACCTGCTCCCTCCCGGATCAG 720
Db 217 LysThrLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgGluGlu 236
QY 721 CTGACCAAGAACCAAGTCAAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 237 MetThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 256
QY 781 GCCGTGGAGTGGAGCAATGGGAGCGCGAGAACCAACTCAAGACCAACGCTCCCGGTG 840
Db 257 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProMet 276
QY 841 CTGGACTCCGAGCGTCTCTCTCTTCTTCTACAGACGCTCACCGTGGACAAGAGCGTGG 900
Db 277 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 296
QY 901 CAGCAGGGGAAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAG 960
Db 297 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 316
QY 961 CAGAAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 317 GlnLysSerLeuSerLeuSerProGlyLys 326
```

RESULT 5

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C&gt;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A&gt;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 &lt;ELL&gt;

A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A:Note: The sequence was determined from the germline gene

P:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A&gt;Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant r

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 &lt;PIN&gt;

A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F:240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83.141-201.247-305/disulfide bonds: #status predicted

F:106.109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.: 7,49e-93 Length: 327

Score: 1579.50 Matches: 298

Percent Similarity: 93.94% Conservative: 12

Best Local Similarity: 90.30% Mismatches: 17

Query Match: 87.90% Indels: 3

DB: 1 Gaps: 1

US-10-733-563-111 (1-990) x G4HU (1-327)

QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGG 60

Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProCysSerArgSerThrSerGlu 20

QY 61 GGCACAGGCGCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCAGGTGACGTGTG 120

Db 21 SerThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40

QY 121 TGGAACTCAGGCGCCTGACACAGCGCGTGCACACTTCCCGGCTGCTCAGTCTCTCA 180

Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 60

QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240

Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrLysThr 80

QY 241 TACATCTGCAAGCTGAATCACAAGCCCGAACAACAGGTGGACAAGAAAGTTGAGCCC 300

Db 81 TyrThrCysAsnValAspHisLysProSerAsnThrLysValAspLysArgValGluSer 100

QY 301 AAATCTGTGCACAAACTCACACATGCCCGTCCCGTCCAGACCTGAACCTCCGGGGGCA 360

Db 101 Lys-----TyrGlyProProCysProSerCysProAlaProGluPheLeuGlyGly 117

QY 361 CGGTCAAGTCTTCT 420







C:Accession: S69339; S72664  
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; PMID:95562687; PMID:7744049  
A:Accession: S69339  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: UNIPARC:UPI0000176P24; EMBL:X81695  
R:Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: UNIPARC:UPI0000176P25; EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Alignment Scores:  
Pred. No.: 2,36e-72 Length: 374  
Score: 1256.50 Matches: 258  
Percent Similarity: 75.14% Conservative: 14  
Best Local Similarity: 71.27% Mismatches: 48  
Query Match: 69.92% Indels: 42  
DB: 2 Gaps: 7

US-10-733-563-111 (1-990) x S69339 (1-374)

```
QY 30 CTGGCACCTCTCCAGAGACCTCTGCGGGGCAACAGCGCCCTGGGCTG-----CCT 83
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 14 ProSerTrpValLeuSerGlnIleThrLeuLysGluSerGlyProThrLeuValLysPro 33
QY 84 GGTCAAGGACTA-----CTCCCGCAACCGGTAC 113
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 34 ThrGlnThrLeuThrLeuThrCysThrPheSerGlyPheSerLeuSerLysSerGlyVal 53
QY 114 GGTGTGCGGAACCTCAGCGCCCT-----CTCCCGCAACCGGTAC 113
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 54 GlyValGlyTrpIleArgGlnProProGlyGlnAlaLeuGluTrpLeuAlaLeuIlePhe 73
QY 138 ---GACCAGCGGTGACACCTTCCCGGTGCTCTACAGTCTCTCAGG-----182
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 TrpAspAspLysArgTyrSerProSerLeuArgThrArgLeuThrIleThrLysAsp 93
QY 193 ACTCTACTCCCTCAGCAGCGGTGACCGTGCCTCC---AGCAGTGGGACCCACAC 239
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 ThrSerLysAsnGln-ValValLeuThrMetThrAsnValAspProAlaAspThrAlaTh 113
QY 240 CTACATCTGCAACGTGAAT-----CACAAAG---CC 266
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 113 rTyTyTyCysGlyTyrSerValGluGlyTyrGlyGlnGlyTyrArgPheHisSerTrpGI 133
QY 267 CAGCAACACCAAGGTGGAGAAAGTTGAGCCCAAAATCTTGTGACAAACTCACACATG 326
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 yGlnGlyThrLeuValThrValSerSerGluProLysSerCysAspLysThrHisCys 153
QY 327 CCCAGCGTCCCGACCACTGAACCTCGCGGGGACCGTCACTCTCTCTCCCTCCCGCCAAA 386
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 sProProCysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProProLy 173
QY 387 ACCCAAGGACACCTCATGATCTCCCGGACCCCTCAGGTGCATCGTGGTGGTGGAGCT 446
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 173 sProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValValAspVa 193
QY 447 GAGCCACGAAGACCTCAGGTCAAGTTCACTGGTACGTGGACGGCGGTGGAGGTGCATAA 506
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 193 lSerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAs 213
QY 507 TGCCAGACAAAGCCCGGGAGGACAGTACACAGCAGGTACCGTGTGGTGGTGGTGGT 566
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 213 nAlaLysThrLysProArgGluGlnTyrAsnSerThrTyrArgValValSerVal 233
```

```
QY 567 CACCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAAGGTCTCCAAACAA 626
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 233 uThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys 253
QY 627 AGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCC 686
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 sAlaLeuProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluPr 273
QY 687 ACAGGTGTACACCTCGCCCCCATCGCGGATGAGCTGACCAAGACCAAGGTCAGCTCAGC 746
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 273 oGlnValTyrThrLeuProProSerArgGluGluMetThrLysAsnGlnValSerLeuTh 293
QY 747 CTGCCTGTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCA 806
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 293 rCysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGI 313
QY 807 GCCGAGAAACAATCAAGACACCGCTCCCGTGTGTGAGCTCCCGAGCGCTCTCTCTCTCT 866
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 313 nProGluAsnAsnTyrLysThrThrProValLeuAspSerAspGlySerPhePheLe 333
QY 867 CTACAGCAAGCTCACCGTGGCAAGAGCAGTGGCAGGAGGAGACGTCCTCTCATGCTC 926
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 uTySerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysE 353
QY 927 CGTGATGATGAGCTCTGCACCAACTACACGAGAGAGAGCTCTCCCTGTCTCTCCGGG 986
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 353 rValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSerLeuSerLeuSerProGI 373
QY 987 TAAA 990
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 373 yLys 374
```

#### RESULT 8

I47160

Ig Gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: I47160

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAAS2218.1; PII

C:Genetics:

A:Gene: IGG2b

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

#### Alignment Scores:

Pred. No.:	3,97e-72	Length:	328
Score:	1253.00	Matches:	232
Percent Similarity:	82.23%	Conservative:	41
Best Local Similarity:	69.88%	Mismatches:	53
Query Match:	69.73%	Indels:	6
DB:	2	Gaps:	3

US-10-733-563-111 (1-990) x I47160 (1-328)

```
QY 1 GCCTCCACCAAGGCGCCATCGTCTTCCCTGGCACCCTCTCTCCAGAGACCTCTCGG 60
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 AlaProLysThrAlaProLeuValTyrProLeuAlaProCysGlyArgAspThrSerGly 20
QY 61 GGCACAGCGCGCTGGGCTGCTGCTCAAGCACTACTTCCCGCAACCGGTGACGGTGTGCG 120
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40
QY 121 TGGAACTCAGCGCGCTGGACCGGGGTGCACACCTTCCCGGGTGTCTACAGTCTCA 180
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 41 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60  
Qy 181 GGACTTACTCTCCAGCAGGTTGGTGAACCGTCCCTCCAGAGTCTGGGACCCAGACC 240  
Db 61 GlyLeuTySerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80  
Qy 241 TACATCTGCAACGTTGAATCAACAAGCCAGCAGCAACCAAGGTGGCAAGAAATTTAGGCC 300  
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrLysValAspLysArgValGlyThr 100  
Qy 301 AAATCTTTGTGACAAATCAACATGCCCCACCGTCCAGCAGCAGCTGAACCTCGCGGGGCA 360  
Db 101 LysThr-----LysProCysProIleCysProAlaCysGluSerProGly--- 116  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGGAGCCCT 420  
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerArgThrPro 136  
Qy 421 GAGTTCACATGCGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAGCTGG 480  
Db 137 GlnValThrCysValValValAspValSerGlnGluAsnProGluValGlnPheSerTrp 156  
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGAGGAGCAGTACAAAC 540  
Db 157 TyrValAspGlyValGluValHisThrAlaGlnThrArgProLysGluGlnPheAsn 176  
Qy 541 AGCAGTACCGTGGTGGAGTCTCAGCTCTCAGTCTGACACAGGCTGGCTGAATGGCAAG 600  
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuAsnGlyLys 196  
Qy 601 GAGTACAAGTCAAGGCTCTCAACAAAGCCCTCCAGCCGCCATCGAGAAACCATCTCC 660  
Db 197 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleThrArgIleIleSer 216  
Qy 661 AAAGCCAAAGGCGCCCGGAGAACCAACAGGTGTACACCTCGCCCACTCCCGGGATGAG 720  
Db 217 LysAlaLysGlnThrArgLysGlnProGlnValTyrThrLeuProProHisAlaGlu 236  
Qy 721 CTGACCAAGAACAGGTGAGCTGAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCCAGCAGATC 780  
Db 237 LeuSerArgSerLysValSerIleThrCysLeuValIleGlyPheTyrProProAspIle 256  
Qy 781 GCCGTGAGTGGGAGCAATGGGCGAG-----CCGAGAACAACTACAAGCACCAGCCT 834  
Db 257 AspValGluTrpGlnArgAsnGlyGlnProGluProGluLysValSerValAspLysAla 296  
Qy 835 CCCGTGCTGGACTCCGACCGCTCTCTTCTCTTCTTCTACAGCAAGCTCACCGTGGACAAGC 894  
Db 277 ProGlnGlnAspValAspGlyThrTyrPheLeuTyrSerLysPheSerValAspLysAla 296  
Qy 895 AGTGGCAGCAGGGGAGCGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGACACACAC 954  
Db 297 SerTrpGlnGlyGlyIlePheGlnCysAlaValMetHisGluAlaLeuHisAsnHis 316  
Qy 955 TACACGAGGAAGAGCCTCTCCTCTCTCTCCGGGTAAA 990  
Db 317 TyrThrGlnLysSerIleSerLysThrProGlyLys 328  
RESULT 9  
S31866  
Ig gamma-1 chain C region - synthetic  
C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R/Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 <F11>  
A/Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PID:CAA49866.1; PID

C/Keywords: immunoglobulin  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region

Alignment Scores:  
Pred. No.: 7,22e-72 Length: 255  
Score: 1249.00 Matches: 231  
Percent Similarity: 96.65% Conservative: 0  
Best Local Similarity: 96.65% Mismatches: 8  
Query Match: 69.50% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x S31866 (1-255)

Qy 274 ACCAAGTGGACAAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACATGCCACCG 333  
Db 17 ThrValAlaGlnAlaAspValGluSerLysSerCysAspLysThrHisThrCysProPro 36  
Qy 334 TGCCACGACCTGNACTCGCGGGGACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 393  
Db 37 CysProAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLysProLys 56  
Qy 394 GACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCAC 453  
Db 57 AspThrLeuMetIleSerArgThrProGluValThrCysValValValAspValSerHis 76  
Qy 454 GAAGACCTGAGGTCAAAGTTCAGTGTGACCGCGTGGAGGTGCAATAATGCCAAG 513  
Db 77 GluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsnAlaLys 96  
Qy 514 ACAAGCCGCGGGAGGACAGTACAACAGCAGCTGAGTGTGGTGGAGTGTGGTGTGGTGT 573  
Db 97 ThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeuThrVal 116  
Qy 574 CTGACACGAGCTGGCTGAATGGCAAGAGTACAAGTGAAGTCTCCAAACAAAGCCCTC 633  
Db 117 LeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLysAlaLeu 136  
Qy 634 CCAGCCCTCATCGAGAAACCATCTCCAAAGCCAAAGCGGACGCCCCAGAACCAAGGT 693  
Db 137 ProAlaProIleGluLysThrIleSerLysAlaLysGlyGlnProArgGluProGlnVal 156  
Qy 694 TACACCTGCTGCCATCCCGGAGTACCTACCAAGAACCAAGTTCAGCTGAGTGTGCTG 753  
Db 157 TyrThrLeuProProSerArgAspGluLeuThrLysAsnGlnValSerLeuThrCysLeu 176  
Qy 754 GTCAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGGCAGCCGAG 813  
Db 177 ValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerAsnGlyGlnProGlu 196  
Qy 814 AACCACTACAGACAGCCCTCCCGTGTGAGTCCGACCGGCTCTCTCTCTCTCTCTCT 873  
Db 197 AsnAsnTyrLysThrThrProProValLeuAspSerAspGlySerPhePheLeuTyrSer 216  
Qy 874 AAGCTCACCTGGACAGACAGTGGCAGCAGGGAACGCTTCTCTCATGCTCCGCTGATG 933  
Db 217 LysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSerValMet 236  
Qy 934 CATGAGCTCTGCACAACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAA 990  
Db 237 HisGluAlaLeuHisAsnHisThrThrGlnLysSerLeuSerLeuSerProGlyLys 255

RESULT 10  
PT0207

Ig gamma chain C region - chimpanzee  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C/Accession: PT0207  
R/Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A/Reference number: PT0207; MUID:91287716; PMID:2062315  
A/Accession: PT0207

A:Molecule type: mRNA  
A:Residues: 1-234 <EHR>  
A:Cross-references: UNIPARC:UPI0000176F05  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:48-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 1,74e-71 Length: 234  
Score: 1243.00 Matches: 229  
Percent Similarity: 98.29% Conservative: 1  
Best Local Similarity: 97.86% Mismatches: 4  
Query Match: 69.17% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x PT0207 (1-234)

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QY 268 AGCACACCAAGGTGGACAGAAAGTTGAGCCCAATCTTTGACAAACTCAGACATGC 327
Db 1 SerAsnThrLysValAspLysValGluProLysSerCysAspThrThrHisThrCys 20
QY 328 CCACCGTCCCGACACCTCAATCTCCCGGCGGACCGTCAAGTCTCTCTCTCCCGCCCAAA 387
Db 21 ProProCysAlaAlaProGluLeuLeuGlyGlyProSerValPheLeuPheProLys 40
QY 388 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCAATGCGTGGTGGACGTG 447
Db 41 ProLysAspThrLeuMetIleSerArgThrProGluValThrCysValValAspVal 60
QY 448 AGCCAGGAAGACCTGAGTCAAGTTCAACTGGTACGTCGAGCGGTGAGGTGCATAT 507
Db 61 SerHisGluAspProGluValLysPheAsnTrpTyrValAspGlyValGluValHisAsn 80
QY 508 GCCAAGACAAAGCCGGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTCCCTC 567
Db 81 AlaLysThrLysProArgGluGluGlnTyrAsnSerThrTyrArgValValSerValLeu 100
QY 568 ACCGCTCTGCACAGGACTTCTATCCCGGATGAGTACCAAGGAGTACCAAGGAGTCTCCAA 627
Db 101 ThrValLeuHisGlnAspTrpLeuAsnGlyLysGluTyrLysCysLysValSerAsnLys 120
QY 628 GCCCTCCAGCCCCCATGAGAAACCATCTCCAAAGCCAAAGGGGAGCCCGAGAACCA 687
Db 121 AlaLeuProAlaProIleGluLysThrLysSerLysAlaLysGlyGlnProArgGluPro 140
QY 688 CAGGTGTACACCTGCCCCATCCCGGATGAGTACCAAGCAGTACCAAGCAGTACGCTGACC 747
Db 141 GlnValTyrThrLeuProSerArgAspGluLeuThrLysAsnGlnValSerLeuThr 160
QY 748 TGCCTGTCAAGGCTTCTATCCCGACATCGCGGTGGAGTGGGAGGAGCAATGGGCAG 807
Db 161 CysLeuValLysGlyPheTyrProSerAspIleAlaValGluTrpGluSerSerGlyGln 180
QY 808 CCGGAGAACAACTACAAGACACGCTCCCGTGTGACTCCGACGGTCTCTTCTTCCTC 867
Db 181 ProGluAsnAsnTyrLysThrThrProProValLeuAspSerAspGlySerPhePheLeu 200
QY 868 TACAGCAAGCTCACCGTGGACAGGACGAGTGGGAGGAGGAAAGTCTTCTCAGCTCC 927
Db 201 TyrSerLysLeuThrValAspLysSerArgTrpGlnGlnGlyAsnValPheSerCysSer 220
QY 928 GTGATGCATGAGGCTCTGCACAAACCACTACACGCGAGAAGAGC 969
Db 221 ValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 234
```

RESULT 11

I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a swine  
A:Reference number: I47158, MUID:95015845, PMID:7930579  
A:Accession: I47158  
A:Status: Preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: UNIPARC:UPI0000115523, EMBL:U03778, NID:G433121, PIDN:AAAS2216.1, PII  
C:Genetics:  
A:Gene: IgG1  
A:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 5,51e-71 Length: 328  
Score: 1235.00 Matches: 231  
Percent Similarity: 81.33% Conservative: 39  
Best Local Similarity: 69.58% Mismatches: 56  
Query Match: 68.73% Indels: 6  
DB: 2 Gaps: 3

US-10-733-563-111 (1-990) x I47158 (1-328)

```
QY 1 GCCTCCACAAGGGCCCATCGTCTTCCCTGGCACCCCTCTCCAGAGACCTCTCTGGG 60
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysGlyArgAspValSerGly 20
QY 61 GGCACAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTGC 120
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrValThr 40
QY 121 TGGAACTCAGCGCGCTGACACGCGCGTGCACACCTTCCCGGCTGCTCTACAGCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60
QY 181 GGACTCTACTCTCAGCAGCGTGTGACCGTGCCTCCAGAGCTGGGGACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80
QY 241 TACATCTCAACGCTGAATCACAAAGCCAGCAACCAAGGTGGACAAAGTGTGAGCCC 300
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrThrLysValAspLysArgVal 98
QY 301 AAATCTTGTGACAAACTCACACATGCCCGTGCACGACCTGCACTCCGCGGGGCA 360
Db 99 ---GlyIleHisGlnProGlnThrCysProIleCysProGlyCysGluValAlaGly 116
QY 361 CGCTCAGTCTTCTCTTCCCGCCAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 117 ProSerValPheIlePheProLysProLysAspThrLeuMetIleSerGlnThrPro 136
QY 421 GAGGTACATCGGTGGTGGACGTGAGCCACGAGACCTCGAGTCAAGTTCAACTGG 480
Db 137 GluValThrCysValValValAspValSerLysGluHisAlaGluValGlnPheSerTrp 156
QY 481 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 540
Db 157 TyrValAspGlyValGluValHisThrAlaGluThrArgProLysGluGluGlnPheAsn 176
QY 541 AGCAGTACCGTGTGGTCAAGCTCTCAGCTCCCGTCCGACACGAGTGGCTGAATGGCAAG 600
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAsnTrpLeuLysGlyLys 196
QY 601 GAGTACAAAGTGCAGGCTCTCCAAAGCCCTCCCGCCCGCCCATCGAGAAACCATCTCC 660
Db 197 GluPheLysCysLysValAsnAsnValAspLeuProAlaProIleThrArgThrIleSer 216
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTGCGCCCGCCATCCCGGATGAG 720
Db 217 LysAlaIleGlyGlnSerArgGluProGlnValTyrThrLeuProProAlaGluGlu 236
QY 721 CTGACCAAGAACACCGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 237 LeuSerArgSerLysValThrThrCysLeuValIleGlyPheTyrProProAspIle 256
```

QY 781 GCCGTGGAGTGGAGAGCAATGGGCAG-----CCGGAGAACAACTACAAAGACCACGGCT 834  
Db 257 HisValGluTrpLysSerAsnGlyGlnProGluProGluAsnThrTyrArgThrThrPro 276  
QY 835 CCCGTGCTGGACTCCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAC 894  
Db 277 ProGlnGlnAspValAspGlyThrPhePheLeuTyrSerLysLeuAlaValAspLysAla 296  
QY 895 AGTGGGACAGGGGAACGCTTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACAC 954  
Db 297 ArgTrpAspHisGlyAspLysPheGluCysAlaValMetHisGluAlaLeuHisAsnHis 316  
QY 955 TACACGACAGAGAGCTCTCCCTGTCTCCGGGTAA 990  
Db 317 TyrThrGlnLysSerIleSerLysThrGlnGlyLys 328

RESULT 12  
147161  
Ig gamma 3 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47161  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMW>

Alignment Scores:  
Pred. No.: 9.89e-71 Length: 328  
Score: 1231.00 Matches: 230  
Percent Similarity: 81.33% Conservative: 40  
Best Local Similarity: 69.28% Mismatches: 56  
Query Match: 68.50% Indels: 6  
DB: 2 Gaps: 3

US-10-733-563-111 (1-990) x I47161 (1-328)

QY 1 GCCTCCCAAGGGCCCATCGTCTTCCCTGGCACCCTCTCTCAAGACGACCTCTGGG 60  
Db 1 AlaProLysThrAlaProSerValTyrProLeuAlaProCysGlyArgAspThrSerGly 20  
QY 61 GGCACAGCGGCGCTGGTGTCTGTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGC 120  
Db 21 ProAsnValAlaLeuGlyCysLeuAlaSerSerTyrPheProGluProValThrMetThr 40  
QY 121 TGGAACTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGGTGTCTCAGTCTCA 180  
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProSerValLeuGlnProSer 60  
QY 181 GGACTCTACTCTCCCTCAGCAGGCTGTGTACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 61 GlyLeuTyrSerLeuSerSerMetValThrValProAlaSerSerLeuSerSerLysSer 80  
QY 241 TACATCTGCAACGTGAATCACAGCCCGACCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
Db 81 TyrThrCysAsnValAsnHisProAlaThrThrThrLysValAspLysArgValGlyThr 100  
QY 301 AAATCTGTGCAAAACTCACACATGCCCGTCCAGCACCTGAACTCGCGGGGCA 360  
Db 101 LysThr-----LysProProCysProLysProGlyCysGluValAlaGly--- 116  
QY 361 CCGTCACTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420

Db 117 ProSerValPheIlePheProProLysProLysAspThrLeuMetIleSerGlnThrPro 136  
QY 421 GAGTTCATCGCTGGTGGTGGACGTGAGCCACGACGACCTGAGGTCAAGTTCACATGG 480  
Db 137 GluValThrCysValValValAspValSerLysGluHisAlaGluValGlnPheSerTrp 156  
QY 481 TACCTGGACCGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGACGACTACAC 540  
Db 157 TyrValAspGlyValGluValHisThrAlaGlyThrArgProLysGluGlnPheAsn 176  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 177 SerThrTyrArgValValSerValLeuProIleGlnHisGlnAspTrpLeuLysGlyLys 196  
QY 601 GAGTACAAAGTGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCC 660  
Db 197 GluPheLysCysLysValAsnAsnValAspLeuProAlaProIleThrArgThrIleSer 216  
QY 661 AAAGCCAAAGGGCAGCCCGACGACACGAGTGTACACCTGCGCCCTCCCGGATGAG 720  
Db 217 LysAlaIleGlyGlnSerArgGluProGlnValTyrThrLeuProProAlaGluGlu 236  
QY 721 CTGACCAAGAACAGGTGACCTGACCTGCTGTGTCAAGGCTTCTATCCAGCGACATC 780  
Db 237 LeuSerArgSerLysValThrValThrCysLeuValIleGlyPheTyrProProAspIle 256  
QY 781 GCCGTGAGTGGGAGAGCAATGGGCAG-----CCGAGAACAACTACAAAGACCCGCT 834  
Db 257 HisValGluTrpLysSerAsnGlyGlnProGluProGluGlyAsnTyrArgThrThrPro 276  
QY 835 CCCGTGCTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACGAGC 894  
Db 277 ProGlnGlnAspValAspGlyThrPhePheLeuTyrSerLysLeuAlaValAspLysAla 296  
QY 895 AGTGGCAGCAGGGGAAACGCTTCTCATGCTCCGTGTATGATGATGAGGCTCTGCACAAAC 954  
Db 297 ArgTrpAspHisGlyGluThrPheGluCysAlaValMetHisGluAlaLeuHisAsnHis 316  
QY 955 TACACGACAGAGCTCTCCCTGTCTCCGGGTAA 990  
Db 317 TyrThrGlnLysSerIleSerLysThrGlnGlyLys 328

RESULT 13  
GHRB  
Ig gamma chain C region - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161  
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
Immunogenetics 18, 387-397, 1983  
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplotype  
A:Reference number: A91749; MUID:84030930; PMID:6313520  
A:Accession: A91749  
A:Molecule type: mRNA  
A:Residues: 1-323 <BER>  
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D  
A:Note: This sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
R:Pratt, D.M.; Mole, L.E.  
Biochem. J. 151, 337-349, 1975  
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin  
A:Reference number: A90290; MUID:76135469; PMID:1243651  
A:Accession: A90290  
A:Molecule type: protein  
A:Residues: 1-47, 'E', '49-71', 'PV', 72-128 <PRA>  
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
A:Reference number: A93928; MUID:83299917; PMID:6193512  
A:Accession: A93928  
A:Molecule type: mRNA  
A:Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:G

A>Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970  
A>Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin

A;Reference number: A90245; MUID:70110015; PMID:5461106  
A;Accession: A90245

A;Molecule type: protein  
A;Residues: 132-143, 'E', 145-161 <FRU>

A;Cross-references: UNIPARC:UPI00001737AC  
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almquist and Wiksell,  
A;Reference number: A94416

A;Accession: A94416  
A;Molecule type: protein

A;Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',  
A;Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE

A;Note: this has the e15 allotypic marker, 185-Ala  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;20-82/Domain: glycoprotein; heterotetramer; immunoglobulin  
F;130-195/Domain: immunoglobulin homology <IM1>

F;236-303/Domain: immunoglobulin homology <IM2>  
F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 5,32e-70 Length: 323

Score: 1219.50 Matches: 227

Percent Similarity: 79.82% Conservative: 34

Best Local Similarity: 69.42% Mismatches: 59

Query Match: 67.86% Indels: 7

DB: 1 Gaps: 2

US-10-733-563-111 (1-990) x GHRB (1-323)

Qy 10 AAGGCCCATCGTCTTCCCTCCGACCTCTCCACAGAGACCTCTCTGGGGGCACAGC 69

Db 4 LysAlaProSerValPheProLeuAlaProCysGlyAspThrProSerSerThrVal 23

Qy 70 GCCCTGGCTGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTCTCGTGGAACTCA 129

Db 24 ThrLeuGlyCysLeuValGlyGlyTyrLeuProGluProValThrValThrTrpAsnSer 43

Qy 130 GCGCGCTTACAGCAGCGGGTGCACACCTTCCCGGTCTCTACAGTCTCTCAGAGCTCTAC 189

Db 44 GlyThrLeuThrAsnGlyValArgThrPheProSerValArgGlnSerSerGlyLeuThr 63

Qy 190 TCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTTACATCTGC 249

Db 64 SerLeuSerSerValValSerValThrSerSerSer-----GlnProValThrCys 80

Qy 250 AACGTGAATCAACACCCAGCAGCAGCAGTGGAGCAAGATTGAGCCCAATCTTGT 309

Db 81 AsnValAlaHisProAlaThrAsnThrLysValAspLysThrValAlaProSerThrCys 100

Qy 310 GACAAACTACTACATGCCCGCCAGCGGTGACCTGAACTCGCGGGGCACCGTCAGTC 369

Db 101 SerLys-----ProThrCysProProProGluLeuLeuGlyGlyProSerVal 116

Qy 370 TTCCTCTTCCCGCCCAACCCAGCAGCAGCTCATGATCTCCCGGACCCCTGAGTCA 429

Db 117 PheIlePheProProLysPheProLysAspThrLeuMetIleSerArgThrProGluValThr 136

Qy 430 TCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 489

Db 137 CysValValValAspValSerGlnAspAspProGluValGlnPheThrTrpThrIleAsn 156

Qy 490 GCGGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGGAGGACGACGTACACAGCAGTAC 549

Db 157 AsnGluInValArgThrAlaArgProProLeuArgGluGlnGlnPheAsnSerThrIle 176

Qy 550 CGTGTGGTGCAGCGTCTCACCCTCTGCACCCAGGACTGGCTGAATGGCAAGAGTACAAG 609

Db 177 ArgValValSerThrLeuProIleThrHisGlnAspTrpLeuArgGlyLysGluPheLys 196

Qy 610 TGCAGGTCTCCACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCAAAACCATCTCCAAAGCCCAA 669

Db 197 CysLysValHisAsnLysAlaLeuProAlaProIleGluLysThrIleSerLysAlaArg 216

Qy 670 GCGAGCCCGCAGAGAACACAGGTGTACACCTCTGCCCTCCAGTACCCGCGATGAGTACCAAG 729

Db 217 GlyGlnProLeuGluProLysValThrMetGlyProProArgGluGluLeuSerSer 236

Qy 730 AACAGGTGACGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCAGCATCCCGCTGGAG 789

Db 237 ArgSerValSerLeuThrCysMetIleAsnGlyPheTyrProSerAspIleSerValGlu 256

Qy 790 TGGGAGAGCAATGGCAGCCGAGAACCACTACAGACCAAGCGCTCCGCTGGTGGTGGTGG 849

Db 257 TrpGluLysAsnGlyLysAlaGluAspAsnTyrLysThrProAlaValLeuAspSer 276

Qy 850 GACGCTCTTCTTCTCTCCTCAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGG 909

Db 277 AspGlySerTyrPheLeuTyrAsnLysLeuSerValProThrSerGluTrpGlnArgGly 296

Qy 910 AACGCTTCTCATGCTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 969

Db 297 AspValPheThrCysSerValMetHisGluAlaLeuHisAsnHisTyrThrGlnLysSer 316

Qy 970 CTCCTCCCTGCTCCGGGTAAA 990

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RESULT 14

G2GP

Ig gamma-2 chain C region - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151

R;Trischmann, T.M.

submitted to the Atlas, April 1975

A;Reference number: A94553

A;Accession: A94553

A;Molecule type: protein

A;Residues: 1-3 <TRI>

A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E

R;Birshtein, B.K.; Hugsain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Amir

A;Reference number: A90352; MUID:71058471; PMID:5538606

A;Accession: A90352

A;Molecule type: protein

A;Residues: 4-68 <BIR>

A;Cross-references: UNIPARC:UPI000017379F

R;Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir

A;Reference number: A90359; MUID:71058486; PMID:5538616

A;Accession: A90359

A;Molecule type: protein

A;Residues: 69-133;312-329 <TUR>

A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1

R;Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665

A;Accession: A90384

A;Molecule type: protein

A;Residues: 134-226 <TRA>

A;Cross-references: UNIPARC:UPI00001737A2

R;Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90385; MUID:75036073; PMID:4609467

A;Accession: A90385





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Qy 361 CGGTCAAGTCTTCTCTTCCCTCCAAACCAAGGACACCTCATGATCTCCGGGACCCCT 420
Db 261 ProSerValPheIlePheProProlsProLysAspThrLeuThrIleSerGlyThrPro 280
Qy 421 GAGTCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 281 GluValThrCysValValValAspValGlyGlnAspAspProGluValGlnPheSerTrp 300
Qy 481 TACGTGACGGGTGGAGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAA 540
Db 301 PheValAspAsnValGluValArgThrAlaArgThrLysProArgGluGluGlnPheAsn 320
Qy 541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 321 SerThrPheArgValValSerAlaLeuProIleGlnHisGlnAspTrpThrGlyGlyLys 340
Qy 601 GAGTCAAGTGCAGGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCC 660
Db 341 GluPheLysCysLysValHisAsnGluAlaLeuProAlaProIleValArgThrIleSer 360
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 151.869 Seconds  
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9198.340 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797  
Sequence: 1 gctccaccaggcccatc.....tctccctgtctccgggtaaa 990

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR SCORES=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
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-NO.MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 05.80.\*

1: uniprot.spot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	97.7	465	2 Q6GMX6 HUMAN	Q6gmxf4 homo sapien
2	1756	97.7	469	2 Q569F4 HUMAN	Q569f4 homo sapien
3	1756	97.7	469	2 Q727P5 HUMAN	Q727p5 homo sapien
4	1756	97.7	475	2 Q5EF85 HUMAN	Q5ef85 homo sapien
5	1756	97.7	475	2 Q6GMW7 HUMAN	Q6gmw7 homo sapien
6	1756	97.7	476	2 Q6GMX1 HUMAN	Q6gmxf1 homo sapien
7	1753	97.6	472	2 Q6N089 HUMAN	Q6n089 homo sapien
8	1752	97.5	473	2 Q6P055 HUMAN	Q6p055 homo sapien
9	1752	97.5	475	2 Q6MZQ6 HUMAN	Q6mzq6 homo sapien
10	1752	97.5	480	2 Q6N094 HUMAN	Q6n094 homo sapien
11	1752	97.5	481	2 Q6N097 HUMAN	Q6n097 homo sapien
12	1751	97.4	330	1 IGHG1 HUMAN	P01857 homo sapien
13	1751	97.4	470	2 Q725W1 HUMAN	Q725w1 homo sapien
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15	1748	97.3	466	2 Q6IN78 HUMAN	Q6in78 homo sapien
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17	1747	97.2	480	2 Q6PJF1 HUMAN	Q6pjf1 homo sapien
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21	1744	97.1	466	2 Q6N096 HUMAN	Q6n096 homo sapien
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24	1687	93.9	475	2 Q5RE17 PONPY	Q5re17 pongo pygma
25	1619.5	90.1	519	2 Q5EBM2 HUMAN	Q5ebm2 homo sapien
26	1615.5	89.9	521	2 Q8N4Y9 HUMAN	Q8n4y9 homo sapien
27	1614.5	89.8	518	2 Q6N030 HUMAN	Q6n030 homo sapien
28	1608	89.5	517	2 Q6N093 HUMAN	Q6n093 homo sapien
29	1604.5	89.3	509	2 Q8NF17 HUMAN	Q8nf17 homo sapien
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31	1603	89.2	465	2 Q6P6C4 HUMAN	Q6p6c4 homo sapien
32	1593	88.6	464	2 Q6MZU6 HUMAN	Q6mzu6 homo sapien
33	1589	88.4	470	2 Q68CM4 HUMAN	Q68cn4 homo sapien
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35	1579.5	87.9	473	2 Q8TC63 HUMAN	Q8tc63 homo sapien
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39	1253	69.7	679	2 Q6PQ8 HUMAN	Q6pq8 homo sapien
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41	1219.5	67.9	323	1 GC RABIT	P01870 oryctolagus
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43	1157	64.4	463	2 Q99LC4 MOUSE	Q99lc4 mus musculus
44	1154	64.2	465	2 Q510J0 RAT	Q510j0 rattus norv
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#### ALIGNMENTS

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DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
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RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;

RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766.1; -, mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGc1; 3.  
DR SMART; SM00407; IGc1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
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Pred. No.: 9,45e-110 Length: 465  
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Qy 481 TACGTGACGGCGGTGGAGTGCATATCCAGACAAAGCCGCGGAGGAGCAGTACAC 540  
Db 296 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTrpAen 315  
Qy 541 AGCAGTACCGGTGGTGGAGCTCTCCACCGTCTCGCACCCAGGACTGGCTGAATGGCAAG 600  
Db 316 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAaspTrpLeuAenGlyLys 335  
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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
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RC TISSUE=Lymph;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
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RA Butterfield Y.N., Krzywinski M.I., Skalska U., Smailus D.B.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC092518; AAH92518.1; -, mRNA.  
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Alignment Scores:  
Pred. No.: 9,46e-110 Length: 469  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0



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Qy 961 CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
Db 460 GlnLysSerLeuSerLeuSerProGlyLys 469

## RESULT 4

QSEFE5\_HUMAN  
ID QSEFE5\_HUMAN PRELIMINARY; PRT; 475 AA.  
AC QSEFE5;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE Anti-RHD monoclonal T125 gammal heavy chain precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
Homo.  
NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RA Gaucher C., Klein P., Belliard R.;  
RT "Sequence determination of the recombinant human anti-RHD monoclonal antibody T125.";  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY894992; AAW82028.1; -, mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_ci.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 475 anti-RHD monoclonal T125 gammal heavy chain.  
FT SEQUENCE 475 AA; 52362 MW; 1367D40DC7D2859 CRC64;  
Alignment Scores:  
Pred. No.: 9,48e-110 Length: 475  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-111 (1-990) x QSEFE5\_HUMAN (1-475)  
Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCCCTGCGACCTCTCTCCAAAGAGACCTCTGGG 60  
Db 146 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 165  
Qy 61 GGCACAGCGCGCTGGCTGGTCAAGCACTACTTCCCGACCGGTGACCGTCTCG 120  
Db 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
Qy 121 TGGAACTCAGCGCGCTGACAGCGCGGTGCACACCTTCCCGCTGTCTTACAGTCTCA 180  
Db 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240  
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
Qy 241 TACATCTGCAACGCTGAATCAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
Db 226 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 245  
Qy 301 AAATCTTGTGCAAAACTCACACATGCCCCAGTCCAGCACCTGAATCTCGCGGGGCA 360  
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 265  
Qy 361 CCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420  
Db 266 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 285  
Qy 421 GAGGTTCACATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480  
Db 286 GluValThrCysValValValValValValValValValValValValValValVal 305  
Qy 481 TACGTGAGCGCGGTGGAGGTGCATAATCCAGAACAAAGCCCGGAGGAGCAGTACAA 540  
Db 306 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 325

QY 541 AGCAGTACCGTGTGTGTGTCAGCTCTCTCACCCTGCTGACACAGGACTGGCTGAATGCGAAG 600  
DB 326 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAenGlyLys 345  
QY 601 GAGTACAGTGTCAAGTCTCCACCAAGCCCTCCAGCCGCCCATCCAGAGAACCAATCTCC 660  
DB 346 GluTyLysCyLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 365  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTCCGCCCATCCCGGATGAG 720  
DB 366 LysAlaLysGlyGlnProHargGluProGlnValTyThrLeuProSerArgAspGlu 385  
QY 721 CTGACCAAGAACAGGTGAGCTGACCTGCTCTTCTTCTACAGCAAGCTCACAGGAGGAGTGG 780  
DB 386 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 405  
QY 781 GCCGTGGAGTGGAGGAGCAATGGCAGCGGAGACCACTACAGACCAAGCTCCCGTG 840  
DB 406 AlaValGluTrpGluSerAenGlyGlnProGluAenAsnTyLysThrProProVal 425  
QY 841 CTGGACTCCGAGCGCTCTCTTCTTCTTCTACAGCAAGCTCACAGGAGGAGTGG 900  
DB 426 LeuAspSerAspGlySerPheLeuTySerLysLeuThrValAspLysSerArgTrp 445  
QY 901 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCAACCACTACAGC 960  
DB 446 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyThr 465  
QY 961 CAGAGAGCGCTCTCCCTGCTCCGGGTAAA 990  
DB 466 GlnTySerLeuSerLeuSerProGlyLys 475

RESULT 5  
Q6GMW7\_HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6GMW7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splice;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Boek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Splice;

Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073782; AAH73782.1; -, mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; Pf07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 51987 MW; 2A1PES5D736860P8 CRC64;  
Alignment Scores:  
Pred. No.: 9,486-110 Length: 475  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-111 (1-990) x Q6GMW7\_HUMAN (1-475)  
QY 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCTCCAGAGGACCTCTGGG 60  
DB 146 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165  
QY 61 GGCACAGCGGCCCTGGCTGCTCAAGGACTACTTCCCGGAAACCGGTGACGGTGG 120  
DB 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyPheProGluProValThrValSer 185  
QY 121 TGGAACTCAGCGCCCTGACACAGCGCGTGACACCTTCCCGGTGTCTCTACAGTCTCA 180  
DB 186 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
QY 181 GGACTTACTCTCCTCAGCAGCGGTGTGACCGTGGCTCCCTCAGCAGCTTGGGACCCAGAC 240  
DB 206 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225  
QY 241 TACATCTCAACGTGAATCAACAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCC 300  
DB 226 TyrlleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 245  
QY 301 AAATCTTGTGACAAACTCACACATGCGCCCGTCCAGCAGCACCTGAACTCGCGGGGCA 360  
DB 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 265  
QY 361 CGGTAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420  
DB 266 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 285  
QY 421 GAGGTTCACATCGT 480  
DB 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 305  
QY 481 TACGTGGAGCGGTGGAGGTGCATTAATCCCAAGACAAAGCCCGGAGAGCAGGTACAAAC 540  
DB 306 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGluGlnTyraen 325  
QY 541 AGCAGTACCGT 600  
DB 326 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAenGlyLys 345  
QY 601 GAGTACAGTGTCAAGTCTCCCAACCAAGCCCTCCAGCCGCCCATCCAGAGAACCAATCTCC 660  
DB 346 GluTyLysCyLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 365  
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTCCGCCCATCCCGGATGAG 720





Qy	841	CTGGACTCCGACGGCTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGACGAGGTGG	900
Db	427	LeuAspSerAspGlySerPhePheLeuTyrSerLeuThrValAspLysSerArgTrp	446
Qy	901	CAGCAGGGGAAAGCTCTCTCATGCTCCGTCATGTCATGAGGCTCTGCACAACCACTACACG	960
Db	447	GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisGlnHisTyrThr	466
Qy	961	CAGAAGAGCCTCTCCCTCTCTCCCGGTAAA	990
Db	467	GlnLysSerLeuSerLeuSerProGlyLys	476
RESULT 7			
Q6N089_HUMAN			
ID	Q6N089	HUMAN PRELIMINARY;	PRT; 472 AA.
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Hypothetical protein DKFP686F15220.		
GN	Name=DKFP686F15220;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RI	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RP	TISSUE=Rectum tumor;		
RC	The German cDNA Consortium;		
RG	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Pobo G., Han M., Wiemann S.;		
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX640627; CAE45781.1; -; mRNA.		
DR	HSSP; P01861; 1ADQ.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG_CL.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_V.		
DR	Pfam; PF07654; Cl-set; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;		
Alignment Scores:			
Pred. No.:	1.51e-109	Length:	472
Score:	1753.00	Matches:	327
Percent Similarity:	99.39%	Conservative:	1
Best Local Similarity:	99.09%	Mismatches:	2
Query Match:	97.55%	Indels:	0
DB:	2	Gaps:	0
US-10-733-563-111 (1-990) x Q6N089_HUMAN (1-472)			
Qy	1	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCTGGCACCTCTCTCCAAGACGACCTCTGGG	60
Db	143	AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly	162
Qy	61	GGCACAGCGCCCTGGGCTGCTGTGTCAAGGACTACTTCCCGCAACCGGTGACGGTTCG	120
Db	163	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	182
Qy	121	TGGAACCTCAGCGCCCTGCACAGCGCGGTGCACACTTCCCGGGTGTCTCTACAGTCCTCA	180
Db	183	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	202
Qy	181	GGACTCTACTCCCTCAGCAGCGGTGGTGAACCGGTGCCTCCAGCAGCTTGGCACCCAGACC	240

RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2].  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Peripheral Nervous System;  
 RA Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065820; AAH65820.1; -, mRNA.  
 DR HSSP; P01861; 1ADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PP07654; C1-set; 3.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

## Alignment Scores:

Pred. No.: 1.76e-109 Length: 473  
 Score: 1752.00 Matches: 327  
 Percent Similarity: 99.09% Conservative: 0  
 Best Local Similarity: 99.09% Mismatches: 3  
 Query Match: 97.50% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x Q6P055\_HUMAN (1-473)

Qy 1 GCCTCCACCAAGGGCCGCTTCCTCCCTGGCACCCTCTCCCAAGAGCACCTCTGGG 60  
 Db 144 AlaserThrySgLyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 163  
 Qy 61 GGCACAGCGCCCTGGGCTGCTGTCAGAGCTACTTCCCGGACCGGTGACGGTGTGCG 120  
 Db 164 GlyThrAlaAlaLeuGlyCySLeuValLysAspTyrPheProGluProValThrValSer 183  
 Qy 121 TGGAACTCAGCGCCCTGACAGCGCGGTGACACACCTTCCCGGCTGTCTCAGTCTCTCA 180  
 Db 184 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 203  
 Qy 181 GGACTCTACTCTCAGCAGCGGTGTGACCGTGCCTCCAGAGCTTGGGACCCAGACC 240  
 Db 204 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 223  
 Qy 241 TACATCTGCAAGTGAATCACAGCCCAAGCCCAAGAGGTGGACAGAAAGTTGAGCCC 300  
 Db 224 TyrIleCyAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 243  
 Qy 301 AAATCTTTGTGACAAACTCACACATGCCACCGTCCAGCAGCCTGAACCTGCGGGGCA 360  
 Db 244 LysSerCyAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 263

Qy 361 CCGTCAGCTTCTCTTCCCTCCCTCCCAAGACACCTCTATGATCTCCCGGACCCCT 420  
 Db 264 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 283  
 Qy 421 GAGGTCACTGCGTGGTGGAGCTGAGCCACCAAGACCTCGAGGTCAAGTTCACATGG 480  
 Db 284 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 303  
 Qy 481 TACGTGACGCGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGACGACGTACAC 540  
 Db 304 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 323  
 Qy 541 AGCAGTACCGTGTGGTTCAGCTCTCCCGTCTCGCACCGAGTGGTGTGTAATGGCAG 600  
 Db 324 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 343  
 Qy 601 GAGTACAGTGCAGAGGTCTCCCAAGACCTCCCGACCCCTCCAGAGAAACCATCTCC 660  
 Db 344 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 363  
 Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTTCCCGGATGAG 720  
 Db 364 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 383  
 Qy 721 CTGACCAAGAACACAGGTTCAGCTCTCCCGTCTGAGTCAAGCTTCTATCCAGGACATC 780  
 Db 384 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 403  
 Qy 781 GCCGTGAGTGGGAGAGCAATGGGACGCGAGAACAACTACAGAGCCAGCCCTCCCGT 840  
 Db 404 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 423  
 Qy 841 CTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGG 900  
 Db 424 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 443  
 Qy 901 CAGCAGGGGAAAGCTTCTCTATGCTCGTATGATGATGAGGTCTGCGACACCATACACG 960  
 Db 444 GlnGlnGlyAsnValPheSerCysSerValMethHisGluGlyLeuHisAsnHisTyrThr 463  
 Qy 961 CAGAAGAGCTCTCCCTGTCTCCGGGTAAA 990  
 Db 464 GlnLysSerLeuSerLeuSerProGlyLys 473  
 RESULT 9  
 Q6MZQ6\_HUMAN  
 ID Q6MZQ6\_HUMAN PRELIMINARY; PRT; 475 AA.  
 AC Q6MZQ6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686G11190.  
 GN Name=DKFZp686G11190;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Esophagus tumor;  
 RA The German cDNA Consortium;  
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640947; CAB45972.1; -, mRNA.  
 DR HSSP; P01861; 1ADQ.  
 DR SMR; Q6MZQ6; 20-475.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.



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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00407; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7BAE255A26F4B8E CRC64;  
  
Alignment Scores:  
Pred. No.: 1.76e-109 Length: 475  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-111 (1-990) x Q6MQ06_HUMAN (1-475)  
  
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCTCTCTCCAAAGAGCACCCTCTGGG 60  
DB 146 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165  
  
QY 61 GGCACAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGACGGTGTGCG 120  
DB 166 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185  
  
QY 121 TGGAACTCAGCGGCGCTGACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCTCA 180  
DB 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205  
  
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGTGACCGTCCCTCAGCAGCTTGGCGACCCAGACC 240  
DB 206 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 225  
  
QY 241 TACATCTCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGAGCAAGAAATTTGAGCCC 300  
DB 226 TyrIleCysAsnValAsnHisLysProSerAenThrLysValAspLysValGluPro 245  
  
QY 301 AAATCTGTGCAAACTCACATGCCCGCCAGCTGCCAGACCTGAACCTCGCGGGGCA 360  
DB 246 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGly 265  
  
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 266 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 285  
  
QY 421 GAGTGCATCATCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 480  
DB 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305  
  
QY 481 TACGTGAGCGGTGGAGTGCATATCCAGACAAAGCCGCGGGAGGAGCAGGTACAAAC 540  
DB 306 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 325  
  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 326 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 345  
  
QY 601 GAGTCAAGTGCAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTCC 660  
DB 346 GluTyrLysCysValValSerAsnLysAlaLeuProAlaProlleGluLysThrIleSer 365  
  
QY 661 AAAGCCAAAGGCGCGCCCGAGAACCAAGGTGTACACCTTGGCCCGCCCATCCCGGATGAG 720  
DB 366 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 385  
  
QY 721 CTGACCAAGAACCGAGTGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 386 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 405  
  
QY 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACAACTACAAGACCCAGCCCTCCCGTG 840  
  
Db 406 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAenTyrLysThrThrProProVal 425  
QY 841 CTGGACTCCGAGCGGCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900  
Db 426 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 445  
QY 901 CAGCAGGGGAAACGTCTTCTCATGTCCGTGTGATGATGAGGTCTGTCACACCAACCACTACACG 960  
Db 446 GlnGlnGlyAsnValPheSerCysSerValMetHisGluGlyLeuHisAsnHisTyrThr 465  
QY 961 CAGAAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990  
Db 466 GlnLysSerLeuSerLeuSerProGlyLys 475  
  
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFP686001196.  
GN Name=DKFP686001196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RC NUCLEOTIDE SEQUENCE.  
RG TISSUE=Esophagus tumor;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAB45776.1; -, mRNA.  
DR HSSP; P01861; 1ADO.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.76e-109 Length: 480  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-111 (1-990) x Q6N094_HUMAN (1-480)  
  
QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTGGCACCCTCTCTCCAAAGAGCACCCTCTGGG 60  
Db 151 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 170  
  
QY 61 GGCACAGCGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCCGGTGACGGTGTGCG 120  
Db 171 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 190  
  
QY 121 TGGAACTCAGCGGCGCTGACAGCGGCTGCACACCTTCCCGGCTGCTCAGTCTCTCA 180  
Db 191 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 210
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Qy	181	GGACTCTACTCCCTCAGCAGCGTGCTGACCGTGCCCTCCAGCAGCTTGCGGCACCCAGACC	240
Db	211	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	230
Qy	241	TACATCTCAACGTCGAATCAACAAGCCACAGCAACAAGGTGGACAAGAAAGTTCGAGCCC	300
Db	231	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro	250
Qy	301	AAATCTTGTCAGAAATCAACATGCCACCGTGCCCGACGACTGAACCTCCGCGGGGCA	360
Db	251	LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly	270
Qy	361	CCGTCAAGTCTTCCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT	420
Db	271	ProSerValPheLeuPheProProlysProLysAspThrLeuMetIleSerArgThrPro	290
Qy	421	GAGTTCACATCGCTGGTGGACGTGAGCCACGAAAGACCTTGAGGTCAAGTTCAACTGG	480
Db	291	GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp	310
Qy	481	TACGTGGACGCGTGGAGGTGCATAATCCAAAGCAACAAGCCGCGGAGGAGCAGTACAAAC	540
Db	311	TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	330
Qy	541	AGCAGTACCGTGGTGGTCCAGCGTCTCTCACCGTCTCGCACAGGACTGGCTGAATGCGAAG	600
Db	331	SerThrTyrArgValValIserValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	350
Qy	601	GAGTACAGTCCAGGCTCTCAACAAGCCCTCCAGCGCCCATCGAGAAACCACTCC	660
Db	351	GluTyrLysCysLysValIserAsnLysAlaLeuProAlaProIleGluLysThrIleSer	370
Qy	661	AAAGCCAAAGGCGACGCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAG	720
Db	371	LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu	390
Qy	721	CTGACCAAGAACCGGTGAGCTGAGCTGCTGCTGCTCAAGGGTCTTATCCAGCGACATC	780
Db	391	LeuThrLysAsnGlnValIserLeuThrCysLeuValLysGlyPheTyrProSerAspIle	410
Qy	781	GCCGTGGAGTGGGAGAGCAATGGCAGCGAGAGAAACAATCAAGACCAACGCTCCCGTG	840
Db	411	AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal	430
Qy	841	CTGACTCCGAGCGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCGTGG	900
Db	431	LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp	450
Qy	901	CAGCAGGGGAACGCTTCTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG	960
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Db	471	GlnLysSerLeuSerLeuSerProGlyLys	480

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DT	05-JUL-2004	(T-EMBLrel. 27, Created)				
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)				
DE		Hypothetical protein DKFp686H20196.				
GN		Name=DKFp686H20196;				
OS		Homo sapiens (Human).				
OC		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC		Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC		Homo.				
OX		NCBI_TaxID=9606;				
OX		(1)				
RN		NUCLEOTIDE SEQUENCE.				
RP						

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RC    TISSUE=Esophagus tumor;
RA    The German cDNA Consortium;
RG    Wambutt R., Heubner D., Meves H.W., Weil B., Amid C., Osanger A.,
RL    Fobo G., Han M., Wiemann S.;
RL    Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR    ENBL; BX640619; CAB45773.1; -, mRNA.
DR    HSSP; P01861; IADQ.
DR    DR
DR    InterPro; IPR003599; Ig.
DR    InterPro; IPR007110; Ig-like.
DR    InterPro; IPR003597; Ig cl.
DR    InterPro; IPR003006; Ig_MHC.
DR    InterPro; IPR003596; Ig_v.
DR    Pfam; PF07654; Cl-set; 3.
DR    SMART; SM00409; Ig; 2.
DR    SMART; SM00407; IGcl; 3.
DR    SMART; SM00406; Ig; 1.
DR    PROSITE; PS50835; IG_LIKE; 4.
DR    PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW    Hypothetical protein.
SQ    SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Alignment Scores:
Pred. No.: 1.76e-109 Length: 481
Score: 1752.00 Matches: 327
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 3
Query Match: 97.50% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x Q6N097 HUMAN (1-481)

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US-10-733-563-111 (1-990) x Q6N097 HUMAN (1-481)

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Qy	61	GCACAGCGGCGCTGGGCTGCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGCG	120
Db	172	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	191
Qy	121	TGGAACTCAGGCGCCCTGACACGAGCGGCTGCACACCTTCCCGCTGTCTCTACAGTCTCA	180
Db	192	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer	211
Qy	181	GGACTCTACTCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGCACCCAGACC	240
Db	212	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	231
Qy	241	TATCTCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGACACAAGAAAGTTGAGCCC	300
Db	232	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysIysValGluPro	251
Qy	301	AAATCTGTGTGCAAAACTCACATATGCCACCGTCCAGCACCTGAACCTCGCGGGGCA	360
Db	252	LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly	271
Qy	361	CGCTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCT	420
Db	272	ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro	291
Qy	421	GAGTCAACATGGGTGGTGGAGTGGCCACGACGACCCCTGAGTCAAGTTCACACTGG	480
Db	292	GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp	311
Qy	481	TACGTGGACGGCGTGGAGGTGCATAATGCCAAGAACAAAGCCGGGAGGAGCAGTACAAC	540
Db	312	TyrValAspGlyValIgluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn	331
Qy	541	AGCAGTACCGTGGTGGTGGTCTCTACCGTCTCTGCACGAGACTGGCTGAATGCGAAG	600
Db	332	SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys	351
Qy	601	GAGTCAAGTGAAGGCTCTCCAAACAAAGCCCTCCACGCCCCCATCGAGAAAACCATCTCC	660

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Db 352 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 371
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Db 372 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 391
QY 721 CTGACCAAGAACAGGTGACCTGACCTGCTGCTGGTCAAGGGTCTTATCCCAAGCACATC 780
Db 392 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 411
QY 781 GCCGTGGAGTGGAGAGCAATGGCGAGCGGAGAGCACTACACAGCACCGCTCCCGTG 840
Db 412 AlaValGluTrpGluSerAsnGlnGlnProGluAsnAsnTyrLysThrProProVal 431
QY 841 CTGGACTCCGAGCGCTCTCTCTCTCTACAGCAAGCTCACCGTCGACAGAGCGAGTGG 900
Db 432 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 451
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Db 452 GlnGlnGlyAsnValPheSerCysSerValMetHisGluGlyLeuHisAsnHisTyrThr 471
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Db 472 GlnLysSerLeuSerLeuSerProGlyLys 481

RESULT 12
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
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GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP PROTEIN SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Fonstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) marker, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
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DR PIR; A93433; GHHU.
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DR PDB; 1AQK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DSI; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1PC1; X-ray; A/B=106-329.
DR PDB; 1PC2; X-ray; D=106-329.
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DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
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DR InterPro; IPR003597; Ig_c1.
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PROSITE; PS00290; IG_MHC; 2.
3D-structure; Direct protein sequencing; Glycoprotein;
Immunoglobulin C region; Immunoglobulin domain.
REGION 1 98
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REGION 111 223
REGION 112 223
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DISULFID 112 112
DISULFID 144 204
DISULFID 250 308
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VARIANT 241 241
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QY 181 GGACTCTACTCCCTCAGCAGCGGTGTCACCGTGGCCCTCCAGCAGCTTGGGCACCCAGACC 240
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QY 241 TACATCTGCAACCGTGAATCAAGCCCAAGCAACCAACCAAGGTGGCAAGAAAGTTGAGCCC 300
Db 81 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 100
QY 301 AAATCTTGTGACAAAACCTCACATGCCACCGGCCAGCAGCAGCTGAAGCTGCGGGGGCA 360
Db 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 120
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCAAGACACACCTCATGATCTCCCGGACCCCT 420
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATGCGTGGTGGACGTGAGCCACCAAGACACCTGAGGTCAAGTTCACCTGG 480
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 160
QY 481 TACGTGACCGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540
Db 161 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGluGlnTyrAen 180
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QY 721 CTGACCAAGAACACAGGTGACCGTGGTCAAGGCTTCTATCCAGCGGATC 780
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QY 841 CTGACCTCCGACGGCTCTTCTCTCTCAGCAAGCTCAGCGTGGAGCAGAGCAGGTGG 900
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AC Q725W1.
DC 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
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RC TISSUE=Spleen;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAHS3984.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
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DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
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US-10-733-563-111 (1-990) x Q725W1\_HUMAN (1-470)

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241 TACATCTCAACGCTGAATCAACAAGCCCAAGCCCAAGAGTGGCAAGAAAGTTTCAGCCC 300
221 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 240
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241 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 260
361 CGCTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATCATCTTCCCGACCTCT 420
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401 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 420
841 CTGGAAGTCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
421 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 440
901 CAGCAGGGGAAACGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
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961 CAGAAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
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AC Q6PUA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 CX NCBI\_TaxID=9606;  
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 RC TISSUE=Primary B-Cells;  
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 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
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 RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.  
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 DR Pfam; PF07654; CI-set; 3.  
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 OC Homo.  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Maximum Match 100%

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Database :

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1756	97.7	371	1	US-08-457-918-7
3	1756	97.7	371	2	US-10-157-408-7
4	1756	97.7	449	1	US-08-458-516-13
5	1756	97.7	467	2	US-08-030-175-41
6	1756	97.7	467	2	US-08-030-175-42
7	1756	97.7	476	1	US-08-378-939-10
8	1756	97.7	547	2	US-09-746-359A-54
9	1756	97.7	567	2	US-09-825-561A-16
10	1756	97.7	571	2	US-09-746-359A-53
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12	1756	97.7	951	2	US-10-282-162-9

13	1752	97.5	475	2	US-09-740-002-27	Sequence 27, Appl
14	1752	97.5	476	2	US-08-487-550-4	Sequence 4, Appl
15	1752	97.5	476	2	US-08-487-550-12	Sequence 12, Appl
16	1752	97.5	476	2	US-09-526-098-4	Sequence 4, Appl
17	1752	97.5	476	2	US-09-526-098-12	Sequence 12, Appl
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20	1752	97.5	476	2	US-09-758-173-4	Sequence 4, Appl
21	1752	97.5	476	2	US-09-758-173-12	Sequence 12, Appl
22	1752	97.5	476	2	US-09-576-424-4	Sequence 4, Appl
23	1752	97.5	476	2	US-09-576-424-12	Sequence 12, Appl
24	1751	97.4	446	2	US-08-397-411-7	Sequence 7, Appl
25	1751	97.4	459	1	US-08-157-101A-7	Sequence 7, Appl
26	1750	97.4	470	2	US-10-104-047-3730	Sequence 3730, Ap
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43	1750	97.4	451	2	US-09-920-171-18	Sequence 18, Appl
44	1750	97.4	451	2	US-09-716-028-14	Sequence 14, Appl
45	1750	97.4	451	2	US-09-716-028-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329



TOPOLOGY: linear  
US-08-457-918-7

## Alignment Scores:

Pred. No.: 2 5e-134 Length: 371  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-457-918-7 (1-371)

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Db 42 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 61
Qy 61 GGCACAGGGCCCTGGGTGCTGCTCAAGACTACTTCCCGCAACCGGTGACGGTGTGC 120
Db 62 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 81
Qy 121 TGGAACTCAGCGCCCTCACCAGCGGCTGCACACTTCCCGGCTGCTCTACAGTCCTCA 180
Db 82 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 101
Qy 181 GGACTCTACTCCTCAGCAGCGGTGCTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 102 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 121
Qy 241 TACATCTGCAACGGTGAATCACAGCCGACGACCAACCAAGGTGGAGCAAGAAAGTTGAGCC 300
Db 122 TyrIleCysAsnValAsnHisGlyProSerAsnThrLysValAspLysValGluPro 141
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 142 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuLeuGlyGly 161
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 162 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 181
Qy 421 GAGTCAATCGTGGTGGAGCTGAGCCAGCAAGACCTGAGGTCAAGTCAACTGCG 480
Db 182 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 201
Qy 481 TACGTGACGGCGTGGAGTGCATAATGCCAGACAAAGCCGCGGAGGACGCTACCAAC 540
Db 202 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 221
Qy 541 AGCAGTACCGTGTGGTCAGCGTCTCTACCGTCTCGCACCAAGGACTGGCTGAATGGCAAG 600
Db 222 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 241
Qy 601 GAGTCAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCC 660
Db 242 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 261
Qy 661 AAAGCAAGGCGGCGCCGAGACCAACAGGTGTACACCTGCCCCCATCCCGGGATGAG 720
Db 262 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 281
Qy 721 CTGACCAAGAACCAAGTCTGACCTGACCTGCTGGTCAAGGCTTCTATCCAGCGCACATC 780
Db 282 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 301
Qy 781 GCGTGGAGTGGGAGAGCAATGGGCGAGCAACTACAGAACCAACCCCTCCCGTG 840
Db 302 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 321
Qy 841 CTGCACTCCGAGCGGTCTCTTCTCTTACAGCAAGCTTACCGTGGGCAAGAGCGGTGG 900
Db 322 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 341
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Qy 901 CAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGTCTGCAACCAACCTACACG 960  
Db 342 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 361  
Qy 961 CAGAAGAGCCTCTCCCTGCTCTCCGGGTAAA 990  
Db 362 GlnLysSerLeuSerLeuSerProGlyLys 371  
RESULT 3  
US-10-157-408-7  
; Sequence 7, Application US/10157408  
; Patent No. 6710169  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/157,408  
; FILING DATE: 28-May-2002  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0444P1C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8228  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Alignment Scores:  
Pred. No.: 2 5e-134 Length: 371  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-10-157-408-7 (1-371)

Qy 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCGGCACCTCTCTCCAGAGCACCTCTCTGGG 60

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Db 42 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 61
Qy 61 GGACAGGGCCCTGGCTGCTGGTCAAGAGCTACTTCCCGCAACCGGTGACGGTGTGCG 120
Db 62 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 81
Qy 121 TGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCGGTGCTTACAGTCTCA 180
Db 82 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 101
Qy 181 GGACTCTACTCTCCAGCAGCGTGGTACCGTGGCTCCAGCAGCTGGGCACCCAGACC 240
Db 102 GlyLeuTyrSerLeuSerValValThrValProSerSerSerLeuGlyThrGlnThr 121
Qy 241 TACATCTGCAACGTGAATCAGACCCGCAACACCAAGGTGGAGCAAGAAAGTTGAGCCC 300
Db 122 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 141
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCTGACCTCGCGGGGCA 360
Db 142 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly 161
Qy 361 CCGTCAGTCTTCTCTTCCCGCAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 162 ProSerValPheLeuPheProLysProLysPheThrLeuMetIleSerArgThrPro 181
Qy 421 GAGTCACTGCTGGTGGTGGAGCTGAGCAGCAGCAGCTGAGTCAAGTCAAGTCACTGG 480
Db 182 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 201
Qy 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGCAAGCCGCGGAGGAGCAGTACAC 540
Db 202 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTrpAsn 221
Qy 541 AGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 222 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 241
Qy 601 GAGTCAAGTCAAGGTCTCAACAAAGCTTCCAGCCCGCCATCGAGAAACCATCTCC 660
Db 242 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 261
Qy 661 AAGCCAAAGGCGCCGAGACACAGTGTACACCTGCGCCCGCCATCCCGGATGAG 720
Db 262 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 281
Qy 721 CTGACCAAGAACCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 282 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 301
Qy 781 GCGGTGAGTGGGAGAGCAATGGCGCGGAGAGCAACCACTACAAGACACCGCTCCCGTG 840
Db 302 AlaValGluTrpGluSerAsnGlyGlnProGluAsnTyrLysThrThrProProVal 321
Qy 841 CTGAGCTCCGACGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 322 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 341
Qy 901 CAGCAGGGGAACGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
Db 342 GlnGlnGlnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 361
Qy 961 CAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 362 GlnLysSerLeuSerLeuSerProGlyLys 371
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## RESULT 4

US-08-458-516-13

; Sequence 13, Application US/08458516

; Patent No. 577085

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

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; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13
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## Alignment Scores:

Pred. No.:	2,646-134	Length:	449
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-111 (1-990) x US-08-458-516-13 (1-449)

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Db	120	AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly	139
Qy	61	GGACAGCGCCCTGGGCTCGCTGGTCAAGCACTACTTCCCGCAACCGGTGACGGTGTGCG	120
Db	140	GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer	159
Qy	121	TGGAATCTAGCGCCCTGACAGCGCGGTGCACACCTTCCCGGTGCTTACAGTCTCTCA	180
Db	160	TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer	179
Qy	181	GGACTCTACTCTCCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	240
Db	180	GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr	199
Qy	241	TACATCTGCAACGTGAATCAAGCCCGCAGCAACCAAGGTGGAGCAAGAAAGTTGAGCCC	300
Db	200	TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro	219
Qy	301	AAATCTTGTGACAAACTCACATGCCACCGTCCAGCAGCTGACCTCGCGGGGCA	360
Db	220	LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuGlyGly	239

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QY 361 CGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 240 ProSerValPheLeuPheProProlYsProlYsAspThrLeuMetIleSerArgThrPro 259
QY 421 GAGTTCACATCGTGTGTGACGTGACGACAGACCCCTGAGTCAAGTTCACCTGG 480
Db 260 GluValThrCysValValValAspValSerHisGluAspProGluValYsPheAsnTrp 279
QY 481 TACGTGGACGGCGTGTGAGTGTCAATGCAAGACAAAGCCGCGGAGGAGCAGTACAA 540
Db 280 TyrValAspGlyValGluValHisAsnAlaYsThrYsProArgGluGluGlnTrpAsn 299
QY 541 AGCAGTACCGTGTGTGACGTCTCACCGTCTGACAGGAGTGTGACAGGAGTGTGAT 600
Db 300 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 319
QY 601 GAGTCAAGTCAAGTCTCCAAACAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCC 660
Db 320 GluTyrLysCysYsValSerAsnLysAlaLeuProAlaProIleGluYsThrIleSer 339
QY 661 AAAGCCAAAGGCGACCCCGGAGAACACAGGAGTGTACACCTGCTCCCGCCATCCCGG 720
Db 340 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 359
QY 721 CTGACCAAGAACAGGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 360 LeuThrLysAsnGlnValSerLeuThrCysLeuValYsGlyPheTyrProSerAspIle 379
QY 781 GCCGTGGAGTGGGAGCAATGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 380 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 399
QY 841 CTGAGTCCGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 400 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 419
QY 901 CAGCAGGGAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 420 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 439
QY 961 CAGAGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 440 GlnLysSerLeuSerLeuSerProGlyLys 449
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## RESULT 5

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US-08-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U. S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,175
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
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; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-030-175-41

Alignment Scores:
Pred. No.: 2,68e-134 Length: 467
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-030-175-41 (1-467)
QY 1 GCCTCCACAAAGGCGCCATCGTCTTCCCTGGCACCTCTCTCCAAAGACACCTCTGGG 60
Db 138 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGCGCTCGCTGCTGCTCAAGGACTACTTCCCGGAAACCGGTGACGGTGTGG 120
Db 158 GlyThrAlaAlaLeuGlyCysLeuValYsAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCGCTGACACAGCGCGGTGACACCTTCCCGGCTGTCTCAGTCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCTGCTGCTCCAGCAGCTTGGGACCCAGACC 240
Db 198 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCACAAAGCCCAAGGACACCTCATGATCTCCCGGACCCCT 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 237
QY 301 AAATCTGTGACAAACTCACACATGCCACCGTCCACAGACCTGAACCTCCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 257
QY 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProProlYsProlYsAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGGTCAATCGTGTGTGAGTGTGAGCCACCAAGACCCCTGAGTCAAGTTCACCTGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValYsPheAsnTrp 297
QY 481 TACGTGGACGGCGTGTGAGTGTGATATCCCAAGACAAAGCCGCGGAGGAGCAGTACAA 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 317
QY 541 AGCAGTACCGTGTGTGAGTGTGCTCACCTGCTGACAGGAGTGTGCTGAATGGCAAG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTCAAGTCAAGGCTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCC 660
Db 338 GluTyrLysCysYsValSerAsnLysAlaLeuProAlaProIleGluYsThrIleSer 357
QY 661 AAAGCCAAAGGCGACCCCGGAGAACACAGGAGTGTACACCTGCTCCCGCCATCCCGG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
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; Sequence 10, Application US/08378939  
; Patent No. 5876961

## GENERAL INFORMATION:

; APPLICANT: CROME, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:

## CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/952640

; FILING DATE: 01-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: ERNST, BARBARA G

; REGISTRATION NUMBER: 30,377

; REFERENCE/DOCKET NUMBER: 1808-118

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 783-6040

; TELEFAX: (202) 783-6031

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-378-939-10

## Alignment Scores:

Pred. No.: 2,69e-134 Length: 476  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 1 Gaps: 0

US-10-733-563-111 (1-990) x US-08-378-939-10 (1-476)

Qy 1 GCCTCCACCAAGGGCCATCGTCTTCCCTGGCACCCTCTCCCAAGAGCACCTCTGGG 60  
Db 147 AlaserThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 166  
Qy 61 GGCACAGCGCCCTGGGCTGCTGTCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTG 120  
Db 167 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 186  
Qy 121 TGGAACTCAGCGCCCTGACACAGCGGCGTGACACCTTCCCGGTGCTCTCAGTCTCTCA 180  
Db 187 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 206  
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCAGCAGCTTGGCCACCCAGACC 240  
Db 207 GlyLeuThrSerLeuSerValValThrValProSerSerSerLeuGlyThrGlnThr 226  
Qy 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAGAAAGTTGAGCCC 300  
Db 227 TyrIleCysAsnValAsnHisLysProSerAnthrLysValAspLysValGluPro 246  
Qy 301 AAATCTTGTCACAAATCTCACACATGCCCGTCCAGCACCTGAACTCGCGGGGGCA 360  
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Db 247 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 266  
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCT 420  
Db 267 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 286  
Qy 421 GAGGTCAATCGCTGGTGGTGGAGCGTGGAGCCACCAAGACCTGAGGTCAAGTTCAGTGG 480  
Db 287 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 306  
Qy 481 TACGTGGACGGGTGGAGTGCATAATGCCAAGCAACAGCCGCGGAGGACGAGTACACAC 540  
Db 307 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 326  
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
Db 327 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 346  
Qy 601 GAGTACAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAG 660  
Db 347 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 366  
Qy 661 AAGCCCAAGGCGCAGCCCGGAGAACCCACAGGTGTACACCTGCCCTCCCTCCCGGATGAG 720  
Db 367 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 386  
Qy 721 CTGACCAAGAACCCAGGTCCAGCTCAGCTCCCTGGTCAAGAGCTTCTATCCAGCCGACATC 780  
Db 387 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 406  
Qy 781 GCCTGGAGTGGGAGAGCAATGGCAGCCGAGAACCAACTACAGACCCAGCCCTCCCTGG 840  
Db 407 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 426  
Qy 841 CTGACTCCGACCGCT 900  
Db 427 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 446  
Qy 901 CAGCAGGGGAACT 960  
Db 447 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 466  
Qy 961 CAGAAGAGCT 990  
Db 467 GlnLysSerLeuSerLeuSerProGlyLys 476

## RESULT 8

US-09-746-359A-54  
; Sequence 54, Application US/09746359A  
; Patent No. 6610286  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Penny  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Xu, Wenfeng  
; APPLICANT: Madden, Karen L.  
; APPLICANT: Kelly, James D.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Blumberg, Hal  
; APPLICANT: Egan, Maribeth A.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Chandrasekhar, Yashmin A.  
; APPLICANT: No. 6610286a, Julia E.  
; TITLE OF INVENTION: Method for Treating Inflammation  
; FILE REFERENCE: 99-108  
; CURRENT APPLICATION NUMBER: US/09/746,359A  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/171,969  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/213,341  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 54

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; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

Alignment Scores:
  Pred. No.:      2,8e-134      Length:      547
  Score:          1756.00      Matches:      328
  Percent Similarity: 99.39%      Conservative: 0
  Best Local Similarity: 99.39%      Mismatches: 2
  Query Match:      97.72%      Indels:      0
  DB:                2          Gaps:        0

US-10-733-563-111 (1-990) x US-09-746-359A-54 (1-547)

Qy 1 GCCTCCCAAGGGCCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGCACCTCTGGG 60
Db 218 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 237
Qy 61 GGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTGTG 120
Db 238 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 257
Qy 121 TGGAACTCAGCGCCCTGACAGCGGCGTGCACACCTTCCCGGCTGCTCTCAGTCTCA 180
Db 258 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 277
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCGCTCCAGCAGCTGGGACCCAGACC 240
Db 278 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 297
Qy 241 TACATCTGCACCTGAATCACAAGCCGAGCAACACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 298 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 317
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 318 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 337
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 338 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 357
Qy 421 GAGGTCAATCGTGGTGGTGGAGGTGAGCCAGACGACCTGAGGTCAAGTTCAACTGG 480
Db 358 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 377
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 378 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 397
Qy 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 398 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 417
Qy 601 GAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCC 660
Db 418 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 437
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATGAG 720
Db 438 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 457
Qy 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 458 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 477
Qy 781 GCCGTGAGTGGGAGAGCAATGGCGAGCGGAGAACCAACTACAGACCAACCCCTCCCGTG 840
Db 478 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 497
Qy 841 CTGAGCTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
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```
Db 498 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 517
Qy 901 CAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGATGAGGTCTGCACAACCATACACG 960
Db 518 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 537
Qy 961 CAGAAGAGCCCTCTCCCTGCTCCGGGTAAA 990
Db 538 GlnLysSerLeuSerLeuSerProGlyLys 547

RESULT 9
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalpha11r/IgGgamma1 polypeptide
US-09-825-561A-16

Alignment Scores:
  Pred. No.:      2,83e-134      Length:      567
  Score:          1756.00      Matches:      328
  Percent Similarity: 99.39%      Conservative: 0
  Best Local Similarity: 99.39%      Mismatches: 2
  Query Match:      97.72%      Indels:      0
  DB:                2          Gaps:        0

US-10-733-563-111 (1-990) x US-09-825-561A-16 (1-567)

Qy 1 GCCTCCCAAGGGCCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGCACCTCTGGG 60
Db 238 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 257
Qy 61 GGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTGTG 120
Db 258 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 277
Qy 121 TGGAACTCAGCGCCCTGACAGCGGCGTGCACACCTTCCCGGCTGCTCTCAGTCTCA 180
Db 278 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 297
Qy 181 GGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCGCTCCAGCAGCTGGGACCCAGACC 240
Db 298 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 317
Qy 241 TACATCTGCACCTGAATCACAAGCCGAGCAACACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 318 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 337
Qy 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 338 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 377
Qy 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCT 420
Db 338 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 357
Qy 421 GAGGTCAATCGTGGTGGTGGAGGTGAGCCAGACGACCTGAGGTCAAGTTCAACTGG 480
Db 358 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 377
Qy 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 378 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 397
Qy 541 AGCAGGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 398 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 417
Qy 601 GAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCC 660
Db 418 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 437
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATGAG 720
Db 438 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 457
Qy 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 458 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 477
Qy 781 GCCGTGAGTGGGAGAGCAATGGCGAGCGGAGAACCAACTACAGACCAACCCCTCCCGTG 840
Db 478 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 497
Qy 841 CTGAGCTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
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QY 361 CGGTGAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db 358 ProSerValPheLeuPheProProLysAspThrLeuMetIleSerArgThrPro 377
QY 421 GAGGTCAATGCGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 378 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 397
QY 481 TACGTGGACGGCGTGGAGGTGCATTAATCCAAAGACAAAGCCCGGGAGGAGCAGTACAA 540
Db 398 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 417
QY 541 AGCAGTACCGTGGTGGTGGAGCTGAGCTCTCCCTGACACCCAGGACCTGCTGAATGGCAAG 600
Db 418 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 437
QY 601 GAGTACAAAGTCAAGGCTCTCCAAACAAAGCCCTCCAGCCGCCATCGAGAAACCAATCTCC 660
Db 438 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaPheIleGluLysThrIleSer 457
QY 661 AAAGCCAAAGGCGACCCCGGAGAACACACAGGTGTACACCCCTGCCCCCATCCCGGGATGAG 720
Db 458 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 477
QY 721 CTGACCAAGAACCCAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 478 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 497
QY 781 GCCGTGGAGTGGAGCAATGGGCGAGCGGAGCAACTACAGACCAACCCCTCCCGTGG 840
Db 498 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 517
QY 841 CTGGAATCCGACGGCTCTCTTCTTCTTACAGCAAGCTCACCCGTGCGACAGAGCAGGTGG 900
Db 518 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 537
QY 901 CAGCGGGGAAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 538 GlnGlnGlyAsnValPheSerCysSerValMethIleGluAlaLeuHisAsnHisTyrThr 557
QY 961 CAGAAGACGCTCTCCCTGCTCCGGGTAA 990
Db 558 GlnLysSerLeuSerLeuSerProGlyLys 567
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## RESULT 10

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US-09-746-359A-53
; Sequence 53, Application US/09746359A
; Parent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
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; ORGANISM: Homo sapiens

US-09-746-359A-53

## Alignment Scores:

Pred. No.:	2,84e-134	Length:	571
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-111 (1-990) x US-09-746-359A-53 (1-571)

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QY 1 GCCTCCAAAGGCCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGCACCTCTCTGGG 60
Db 242 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 261
QY 61 GGCACAGCGGCGCTGGGCTGCTGGTCAAGACTACTTCCCGGAACCGGTGACGTGCG 120
Db 262 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 281
QY 121 TGGAACTCAGCGCGCTGACACGCGGTGCACACTTCCCGGCTGCTTACAGTCCCTCA 180
Db 282 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 301
QY 181 GGACTCTACTCTCCAGCAGCGTGTGACCGCTGCGCTCCAGCAGCTTGGGCACCCAGACC 240
Db 302 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 321
QY 241 TACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGGACAAAGATTGAGCCC 300
Db 322 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 341
QY 301 AAATCTGTGACAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCGCGGGGCA 360
Db 342 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 361
QY 361 CCGTCAGTCTTCTCTTCTCCCTCCCAAAACCCAAAGACACCTCATGATCTCCCGGACCCCT 420
Db 362 ProSerValPheLeuPheProProLysAspThrLeuMetIleSerArgThrPro 381
QY 421 GAGTCAATGCGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 382 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 401
QY 481 TACGTGGACGGTGGAGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAGTACAAAC 540
Db 402 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 421
QY 541 AGCAGTACCGTGGTGGTGGAGCTCTCCCTGACACCCAGGACCTGCTGAATGGCAAG 600
Db 422 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 441
QY 601 GAGTCAATGCGTGGTGGAGCTTCCAAACAAAGCCCTCCAGCCGCCATCGAGAAACCAATCTCC 660
Db 442 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaPheIleGluLysThrIleSer 461
QY 661 AAAGCCAAAGGCGACCCCGGAGAACCAAGGTGTACACCTTCCCGGCTGCTGAGTACGAG 720
Db 462 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 481
QY 721 CTGACCAAGAACCCAGGTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 482 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 501
QY 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCAACTCAAGACCAACCCCTCCCGTGG 840
Db 502 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 521
QY 841 CTGGAATCCGACGGCTCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 522 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 541
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QY 61 GGCACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCAGTGGTGG 120
Db 642 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 661
QY 121 TGGAACTCAGGCGCTGACACAGCGCGTGACACCTTCCCGGCTGTCTCAAGTCTCA 180
Db 662 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 681
QY 181 GGACTTACTCCCTCAGCAGCGTGTGACCGCTGCTCCAGCAGCTTGGGCACCCAGACC 240
Db 682 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 701
QY 241 TACATCTGCAAGCTGAATCAACAGCCAGCCAGCAACACCAAGGTGGACAGAAAGTTGAGCC 300
Db 702 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 721
QY 301 AAATCTGTGACAAACTCACACATGCCACCGTCCCGACACCTGAACTCGCGGGGCA 360
Db 722 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuLeuGly 741
QY 361 CGGTCAAGTCTTCTCTTCCCGCCAAACCCAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db 742 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 761
QY 421 GAGTCAATGCGTGGTGTGACGTGACGTCACGACGACGACGACGACGACGACGACG 480
Db 762 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 781
QY 481 TACGTGACGCGCTGAGTGCATTAATCCCAAGACAAAGCCGCGGAGGACGATACAAAC 540
Db 782 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 801
QY 541 AGCAGTACCGTGTGGTGTGACGCTCTCCACCGTCTGACACGAGGATGGCTGAATGGCAAG 600
Db 802 SerThrTyrArgValValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 821
QY 601 GAGTCAAGTGTGAGGTCTCCAAAGCCCTCCAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660
Db 822 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 841
QY 661 AAAGCAAAGCGAGCCCGAGAACACAGGTGTACACCTGCGCCCATCCCGGATGAG 720
Db 842 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 861
QY 721 CTGACCAAGAACAGCTCAGCTCAGCTGCTTCTTCTTCAAGGCTTCTATCCAGCGACATC 780
Db 862 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 881
QY 781 GCCGTGGAGTGGAGACAATGGCGAGCGGAGAACAACTACAGACCAACGACCCCTCCGCTG 840
Db 882 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 901
QY 841 CTGGAATCCGAGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 902 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 921
QY 901 CAGCAGGGGAAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 960
Db 922 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 941
QY 961 CAGAAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 942 GlnLysSerLeuSerLeuSerProGlyLys 951
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## RESULT 13

US-09-740-002-27

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; Sequence 27, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
```

```
; TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-740-002-27
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Alignment Scores: 5.68e-134 Length: 475
Pred. No.: 1752.00 Matches: 327
Score: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 3
Query Match: 97.50% Indels: 0
DB: 2 Gaps: 0
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US-10-733-563-111 (1-990) x US-09-740-002-27 (1-475)

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QY 1 GCCTCCACAAAGGCGCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTGGG 60
Db 146 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 165
QY 61 GGCACAGCGGCTGGCTGCTGCTCAAGGACTACTTCCCGAACCAGTGGTGGTGG 120
Db 166 GlyThrAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 185
QY 121 TGGAACTCAGGCGCTGACGCGGTGACACCTTCCCGGCTGTCTCAAGTCTCA 180
Db 186 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 205
QY 181 GGAATCTGTGACAAACTCACACATGCCACCGTCCCGACACCTTCCCGGATGAG 240
Db 206 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 225
QY 241 TACATCTGCAAGCTGAATCAACAGCCAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCC 300
Db 226 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 245
QY 301 AAATCTGTGACAAACTCACACATGCCACCGTCCCGACACCTGAACTCGCGGGGCA 360
Db 246 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 265
QY 361 CGGTCAAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
Db 266 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 285
QY 421 GAGTCAATGCGTGGTGTGACGTGACGTCACGACGACGACGACGACGACGACGACG 480
Db 286 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 305
QY 481 TACGTGACGCGCTGAGTGCATTAATCCCAAGACAAAGCCGCGGAGGACGATACAAAC 540
Db 306 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnThrAsn 325
QY 541 AGCAGTACCGTGTGGTGTGACGCTCTCACCGTCTTCCAGCAGGACTGGCTGAATGGCAAG 600
Db 326 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 345
QY 601 GAGTCAAGTGTGAGGTCTTCCAAAGCCCTTCCAGCCCGCCCATCGAGAAACCATCTTCC 660
Db 346 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 365
QY 661 AAAGCAAAGCGAGCCCGAGAACCAAGTGTACACCTTCCCGGATGAG 720
Db 366 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 385
```





APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-487-550-12

Alignment Scores:  
Pred. No.: 5,68e-134 Length: 476  
Score: 1752.00 Matches: 327  
Percent Similarity: 99.09% Conservative: 0  
Best Local Similarity: 99.09% Mismatches: 3  
Query Match: 97.50% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-111 (1-990) x US-08-487-550-12 (1-476)

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Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCACCTCTCTCAAGAGCACCTCTGGG 60
Db 147 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 166
Qy 61 GGCACAGCGCGCGCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGTG 120
Db 167 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 186
Qy 121 TGGAACTCAGCGCGCTCACACAGCGGCTGCACACTTCCCGGCTGCTTACAGTCCTCA 180
Db 187 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 206
Qy 181 GGACTCTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 207 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 226
Qy 241 TACATCTGCACAGTGAATCACAGCCGACACACACAGGTGGACAGAAAGTTGAGCCC 300
Db 227 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysAlaGluPro 246
Qy 301 AAATCTGTGACAAATCACACATGCCACCGTCCCGACACCTGAACTCGCGGGGCA 360
Db 247 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 266
Qy 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
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Db 267 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 286
Qy 421 GAGGTCAATCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 287 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 306
Qy 481 TACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGACGAGTACAC 540
Db 307 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 326
Qy 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 327 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 346
Qy 601 GAGTACAAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCC 660
Db 347 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 366
Qy 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAG 720
Db 367 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 386
Qy 721 CTGACCAAGAACCAAGGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATC 780
Db 387 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 406
Qy 781 GCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACCAAGTGGTGGTGGTGGTGGTGG 840
Db 407 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 426
Qy 841 CTGGACTCCGACGGCTCCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG 900
Db 427 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 446
Qy 901 CAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCATACAG 960
Db 447 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 466
Qy 961 CAGAAGAGCCCTCTCCCTGCTCTCCGGGTAAA 990
Db 467 GlnLysSerLeuSerLeuSerProGlyLys 476
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Search completed: January 28, 2006, 08:48:58  
Job time : 51.1441 secs



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:44:22 ; Search time 120.901 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-111  
Perfect score: 1797  
Sequence: 1 gcctccaccaaggcccatc.....tctccctgtctccggtaaa 990

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_epool\_p/US10733563/runat\_27012006.180007.4900/app\_query.fasta.1.2716  
-DB=Published Applications AA Main -QFMT=fastan -SUFFIX=n2p.rapbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=1  
-MATRIX=blosum62 -TRANS=human4.0.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext  
-HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 -CGEN 1 1.497 @runat\_27012006.180007.4900 -NCPU=6 -ICPU=3  
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-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main:  
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3: /cgn2\_6/ptodata/1/pubaa/US09\_PUBCOMB.pcp:\*  
4: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pcp:\*  
5: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pcp:\*  
6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1765	98.2	333	4	US-10-733-563-111
2	1765	98.2	333	4	US-10-733-563-111
3	1765	98.2	336	4	US-10-733-563-111
4	1765	98.2	448	4	US-10-733-563-111
5	1765	98.2	448	4	US-10-733-563-111
6	1765	98.2	448	4	US-10-733-563-111
7	1765	98.2	448	4	US-10-733-563-111
8	1765	98.2	448	4	US-10-733-563-111
9	1765	98.2	448	4	US-10-733-563-111
10	1765	98.2	467	4	US-10-733-563-111
11	1765	98.2	467	4	US-10-733-563-111

12	1765	98.2	467	4	US-10-731-984-7	Sequence 7, Appl
13	1765	98.2	467	4	US-10-731-984-23	Sequence 23, Appl
14	1760	97.9	330	4	US-10-733-563-110	Sequence 110, Appl
15	1759	97.9	473	4	US-10-467-253-13	Sequence 13, Appl
16	1758	97.8	469	4	US-10-404-724-72	Sequence 72, Appl
17	1756	97.7	332	3	US-09-990-586-98	Sequence 98, Appl
18	1756	97.7	332	4	US-10-310-113-167	Sequence 167, Appl
19	1756	97.7	333	4	US-10-230-880-98	Sequence 98, Appl
20	1756	97.7	333	4	US-10-272-899A-8	Sequence 8, Appl
21	1756	97.7	356	4	US-10-272-899A-72	Sequence 72, Appl
22	1756	97.7	371	4	US-10-157-408-7	Sequence 7, Appl
23	1756	97.7	371	4	US-10-097-044A-7	Sequence 7, Appl
24	1756	97.7	371	4	US-10-769-247-7	Sequence 7, Appl
25	1756	97.7	444	4	US-10-150-475A-6	Sequence 6, Appl
26	1756	97.7	444	4	US-10-704-522-6	Sequence 6, Appl
27	1756	97.7	444	4	US-10-645-215-6	Sequence 6, Appl
28	1756	97.7	444	6	US-11-136-538-7	Sequence 7, Appl
29	1756	97.7	445	4	US-10-320-231A-79	Sequence 79, Appl
30	1756	97.7	445	4	US-10-408-901-34	Sequence 34, Appl
31	1756	97.7	445	4	US-10-408-901-42	Sequence 42, Appl
32	1756	97.7	445	5	US-10-867-506-79	Sequence 79, Appl
33	1756	97.7	445	5	US-10-937-596-3	Sequence 3, Appl
34	1756	97.7	447	3	US-03-256-156-1	Sequence 1, Appl
35	1756	97.7	447	5	US-10-684-957-17	Sequence 17, Appl
36	1756	97.7	447	5	US-10-684-957-19	Sequence 19, Appl
37	1756	97.7	447	5	US-10-684-957-21	Sequence 21, Appl
38	1756	97.7	447	5	US-10-684-957-32	Sequence 32, Appl
39	1756	97.7	447	6	US-11-010-797-2	Sequence 2, Appl
40	1756	97.7	448	4	US-10-378-567-2	Sequence 2, Appl
41	1756	97.7	448	5	US-10-985-584-18	Sequence 18, Appl
42	1756	97.7	449	5	US-10-635-908-16	Sequence 16, Appl
43	1756	97.7	449	5	US-10-635-908-18	Sequence 18, Appl
44	1756	97.7	449	5	US-10-476-265-12	Sequence 12, Appl
45	1756	97.7	449	5	US-10-985-584-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-272-899A-10  
; Sequence 10, Application US/10272899A  
; Publication No. US20040033561A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Keefe, Theresa L.  
; APPLICANT: Healy, Judith Jacques  
; APPLICANT: Newman, Walter  
; APPLICANT: Ponath, Paul  
; APPLICANT: Bruce Key  
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,  
; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF  
; TITLE OF INVENTION: USE THEREFOR  
; FILE REFERENCE: MP101-244P2RM  
; CURRENT APPLICATION NUMBER: US/10/272.899A  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/350,166  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: 60/392,364  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 333  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human IgG1-FcRmut protein  
US-10-272-899A-10

Alignment Scores: 7.05e-113 Length: 333  
Pred. No.: 1765.00 Matches: 330  
Score: 100.00% Conservativeness: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00%

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Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-111 (1-990) x US-10-272-899A-10 (1-333)
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Qy 61 GGCAAGGGCCCTGGGTGCTGCTGCTCAAGACTACTTCCCGCAACCGGTGACGGTGTG 120
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43
Qy 121 TGGAACTCAGCGCCCTGACCAGGGGTGCACACCTTCCCGGTCTCTACAGTCTCA 180
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 63
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGAC 240
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83
Qy 241 TACATCTGCAACGTAATCAACGCCGACGACCAACCAAGGTGGACAGAAAGTTGAGCC 300
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103
Qy 301 AAATCTTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123
Qy 361 CCCTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 124 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 143
Qy 421 GAGTCCATCGCTGGTGGAGCTGAGCCACGAGACCTGAGGTCAAGTTCACATGG 480
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163
Qy 481 TACGTGAGCGCGTGGAGTGCATAATGCCAAGACCAAGCGCGGGAGGACGACTACAC 540
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 183
Qy 541 AGCAGTACCGTGTGGTGCAGCGTCTCACCGCTCTGCACACGAGGACTGGCTGAATGGCAAG 600
Db 184 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 203
Qy 601 GAGTACAGTGCAGGCTCCACAAAGCCCTCCAGCGCCCTCGAGAAACCAATCTCC 660
Db 204 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 223
Qy 661 AAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTACACCTGCCCTCCCTCCCGGATCAG 720
Db 224 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 243
Qy 721 CTGACCAAGAACCAAGTGCAGCTGACCTGCTCAAGGCTTCTATCCAGCGACATC 780
Db 244 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 263
Qy 781 GCCGTGAGTGGGAGAGCAATGGGAGCGGAGAACCACTAACAGACACCGCTCCCGTG 840
Db 264 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 283
Qy 841 CTGGACTCCGAGCGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900
Db 284 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 303
Qy 901 CAGCAGGGGAACTCTTCTCATGTCTCGTGTGATGAGGTCTGTGCACCAACCACTACAG 960
Db 304 GlnGlnGlnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 323
Qy 961 CAGAAAGCCCTCTCCCTGTCTCCGGGTAAA 990
Db 324 GlnLysSerLeuSerLeuSerProGlyLys 333
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RESULT 2
US-10-733-563-114
; Sequence 114, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-PCRmut protein
US-10-733-563-114
Alignment Scores:
Pred. No.: 7,05e-113 Length: 333
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-111 (1-990) x US-10-733-563-114 (1-333)
Qy 1 GCCTCCCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCTCCAGAGACACCTCTGGG 60
Db 4 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 23
Qy 61 GGCAAGGGCCCTGGGTGCTGCTGCTCAAGACTACTTCCCGCAACCGGTGACGGTGTG 120
Db 24 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 43
Qy 121 TGGAACTCAGCGCCCTGACCAGCGGTGCACACCTTCCCGGTCTCTACAGTCTCA 180
Db 44 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSer 63
Qy 181 GGACTCTACTCCCTCAGCAGCGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGAC 240
Db 64 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 83
Qy 241 TACATCTGCAACGTAATCAACGCCGACGACCAACCAAGGTGGACAGAAAGTTGAGCC 300
Db 84 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 103
Qy 301 AAATCTTTGTGACAAACTCACACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 104 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 123
Qy 361 CCCTCAGTCTTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 124 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 143
Qy 421 GAGTCCATCGCTGGTGGAGCTGAGCCACGAGACCTGAGGTCAAGTTCACATGG 480
Db 144 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 163
Qy 481 TACGTGAGCGCGTGGAGTGCATAATGCCAAGACCAAGCGCGGGAGGACGACTACAC 540
Db 164 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 183
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US-10-171-452A-54

Alignment Scores:  
Pred. No.: 7,31e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-171-452A-54 (1-448)

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QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTTCTCCCGACCGGTGACGGTGTG 120  
DB 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158  
QY 121 TGGAACTCAGCGCCCTGACAGCGCGTGCACACTTCCCGGCTGTCTTACAGTCTCA 180  
DB 159 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178  
QY 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCACCAGACC 240  
DB 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198  
QY 241 TACATCTGCAACGTGAATCACAAGCCCAAGCCACACACCAAGGTGGACAAAGATTGAGCC 300  
DB 199 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysValGluPro 218  
QY 301 AAATCTGTGTGACAAATCACAATGCCACATGCCACCGTCCAGCACCTGAACTCGCGGGGCA 360  
DB 219 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuAlaGlyAla 238  
QY 361 CCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCTCATGANTCCCGGACCCCT 420  
DB 239 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 258  
QY 421 GAGTCCATCGGTGGTGGACGTGAGCCACGACGACCTGAGTCAAGTCAAGTTCAGTGG 480  
DB 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 278  
QY 481 TACGTGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAAC 540  
DB 279 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTyrAen 298  
QY 541 AGCAGTACCGTGGTGGTCCAGGTCTCTACCGTCTGCAACGAGGACTGGCTGAATGGCAAG 600  
DB 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAenTrpLeuAenGlyLys 318  
QY 601 GAGTACAGTGCAGGTCTCCACAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCCATCTCC 660  
DB 319 GluTyrLysCysLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 338  
QY 661 AAAGCCAAAGCGAGCCCGGAGAACCAAGTGTACACCTGCCCTCCATCCCGGAGTACAG 720  
DB 339 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358  
QY 721 CTGACCAAGAACCGAGTGCAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGGCAATC 780  
DB 359 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378  
QY 781 GCCGTGGAGTGGAGAGCAATGGGAGCGGAGAGAACAACTACAGACCAACGCTCCCGTG 840  
DB 379 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyrLysThrThrProProVal 398  
QY 841 CTGAGCTCCGAGCGCTCTTCTCTCTCTACAGCAGCTCACCGTGGACAAAGCAGGCTGG 900  
DB 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418  
QY 901 CAGCAGGGGAAACGTCTTCTCATGTCTCCGTGATGATGAGGCTCTGTCACAAACACTTACACG 960

DB 419 GlnGlnGlyAenValPheSerCysSerValMethHisGluAlaLeuHisAenHisTyrThr 438  
QY 961 CAGAAGAGCCTCTCCCTGTCTCTCGGGTAAA 990  
DB 439 GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 6

US-10-353-708-42  
; Sequence 42, Application US/10353708  
; Publication No. US20030219403A1

; GENERAL INFORMATION:

; APPLICANT: Frewin, Mark

; APPLICANT: Waldmann, Herman

; APPLICANT: Gorman, Scott

; APPLICANT: Hale, Geoff

; APPLICANT: Rao, Patricia

; APPLICANT: Kornaga, Tadeusz

; APPLICANT: Ringler, Douglas

; APPLICANT: Cobboid, Stephen

; APPLICANT: Winsor-Hines, Dawn

; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen

; FILE REFERENCE: 695458-73

; CURRENT APPLICATION NUMBER: US/10/353,708

; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: US10/171,452

; PRIOR FILING DATE: 2002-06-13

; PRIOR APPLICATION NUMBER: US60/373,471

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US60/373,470

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: US60/345,194

; PRIOR FILING DATE: 2002-10-19

; PRIOR APPLICATION NUMBER: GB0122724.8

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: GB0114517.6

; PRIOR FILING DATE: 2001-06-14

; NUMBER OF SEQ ID NOS: 60

; SEQ ID NO 42

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Heavy chain of humanized antibody

US-10-353-708-42

Alignment Scores:  
Pred. No.: 7,31e-113 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-353-708-42 (1-448)

QY 1 GCCTCCACAGGGCCCATCGTCTTCCCTCGGCACCTCTCTCCAGAGCACTCTCGG 60  
DB 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138  
QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTTCTTCCCGGAGTGTGCGTGTGCG 120  
DB 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158  
QY 121 TGGAACTCAGCGCCCTGACAGCGCGGTGCACACTTCCCGGCTGTCTTACAGTCTCA 180  
DB 159 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178  
QY 181 GGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCAACGAGACC 240  
DB 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198  
QY 241 TACATCTGCAACGTGAATCACAAGCCCAAGTGGACCAACCAAGGTTGAGGCC 300

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Db 199 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
QY 301 AAATCTTGTCACAACTCAGCATGCCCGTCCAGCAGCACTGAATCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCGTCAGCTCTCTCCCTCCCAAAACCCAGGACCCCTCATGATCTCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 258
QY 421 GAGGTCAATGCGTGGTGGAGCTGAGCCAGCAAGACCCCTGAGCTCAAGTTCAACTGG 480
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACCGCGTGGAGGTGATATCCCAAGACAAAGCCCGGAGGAGCAGTACAAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 298
QY 541 AGCAGGTACCGTGGTGGAGCTCTCAGCTCTCAGCTCTGCAAGGAGTGGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAGTCAAGGTCTCCAAACAAAGCCCTCCAGGCCCCCATCGAGAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 338
QY 721 CTGACCAAGACCGTGGAGCAATGGGAGCGAGCAAGCACTCAAGAGCTTCTATCCAGGACATC 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
QY 781 GCCGTGAGTGGGAGAGCAATGGGAGCGAGCAAGCACTCAAGAGCTTCTATCCAGGACATC 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnValTyrLysThrProProVal 398
QY 841 CTGACATCCGAGCGCTCTCTTCTTCTTACAGCAAGCTCAACGTCGACAGCAGGTGG 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
QY 901 CAGCAGGGGACGCTCTCTCATGCTCCGTCATGTCATGAGGTCTTGCACAACTACACG 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMethHisGluAlaLeuHisAsnHisTyrThr 438
QY 961 CAGAGAGCCCTCTCCCTGCTCCGGGTAAA 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448
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RESULT 7
US-10-353-708-54
; Sequence 54, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10353708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
```

```
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 54
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-54

Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-353-708-54 (1-448)

QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCTCCGACCCCTCTCCAAAGACCACTCTGGG 60
Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerLysSerThrSerGly 138
QY 61 GGCACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGGTCTG 120
Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCCCTGACAGCGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCTCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGACCCAGACC 240
Db 179 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTGAATCAAGCCCAAGCCAGCAACACCAAGGTGGACAAAGATTGAGCCC 300
Db 199 TyrileCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
QY 301 AAATCTTGTCACAACTCAGCATGCCCGTCCAGCAGCACTGAATCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCGTCAGCTCTCTCTCCCTCCCAAAACCCAGGACCCCTCATGATCTCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProLysProLysProLysAspThrLeuMetIleSerArgThrPro 258
QY 421 GAGGTCAATGCGTGGTGGAGCTGAGCCAGCAAGACCCCTGAGCTCAAGTTCAACTGG 480
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACCGCGTGGAGGTGATATCCCAAGACAAAGCCCGGAGGAGCAGTACAAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTrpAsn 298
QY 541 AGCAGGTACCGTGGTGGAGCTCTCAGCTCTCAGCTCTGCAAGGAGTGGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAGTCAAGGTCTCCAAACAAAGCCCTCCAGGCCCCCATCGAGAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 338
QY 661 AAAGCCAAAGGGCAGCCCGGAGCAAGTGTACACCTCTCCCGCCCATCTCCCGGATGAG 720
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Db 339 LysAlaLysGlyGlnProArgGluProGlnValThrLeuProProSerArgAspGlu 358
Qy 721 CTGACCAAGAACACCGGTGAGCTGACCTGCTCCCTGGTCAAGAGCTTCTATCCAGCGACATC 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACAACTACAGACCAACCGCTCCCGTG 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
Qy 841 CTGGAACCTCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy 901 CAGCAGGGAACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
Qy 961 CAGAGAGCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 8
; Sequence 8, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
US-10-733-563-111 (1-990) x US-10-731-984-8 (1-448)

Alignment Scores:
Pred. No.: 7,31e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-731-984-8 (1-448)
Qy 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCGCACCTCTCTCCAGAGCACCTCTGGG 60
Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
Qy 61 GGCACAGCGGCGCTGGGTCTGCTGCTCAAGGACTACTTCCCGGACCGGTGACGGTGTG 120
Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
Qy 121 TGGAACTCAGCGCGCTGACAGCGGGGTGACACCTCTCCCGGTGCTTACAGTCTCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
Qy 181 GGACTCTACTCTCTCAGCAGCGGTGTGACCTGCGCTCCAGCAGCTTGGGACCCAGACC 240
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerLeuGlyThrGlnThr 198
Qy 241 TACATCTGCAACGTGAATCAACAGCCCGACCAACCAAGGTGGACAAAGAAATTGAGCCC 300
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Db 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 218
Qy 301 AAATCTTGTGACAAACTCACACATGCCCGTCCAGCACCTGAACCTCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 238
Qy 361 CCGTCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 239 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 258
Qy 421 GAGTTCACATCGTGGTGTGAGCTGAGCCACGAGACCTCTGAGGTCAAGTTCACCTGG 480
Db 259 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 278
Qy 481 TACGTGGAGCGCGTGGAGTGCATAATGCCAAGACCAAGCCGCGGAGGAGCAGGTACAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 298
Qy 541 AGCACGTACCGTGGTCTCAGCGTCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGCG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
Qy 601 GAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCATCGAGAAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 338
Qy 661 AAAGCCAAAGGCGCCCGGAGAACACACAGGTGTACACCTCCCGCCATCCCGGATGAG 720
Db 339 LysAlaLysGlyGlnProArgGluProGlnValThrLeuProProSerArgAspGlu 358
Qy 721 CTGACCAAGAACACCGGTGAGCTGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
Qy 781 GCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACAACTACAGACCAACCGCTCCCGTG 840
Db 379 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 398
Qy 841 CTGCACTCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 399 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 418
Qy 901 CAGCAGGGAACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 419 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 438
Qy 961 CAGAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448
```

```
RESULT 9
; Sequence 24, Application US/10731984
; Publication No. US20040175381A1
; GENERAL INFORMATION:
; APPLICANT: WINDSOR-HINES, Dawn
; APPLICANT: RAO, Patricia
; APPLICANT: RINGLER, Douglas J.
; TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
; FILE REFERENCE: TLN-022
; CURRENT APPLICATION NUMBER: US/10/731,984
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: 60/431839
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Sequence
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US-10-731-984-24
Alignment Scores:
Pred. No.: 7,34e-113 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-731-984-24 (1-448)
QY 1 GCCTCCACCAAGGCGCCATCGTCTCCCTCGGACCCCTCTCCACAGCAGCACTCTGGG 60
Db 119 AlaserThrLySGlyProSerValPheProLeuAlaProSerSerLySerThrSerGly 138
QY 61 GGCACAGCGCGCCCTGGCTGCTGTCAAGGACTACTTCCCGAACCCTGACCGGTGTGCG 120
Db 139 GlyThrAlaLeuLeuGlyCysLeuValLySAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCGCCCTGACAGCGGCGTGACACCTTCCCGGTGTCTCAGTCTCTCA 180
Db 159 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGCC 240
Db 179 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
Db 199 TyrileCysAenValAenHisLySProSerAenThrLySValAspLySValGluPro 218
QY 301 AAATCTGTGTGACAAACTCACACATGCCCCACCGTCCAGCACTGAACTCGCGGGGCA 360
Db 219 LySserCysAspLySThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCGTCAGTCTCTCTTCCCTCCCAAAACCCAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProProLySProLySAspThrLeuMetileSerArgThrPro 258
QY 421 GAGGTCAATCGTGTGGAGTGTGAGCCACCAAGACCCCTGAGGTCAAGTTCAACTTGG 480
Db 259 GluValThrCysValValValAspValSerHisGluAspProGluValLySAspThr 278
QY 481 TACGTGAGCGCGTGGAGGTGCTATATCCCAAGACAAAGCCGCGGAGGAGCAGTACAC 540
Db 279 TyrValAspGlyValGluValHisAenAlaLySThrLySProArgGluGlnTyrAen 298
QY 541 AGCAGCTACCGTGTGTGAGGTCTCTCACCGTCTCGCACAGGACTGGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspThrPleuAenGlyLyS 318
QY 601 GAGTACAAGTCAAGGTCTCCAAAGCCCTCCAGCCCTCCAGCCCTCAGAGAAACCATCTCC 660
Db 319 GluTyrLySValValSerAenLySAlaLeuProAlaProIleGluLySThrIleSer 338
QY 661 AAAGCCAAAGCGCGCCCGGAGAACCAACAGGTGTACACCTGCGCCCTCCATCCCGGAGTAG 720
Db 339 LySAlaLySGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 358
QY 721 CTGACCAAGAACCAAGGTGAGCTGACCGTCTCGTGTCAAAGGCTTCTATCCAGCGCATC 780
Db 359 LeuThrLySAenGlnValSerLeuThrCysLeuValLySGlyPheTyrProSerAspIle 378
QY 781 GCCGTGAGTGGGAGAGCAATGGGCGAGCGGAGAACCACTACAAGACCAACCGCTCCCGTG 840
Db 379 AlaValGluTTPGluSerAenGlyGlnProGluAenAenTyrLySThrProProVal 398
QY 841 CTGACTCCGAGCGGTCTCTTCTTCTACAGCAAGCTCACCGTGGGACAAGAGCAGGTGG 900
Db 399 LeuAspSerAspGlySerPheLeuTyrSerLySLeuThrValAspLySAspArgTTP 418
QY 901 CAGCAGGGGAAGCTTCTCTCATGCTCCGTGATGATGAGGCTCTGACACCAACCACTACACG 960

Db 419 GlnGlnGlyAenValPheSerCysSerValMethisGluAlaLeuHisAenHisTyrThr 438
QY 961 CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 990
Db 439 GlnLySserLeuSerLeuSerProGlyLyS 448

RESULT 10
US-10-171-452A-53
; Sequence 53, Application US/10171452A
; Publication No. US20030108518A1
; GENERAL INFORMATION:
; APPLICANT: Prewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobboid, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: TRX1 Antibody and Uses Therefor
; FILE REFERENCE: 695458-59
; CURRENT APPLICATION NUMBER: US/10171.452A
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-171-452A-53

Alignment Scores:
Pred. No.: 7,34e-113 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-171-452A-53 (1-467)
QY 1 GCCTCCACCAAGGCGCCATCGTCTCCCTCGGACCCCTCTCCACAGCAGCACTCTGGG 60
Db 138 AlaserThrLySGlyProSerValPheProLeuAlaProSerSerLySThrSerGly 157
QY 61 GGCACAGCGCGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCCTGACCGGTGTGCG 120
Db 158 GlyThrAlaLeuLeuGlyCysLeuValLySAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCGCCCTGACAGCGGCGTGACACCTTCCCGGTGTCTCAGTCTCTCA 180
Db 178 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGACCCAGCC 240
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
Db 218 TyrileCysAenValAenHisLySProSerAenThrLySValAspLySValGluPro 237
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```
QY 301 AAATCTGTGACAAACTCACACATGCCACCGTCCCGAGCACCTGAACTCCGGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProPocCysProAlaProGluLeuAlaGlyAla 257
QY 361 CGGTCAAGTCTTCTCTCCCTCCCAAAACCCAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTTCACATCGTGTGTGTGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGACGGGTGGAGGTGATTAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGTGTGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleGluLysThrIleSer 357
QY 661 AAAGCAAAGGCGACCCCGAGAAACCAAGGTGTACACCTGCCCCCATCCCGGATGAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGACCCAGTCCAGCTGACCTGACCTGCTGCTCAAGGCTTCTATCCAGCAGATC 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGAGTGGAGAGCAATGGGAGCGGAGCAACCACTCAAGACCAACCGCTCCCGTG 840
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417
QY 841 CTGACCTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGACAGCAGCGTGG 900
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGACGCTCTTCTCATGCTCCCGTGTGATGATGAGGTCTGTCACAACTACAG 960
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCTCTCCCTGTCTCCGGGTAA 990
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467
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## RESULT 11

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US-10-733-708-53
; Sequence 53, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
; APPLICANT: Frewin, Mark
; APPLICANT: Waldmann, Herman
; APPLICANT: Gorman, Scott
; APPLICANT: Hale, Geoff
; APPLICANT: Rao, Patricia
; APPLICANT: Kornaga, Tadeusz
; APPLICANT: Ringler, Douglas
; APPLICANT: Cobbold, Stephen
; APPLICANT: Winsor-Hines, Dawn
; TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
; FILE REFERENCE: 695458-73
; CURRENT APPLICATION NUMBER: US/10/353,708
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US10/171,452
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US60/373,471
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US60/373,470
; PRIOR FILING DATE: 2002-04-18
```

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; PRIOR APPLICATION NUMBER: US60/345,194
; PRIOR FILING DATE: 2002-10-19
; PRIOR APPLICATION NUMBER: GB0122724.8
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: GB0114517.6
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 53
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Heavy chain of humanized antibody
US-10-353-708-53
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Alignment Scores:
Pred. No.: 7,34e-113 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0
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US-10-733-563-111 (1-990) x US-10-353-708-53 (1-467)

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Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGGGCCCTCGGTGCTGCTGCTCAAGACTACTTCCCGAACCCGGTGAAGGTGTCG 120
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCCCTGACGAGCGGGTGCACACCTTCCCGGTCTCTCAGTCCCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCCAGACC 240
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCACAGCCCAACCAACCAAGGTGGACAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLysValGluPro 237
QY 301 AAATCTGTGACAAACTCACACATGCCACCGTCCCGGAGCAGCTGAACTCCGGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CGGTCAAGTCTTCTCTCCCTCCCAAAACCCAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProProlsProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTTCACATCGTGTGTGTGAGCTGAGCCACGAGACCCCTGAGGTTCAACTGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGACGGGTGGAGGTGATTAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGTGTGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCGCCCATCGAGAAACCATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlleGluLysThrIleSer 357
QY 661 AAAGCAAAGGCGACCCCGAGAAACCAAGGTGTGACACCTTCCCGGTCTCTCAGTCCCTCA 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
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## Alignment Scores:

```
Pred. No.: 7,34e-113 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-731-984-23 (1-467)

QY 1 GCCTCCACCAAGGGCCCATCGTCTTCCCGTGGCACACCTCTCTCCAGAGCACCTCTGGG 60
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGGCCCTGGGCTCGCTGCTCAAGACTACTTCCCGAACCGGTGACGGTGTGC 120
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGGCGCCCTGACACAGCGGTGCACACTTCCCGGTGTCTTACAGTCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCCAGACC 240
Db 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGCTGAATCACAAGCCCAAGCCACCAAGGTGGACAAAGATTGAGGCC 300
Db 218 TyrlleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237
QY 301 AAATCTTGACAAACTCACACATGCCACCGTCCCGTCCAGCACCTGAACTCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CGGTGAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCTCT 420
Db 258 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGGTCAATCGTGGTGGAGCTGACCGACGACGACCGTGGTCAAGTTCACATCGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGAACGGGTGAGGTGCATATGCAAGACAAAGCCCGGGAGGAGCAGTACAAAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGGTGGTTCAGGTCTCTACCGTCTGACACGAGTGTGCTGAATGGCAAG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAAGTGCAGGTCTCCAAACAAAGCCCTCCAGACCCCTCCAGACCAACCATCTCC 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGACGCCCGGAGAACACAGGTGTACACCTGCTCCCGCCATCCCGGGATGAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGAACCCAGGTGACCTGCTGCTGGTCAAGGGCTTCTATCCAGCGACATC 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCGGTGAGTGGGAGCAATGGGCGAGCGGAGAACACTACAAGACCCGCTCCCGTGG 840
Db 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProProVal 417
QY 841 CTGGACTCCGAGGGCTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAGAGCAGGTGG 900
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATAGGTGCTGCAACCACTACACG 960
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
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Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 14
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; Sequence 110, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Ponath, Paul
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 10/272,899
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/392,364
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/350,166
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human IgG1-FcRmut protein
US-10-733-563-110

Alignment Scores:
Pred. No.: 1.55e-112 Length: 330
Score: 1760.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.94% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-111 (1-990) x US-10-733-563-110 (1-330)

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QY 61 GGCACAGCGGCCCTGGGCTCGCTGCTCAAGACTACTTCCCGAACCCGGTGAAGGTGTG 120
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGGCGCCCTGACACGCGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAACGCTGAATCACAAGCCCAAGCAACCAAGGTGGACAAAGATTGAGGCC 300
Db 81 TyrlleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTTGACAAACTCACACATGCCACCGTCCCGTGGCACACCTGAATCTCCGGGGCA 360
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 120
QY 361 CGGTGAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCTCT 420
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATCGTGGTGGAGCTGACCGACGACGACCGTGGTCAAGTTCACATCGG 480
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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:46:13 ; Search time 12.6351 Seconds  
(without alignments)  
1696.980 Million cell updates/sec

Title: US-10-733-563-111

Perfect score: 1797

Sequence: 1 gctccaccaggcccatc.....tctccctgtctccggtaaa 990

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10733563 @CNC 1.1.1 @runat\_27012006\_180008\_4917  
-NCPU=6 -ICPU=3 -NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA New:  
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4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1765	98.2	448	7	US-11-158-505-8	Sequence 8, Appli
2	1765	98.2	448	7	US-11-158-505-24	Sequence 24, Appli
3	1765	98.2	467	7	US-11-158-505-5	Sequence 5, Appli
4	1765	98.2	467	7	US-11-158-505-7	Sequence 7, Appli
5	1765	98.2	467	7	US-11-158-505-21	Sequence 21, Appli
6	1765	98.2	467	7	US-11-158-505-23	Sequence 23, Appli
7	1756	97.7	335	7	US-11-024-251-35	Sequence 35, Appli
8	1756	97.7	444	7	US-11-172-320-6	Sequence 6, Appli
9	1756	97.7	444	7	US-11-173-969-6	Sequence 6, Appli
10	1756	97.7	451	7	US-11-158-505-33	Sequence 33, Appli

11	1756	97.7	551	7	US-11-022-289-7	Sequence 7, Appli
12	1756	97.7	551	7	US-11-022-289-8	Sequence 8, Appli
13	1756	97.7	557	7	US-11-022-289-4	Sequence 4, Appli
14	1756	97.7	557	7	US-11-022-289-5	Sequence 5, Appli
15	1756	97.7	557	7	US-11-022-289-6	Sequence 6, Appli
16	1754	97.6	592	6	US-10-016-686-4	Sequence 4, Appli
17	1753	97.6	447	7	US-11-102-621-132	Sequence 132, App
18	1752	97.5	476	7	US-11-139-499-4	Sequence 4, Appli
19	1752	97.5	476	7	US-11-139-499-12	Sequence 12, Appli
20	1751	97.4	330	6	US-10-886-383-6	Sequence 6, Appli
21	1751	97.4	330	6	US-10-493-909-20	Sequence 20, Appli
22	1751	97.4	330	7	US-11-022-289-11	Sequence 11, Appli
23	1751	97.4	330	7	US-11-075-351-1	Sequence 1, Appli
24	1751	97.4	330	7	US-11-165-141-15	Sequence 15, Appli
25	1751	97.4	330	7	US-11-102-621-3	Sequence 3, Appli
26	1751	97.4	330	7	US-11-102-621-7	Sequence 7, Appli
27	1750	97.4	447	7	US-11-102-621-130	Sequence 130, App
28	1750	97.4	447	7	US-11-102-621-131	Sequence 131, App
29	1750	97.4	449	7	US-11-154-337-17	Sequence 17, Appli
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31	1750	97.4	451	6	US-10-923-327-9	Sequence 9, Appli
32	1750	97.4	451	6	US-10-923-327-11	Sequence 11, Appli
33	1750	97.4	452	7	US-11-120-338-14	Sequence 14, Appli
34	1750	97.4	452	7	US-11-107-028-32	Sequence 32, Appli
35	1750	97.4	452	7	US-11-106-820-26	Sequence 26, Appli
36	1750	97.4	471	7	US-11-106-820-25	Sequence 25, Appli
37	1750	97.4	548	7	US-11-022-289-3	Sequence 3, Appli
38	1750	97.4	557	7	US-11-022-289-2	Sequence 2, Appli
39	1750	97.4	564	7	US-11-022-289-10	Sequence 10, Appli
40	1750	97.4	667	7	US-11-096-046-25	Sequence 25, Appli
41	1750	97.4	692	6	US-10-981-356A-26	Sequence 26, Appli
42	1750	97.4	695	7	US-11-096-046-26	Sequence 26, Appli
43	1749	97.3	449	7	US-11-080-587-6	Sequence 6, Appli
44	1748	97.3	330	7	US-11-102-621-71	Sequence 71, Appli
45	1748	97.3	446	7	US-11-102-621-121	Sequence 121, App

ALIGNMENTS

RESULT 1  
US-11-158-505-8  
; Sequence 8, Application US/11158505  
; Publication No. US20060002921A1  
; GENERAL INFORMATION:  
; APPLICANT: WINSOR-HINES, DAWN  
; APPLICANT: RAO, PATRICIA  
; APPLICANT: RINGLER, DOUGLAS J  
; APPLICANT: PONATH, PAUL  
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE  
; TITLE OF INVENTION: INDUCTION IN PRIMATES  
; FILE REFERENCE: TLN-031  
; CURRENT APPLICATION NUMBER: US/11/158,505  
; PRIOR FILING DATE: 2005-06-21  
; PRIOR APPLICATION NUMBER: 60/582,181  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1  
; OTHER INFORMATION: antibody heavy chain construct  
US-11-158-505-8

Alignment Scores:  
Pred. No.: 3.3e-115 Length: 448  
Score: 1765.00 Matches: 330  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.22% Indels: 0  
DB: 7 Gaps: 0



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US-10-733-563-111 (1-990) x US-11-158-505-8 (1-448)
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Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCGCTCACCAGCGCGCTGCACACTTCCCGCTGTCTCTACAGTCCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
Db 179 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 198
QY 241 TACATCTGCAACGTAATCACAAGCCCGACACACCAAGGTGGACAAAGATTGAGCCC 300
Db 199 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 218
QY 301 AAATCTTGTGACAAACTCACAATGCCCGCCAGCACCTGAACTCGCGGGGCA 360
Db 219 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 238
QY 361 CCGTCAGTCTTCTCTTCCCGCCAAAACCCAAAGGACCCCTCATGATCTCCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 258
QY 421 GAGGTCAATCGGTGGTGGACGTGAGCCAGCCAGCAGACCTGAGGTCAAGTTCACCTGG 480
Db 259 GluValThrCysValValAlaAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysValAspLysValGluPro 298
QY 541 AGCAGTACCTGTGGTGTGAGTCTCTACCGTCTCTGCAACGAGACTGGCTGAATGGCAAG 600
Db 299 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 318
QY 601 GAGTACAGTGCAGGTCCTCAACAAAGCCTCCAGCGCCCGCCATCGAGAAACCATCTCC 660
Db 319 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 338
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QY 721 CTGACCAAGAACCAAGGTGAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGCGACATC 780
Db 359 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 378
QY 781 GCCGTGGAGTGGGAGAGCAATGGCGAGCCGCGAGACACTACAGACCCGCTCCCGTG 840
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QY 841 CTGACCTCCGAGCGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTGG 900
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RESULT 2
US-11-158-505-24
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; Sequence 24, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PORATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 24
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-24
Alignment Scores:
Pred. No.: 3,3e-115 Length: 448
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-111 (1-990) x US-11-158-505-24 (1-448)
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QY 1 GCCTCCACAAAGGCCCCATCGGTCTTCCCTCGCACCCCTCTCCAAAGAGACCTCTCTGGG 60
Db 119 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 138
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Db 139 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 158
QY 121 TGGAACTCAGCGCGCTGACCGCGGTGCACACCTTCCCGGTGTCTCTACAGTCCTCA 180
Db 159 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 178
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACC 240
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QY 241 TACATCTGCAACGTAATCACAAGCCCGACCAACCAAGGTGGCAAGAAAGTTGAGCCC 300
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QY 361 CCGTCAGTCTTCTCTTCCCGCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCT 420
Db 239 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 258
QY 421 GAGGTCAATCGGTGGTGGAGCTGAGCCAGCAACCAAGACCCCTGAGGTCAAGTTCACCTGG 480
Db 259 GluValThrCysValValAlaAspValSerHisGluAspProGluValLysPheAsnTrp 278
QY 481 TACGTGACGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 279 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 298
QY 541 AGCAGTACCGTGTGGTGTGAGTCTCTCACCGTCTCTGCAACGAGGACTGGCTGAATGGCAAG 600
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Db 299 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAenGlyLys 318
QY 601 GAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGAGCCCTCCATCAGAGAAACCAATCTCC 660
Db 319 GluTyLysCysLysValSerAenLysAlaLeuProAlaProLleGluLysThrIleSer 338
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCTCCATCCCGGAGTACG 720
Db 339 LysAlaLysGlnProArgGluProGlnValTyThrLeuProProSerArgAspGlu 358
QY 721 CTGACCAAGAACCCAGTGCAGCTGACCTGCTCCAGAGGCTTCAAGGCTTCTATCCAGGACATC 780
Db 359 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 378
QY 781 GCCGTGGAGTGGAGAGCAATGGCGAGCGGAGAGCAACAACTCAAGACCAAGCTCCCGTG 840
Db 379 AlaValGluTrpGluSerAenGlnProGluAenAenTyLysThrProProVal 398
QY 841 CTGGACTCCGAGCGGTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 399 LeuAepSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 418
QY 901 CAGCAGGGGAAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
Db 419 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyThr 438
QY 961 CAGAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 439 GlnLysSerLeuSerLeuSerProGlyLys 448

RESULT 3
US-11-158-505-5
; Sequence 5, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLM-031
; CURRENT APPLICATION NUMBER: US/11/158.505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent in ver. 3.3
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-5

Alignment Scores:
Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-5 (1-467)

QY 1 GCCTCCACAAAGGGCCCATCGTCTTCCCTCCCTGGCACCTCTCTCCAGAGCACTCTCGG 60
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCAACAGCGCCCTGGGTGCTGCTCAAGGACTACTTCCCGCAACCGGTGACGGTGTGCG 120
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Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyRpeProGluProValThrValSer 177
QY 121 TGGAACTCAGGCGCCTGACCAAGCGGTGCACACTTCCCGGCTGTCTTCAAGTCCCTCA 180
Db 178 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACC 240
Db 198 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTCAGACCTGAATCAACAGCCCAAGCAACCAAGGTGGGACAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAenValAenHisLysProSerAenThrLysValAspLysLysValGluPro 237
QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCACTGAATCTCGCGGGGCA 360
Db 238 LysSerCysAepLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 258 ProSerValPheLeuPheProProLysPheProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 CAGTCAATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 297
QY 481 TACGTGAGCGCGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAAC 540
Db 298 TyrValAepGlyValGluValHisAenAlaLysThrLysProArgGluGlnGlnTrpAen 317
QY 541 AGCACGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 318 SerThrTyArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAenGlyLys 337
QY 601 GAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGAGCCCTCCATCAGAGAAACCAATCTCC 660
Db 338 GluTyLysCysLysValSerAenLysAlaLeuProAlaProLleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCGCCCTCCATCCCGGAGTACG 720
Db 358 LysAlaLysGlnProArgGluProGlnValTyThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGAACCCAGTGCAGCTGACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
Db 378 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 397
QY 781 GCCGTGGAGTGGAGAGCAATGGCGAGCGGAGAGCAACAACTCAAGACCAAGCTCCCGTG 840
Db 398 AlaValGluTrpGluSerAenGlyGlnProGluAenAenTyLysThrProProVal 417
QY 841 CTGGACTCCGAGCGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 418 LeuAepSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
Db 438 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAenHisTyThr 457
QY 961 CAGAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 4
US-11-158-505-7
; Sequence 7, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
```

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; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-7

Alignment Scores:
Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-7 (1-467)

QY 1 GCCTCCACCAAGGCGCCATCGGCTTCCCTCGGACCCCTCTCCAGAGCACTCTGGG 60
DB 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTTCCCGCAACCGGTACCGGTGCG 120
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCCCTCGGCTGCTGCTCAAGGACTTCCCGGTGCTCTACAGTCTCA 180
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGGTGTGACCGTGCCTCCAGCAGTGGGGACCCAGACC 240
DB 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAACGTGAATCAACAGCCCAAGCAACCAAGGTGGACAGAAAGTTGAGCC 300
DB 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237
QY 301 AAATCTTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCGCGGGGCA 360
DB 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTTCTTCCCTCCCAAGCAACCAAGGACCCCTCATGATCTCCCGGACCCCT 420
DB 258 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGGTTCATCGTGGTGGTGGCTGAGCCACCAAGACCCCTGAGTCAAGTCAAGTCACTGG 480
DB 278 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGACCGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGACAGTACAAC 540
DB 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGGTGGTGGCTGCTACCGTCTCGACAGGACTGGCTGAATGGCAAG 600
DB 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCC 660
DB 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 357
QY 661 AAAGCCAAAGGCGCCCGGAGAACCAACAGGTGTACACCCCTGCCCCCATCCCGGGATGAG 720
DB 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
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QY 721 CTGACCAAGAACGAGGTACGCTGACCTGCTGCTCAAGGCTTCTATCCAGGACATC 780
DB 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGGAGTGGGAGAGCAATGGSCAGCCGAGAACAACTACAGAACCCAGCCCTCCCGTG 840
DB 398 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417
QY 841 CTGGACTCCGACGCGCTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGG 900
DB 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGATGAGGCTTCGCAACCACTACACG 960
DB 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCCTCTCCCTGCTCTCCGGGTAAA 990
DB 458 GlnLysSerLeuSerLeuSerProGlyLys 467

RESULT 5
US-11-158-505-21
; Sequence 21, Application US/11/158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-21

Alignment Scores:
Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-158-505-21 (1-467)

QY 1 GCCTCCACCAAGGCGCCATCGGCTTCCCTCGGACCCCTCTCCAGAGCACTCTGGG 60
DB 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTTCCCGCAACCGGTGAGCGGTGCG 120
DB 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCCCTCGGCTGCTGCTCAAGGACTTCCCGGTGCTCTACAGTCTCA 180
DB 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCCCTCAGCAGGTGTGACCGTGCCTCCAGCAGTGGGGACCCAGACC 240
DB 198 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 217
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QY 241 TACATCTGCAAGCTGAATCAACAGCCCGACCAACCAAGGTGGACAGAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAenThrLysValAspLysValGluPro 237
QY 301 AAATCTTGCAAAACTCACACATGCCACCGTCCCGACGACCTGAACCTCGCGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAACCAAGACACCTCATATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTCAATGCTGGTGGTGAACCGACCGAAGACCTGAGGTCAAGTTCACCTGG 480
Db 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGAGCGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGTACAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTCAATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 357
QY 661 AAAGCCAAAGGCGCGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATCAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGAACCAAGGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGGACCATC 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAGACACCGCTCCCGTG 840
Db 398 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417
QY 841 CTGACCTCGAGCGGTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCGGTGG 900
Db 418 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 437
QY 901 CAGCAGGGGAACGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCAACACCACTACAC 960
Db 438 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 457
QY 961 CAGAAGAGCCTCTCCCTGCTCTCCGGGTAAA 990
Db 458 GlnLysSerLeuSerLeuSerProGlyLys 467
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## RESULT 6

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US-11-158-505-23
; Sequence 23, Application US/11158505
; Publication No. US2006002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 23
; LENGTH: 467
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-23
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## Alignment Scores:

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Pred. No.: 3,29e-115 Length: 467
Score: 1765.00 Matches: 330
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.22% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-111 (1-990) x US-11-158-505-23 (1-467)
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QY 1 GCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCTCTCCCAAGAGCACCTCTGGG 60
Db 138 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 157
QY 61 GGCACAGCGCCCTCGGTGCTGCTCAAGGACTACTTCCCGAACCCTGACGGTGTGCG 120
Db 158 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 177
QY 121 TGGAACTCAGCGCCCTCGACCAAGCGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 180
Db 178 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 197
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCTGCTCCCTCCACAGCTGGGACCCAGACC 240
Db 198 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 217
QY 241 TACATCTGCAAGCTGAATCAACAGCCCGACCAACCAAGGTGGACAGAGAAAGTTGAGCCC 300
Db 218 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 237
QY 301 AAATCTTGCAAAACTCACACATGCCACCGTGGCCCGACGACCTGAACCTCGCGGGGCA 360
Db 238 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuAlaGlyAla 257
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAACCAAGACACCTCTCATGATCTCCCGGACCCCT 420
Db 258 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 277
QY 421 GAGTCAATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 278 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 297
QY 481 TACGTGGAGCGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGGAGCAGTACAC 540
Db 298 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGlnTyrAsn 317
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
Db 318 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 337
QY 601 GAGTCAATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
Db 338 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProLysThrIleSer 357
QY 661 AAAGCCAAAGGCGCGCCCGGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGATCAG 720
Db 358 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 377
QY 721 CTGACCAAGAACCAAGGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGGACCATC 780
Db 378 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 397
QY 781 GCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAGACACCGCTCCCGTG 840
Db 398 AlaValGluTyrGluSerAsnGlyGlnProGluAsnAsnTyrLysThrProProVal 417
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Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-172-320-6 (1-444)

QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCCGACCTCTCTCCAGAGCACCTCTGGG 60  
DB 115 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 134  
QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGTGTG 120  
DB 135 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 154  
QY 121 TGGAACTCAGGCGCTCAGACAGCGCGTGCACACCTTCCCGGTGTCTCAGTCTCTCA 180  
DB 155 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 174  
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGGTGCCCTCCAGCAGCTTGGGCACCCAGACC 240  
DB 175 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 194  
QY 241 TACATCTGCAGCTGAATCAACAGCCCGAGCAACCAACAGGTGGACAGAAAGTTGAGCCC 300  
DB 195 TyrIleCysAenValAsnHisLysProSerAenThrLysValAspLysLysValGluPro 214  
QY 301 AAATCTGTGCAAAACTCACACATGCCCGTCCCGTCCGACACCTGAATCGCGGGGCA 360  
DB 215 LysSerCysAspLysThrHisThrCysProCysProCysProAlaProGluLeuGlyGly 234  
QY 361 CGGTGAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 235 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 254  
QY 421 GAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
DB 255 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 274  
QY 481 TACGTGGAGCGGTGAGTGCATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 275 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgLysGlnThrAsn 294  
QY 541 AGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
DB 295 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 314  
QY 601 GAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 315 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 334  
QY 661 AAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCGCCCTCCCGGATGAG 720  
DB 335 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 354  
QY 721 CTGACCAAGAACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 355 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 374  
QY 781 GCCGTGGAGTGGAGAGCATGGGAGCGCGGAGAACAACTCAAGACCAACGCTCCCGT 840  
DB 375 AlaValGluTrpGluSerAsnGlyGlnProGluAenAsnTyrLysThrThrProProVal 394  
QY 841 CTGGACTCCGAGGTCT 900  
DB 395 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 414  
QY 901 CAGCAGGGGAAAGCTTCT 960  
DB 415 GlnGlnGlyAenValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 434  
QY 961 CAGAAAGCCT 990

Db 435 GlnLysSerLeuSerLeuSerProGlyLys 444

## RESULT 9

US-11-173-969-6  
; Sequence 6, Application US/11173969  
; Publication No. US20050271672A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/11/173,969  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/150,475  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6  
US-11-173-969-6

## Alignment Scores:

Pred. No.:	1,38e-114	Length:	444
Score:	1756.00	Matches:	328
Percent Similarity:	99.39%	Conservative:	0
Best Local Similarity:	99.39%	Mismatches:	2
Query Match:	97.72%	Indels:	0
DB:	7	Gaps:	0

US-10-733-563-111 (1-990) x US-11-173-969-6 (1-444)

QY 1 GCCTCCACAGGGCCCATCGGTCTTCCCTCCGACCTCTCTCCAGAGCACCTCTGGG 60

DB 115 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 134

QY 61 GGCACAGCGCCCTCGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACGTGTG 120

DB 135 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 154

QY 121 TGGAACTCAGGCGCTCAGACAGCGCGTGCACACCTTCCCGGTGTCTCAGTCTCTCA 180

DB 155 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 174

QY 181 GGACTCTACTCTCCCTCAGCAGCGTGTGACCGGTGCCCTCCAGCAGCTTGGGCACCCAGACC 240

DB 175 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 194

QY 241 TACATCTGCAACGTGAATCAACAGCCCGAGCAACCAACAGGTGGACAGAAAGTTGAGCCC 300

DB 195 TyrIleCysAenValAsnHisLysProSerAenThrLysValAspLysLysValGluPro 214

QY 301 AAATCTGTGCAAAACTCACACATGCCCGTCCCGTCCGACACCTGAATCGCGGGGCA 360

DB 215 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuGlyGly 234

QY 361 CGGTGAGTCTTCT 420

DB 235 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 254

QY 421 GAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

DB 255 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 274

QY 481 TACGTGGAGCGGTGAGTGCATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 275 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgLysGlnThrAsn 294







; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 7  
; LENGTH: 551  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-7  
Alignment Scores:  
Pred. No.: 1.37e-114 Length: 551  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0  
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DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 20  
QY 61 GGCACAGCGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGG 120  
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluProValThrValSer 40  
QY 121 TGGAACTCAGCGGCCCTGACAGCGGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCA 180  
DB 41 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 181 GGACTCTACTCTCCAGAGGGTGTGACGTGCGCTCCAGCAGCTTGGGACCCAGACC 240  
DB 61 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
QY 241 TACATCTGCAACGTGAATCACAGCCCAAGCCAGCACCAAGGTGGACAAGAAAGTTGAGCCC 300  
DB 81 TyrileCysAenValAenHisGlyProSerAenThrLysValAspLysValGluPro 100  
QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCGCGGGGCA 360  
DB 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 120  
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGACACCTCATGATCTCCCGGACCCCT 420  
DB 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140  
QY 421 GAGGTACATCGTGGTGGTGGAGTGGAGCCAGCAGACCCCTGAGGTCAAGTTCACCTGG 480  
DB 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 160  
QY 481 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAA 540  
DB 161 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTyrAen 180  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 181 SerThrTyArgValValSerValLeuThrValLeuHisGlnAenTrpLeuAenGlyLys 200  
QY 601 GAGTACAGTGCAGGTCTCCAAACAGCCCTCCCGCCCGCCCATCGAGAAACCATCTCC 660  
DB 201 GluTyLysCysLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 220  
QY 661 AAAGCCAAAGGCGCCCGCCGAGAACCAACAGTGTACACCTCGCCCGCCCATCGGAGTAC 720  
DB 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
QY 721 CTGACCAAGAACAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGGACATC 780

DB 241 LeuThrLysAenGlnValSerLeuThrCysLeuValLysGlyPheTyProSerAspIle 260  
QY 781 GCCGTGGAGTGGGAGAGCAATGGGCGAGGAGAACTACAGACCAAGACCCAGCTCCCGTG 840  
DB 261 AlaValGluTrpGluSerAenGlyGlnProGluAenLysThrLysThrProProVal 280  
QY 841 CTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGTGGACAAGACGAGGTGG 900  
DB 281 LeuAenSerAspGlySerPhePheLeuTySerLysLeuThrValAspLysSerArgTrp 300  
QY 901 CAGCAGGGGACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCATACAG 960  
DB 301 GlnGlnGlyAenValPheSerCysSerValMethHisGluAlaLeuHisAenHisTyThr 320  
QY 961 CAGAAGAGCCCTCTCCCTGTCTCCGGGTAAA 990  
DB 321 GlnLysSerLeuSerLeuSerProGlyLys 330  
RESULT 12  
US-11-022-289-8  
; Sequence 8, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 551  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-8  
Alignment Scores:  
Pred. No.: 1.37e-114 Length: 551  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0  
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DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSergly 20  
QY 61 GGCACAGCGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGG 120  
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspThrPheProGluProValThrValSer 40  
QY 121 TGGAACTCAGCGGCCCTGACAGCGGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCA 180  
DB 41 TrpAenSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 181 GGACTCTACTCTCCAGAGGGTGTGACGTGCGCTCCAGCAGCTTGGGACCCAGACC 240  
DB 61 GlyLeuTySerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80  
QY 241 TACATCTGCAACGTGAATCACAGCCCAAGCCAGCACCAAGGTGGACAAGAAAGTTGAGCCC 300  
DB 81 TyrileCysAenValAenHisGlyProSerAenThrLysValAspLysValGluPro 100  
QY 301 AAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCGCGGGGCA 360  
DB 101 LysSerCysAspLysThrHisThrCysProCysProAlaProGluLeuLeuGlyGly 120  
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGACACCTCATGATCTCCCGGACCCCT 420  
DB 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140  
QY 421 GAGGTACATCGTGGTGGTGGAGTGGAGCCAGCAGACCCCTGAGGTCAAGTTCACCTGG 480  
DB 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAenTrp 160  
QY 481 TACGTGGACGGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAA 540  
DB 161 TyrValAspGlyValGluValHisAenAlaLysThrLysProArgGluGlnTyrAen 180  
QY 541 AGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600  
DB 181 SerThrTyArgValValSerValLeuThrValLeuHisGlnAenTrpLeuAenGlyLys 200  
QY 601 GAGTACAGTGCAGGTCTCCAAACAGCCCTCCCGCCCGCCCATCGAGAAACCATCTCC 660  
DB 201 GluTyLysCysLysValSerAenLysAlaLeuProAlaProIleGluLysThrIleSer 220  
QY 661 AAAGCCAAAGGCGCCCGCCGAGAACCAACAGTGTACACCTCGCCCGCCCATCGGAGTAC 720  
DB 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
QY 721 CTGACCAAGAACAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGGACATC 780

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QY 361 CCGTCAGTCTTCTCTCCCTCCCAAAACCCAGGACACCCCTCATGATCTCCGGACCCCT 420
Db 121 ProSerValPheLeuPheProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGGTCAATCGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGG 480
Db 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TACGTGACGGCGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGGACGAGTACAAAC 540
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGTACCGGTGGTCCAGCTCTCCAGCTCTCCAGCTCTCCAGCTCTCCAGCTCTCCAG 600
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTACAGTGCAGAGTCTCCAAAGCCCTCCAGCTCTCCAGCTCTCCAGCTCTCCAGCTCC 660
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 220
QY 661 AAAGCCAAAGGCGACCCCGGAGAACACAGGTGTACACCTGCTCCCGCCCATCCCGGATGAG 720
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGACCGGTCCAGCTCTCCAGCTCTCCAGCTCTCCAGCTCTCCAGCTCTCCAG 780
Db 241 LeuThrLysAsnGlnValSerLysThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGGAGTGGGAGCAATGGGCGAGGAGAACTCAAGAGCTTCTCAAGAGCTTCTCAAG 840
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnLysThrLysThrProProVal 280
QY 841 CTGAGTCCGACGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
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QY 961 CAGAAGAGCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330
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## RESULT 13

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US-11-022-289-4
; Sequence 4, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-4

Alignment Scores:
Pred. No.: 1.37e-114 Length: 557
Score: 1756.00 Matches: 328
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 97.72% Indels: 0
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DB: 7 Gaps: 0
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QY 1 GCCTCCACCAAGGCGCCATCGGTCTTCCCTCGCACCCCTCTCCAAAGAGCACCTCTGGG 60
Db 1 AlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20
QY 61 GGCAACAGCGGCGCTGGCTGCTCAAGGACTTACTTCCCGCAACCGGTGACGGTGTG 120
Db 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40
QY 121 TGGAACTCAGCGCGCTTGACGAGCGGCGTGCACACCTTCCCGGTCTCTACAGTCTCTCA 180
Db 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60
QY 181 GGACTCTACTCTCCCTCAGCAGCGTGGTGCACCGTGCCTTCCAGCAGCTTGGGCGCCAGACC 240
Db 61 GlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeuGlyThrGlnThr 80
QY 241 TACATCTGCAACGTGAATCAAGCCCGAGCAACCAAGGTGGACAAGAAAGTTGAGCCC 300
Db 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100
QY 301 AAATCTTGTGACAAACTCAGATGCCACCGTCCCGACGACCTGAACTCGCGGGGCA 360
Db 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGlyGly 120
QY 361 CCGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCT 420
Db 121 ProSerValPheLeuPheProProLysProLysAspThrLeuMetIleSerArgThrPro 140
QY 421 GAGTGCATCGTGGTGGAGTGCATATGCCAAGCAAGCCCGGAGGAGGAGTCAAGTCAATCG 480
Db 141 GluValThrCysValValAspValSerHisGluAspProGluValLysPheAsnTrp 160
QY 481 TAGCTGACCGCGTGGAGTGCATATGCCAAGCAAGCCCGGAGGAGGAGTCAAGTCAAG 540
Db 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180
QY 541 AGCAGGTACCGTGGTGGTGCACCGTCTCCAGCAGGACTCGCTGAATGGCAAG 600
Db 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200
QY 601 GAGTCAAGTGCAGAGTCTCCAAAGCCCTTCCAGCGCCCATCGAGAAAACCATCTCC 660
Db 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProlLeGluLysThrIleSer 220
QY 661 AAAGCCAAAGGCGCGCCCGGAGAACACAGGTGTACACCTTCCAGCGCCCATCGAGAAAACCATCTCC 720
Db 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240
QY 721 CTGACCAAGAACAGGTGCAGCTGACCTGGCTCAAGGCTTCTTATCCAGCGACATC 780
Db 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260
QY 781 GCCGTGGAGTGGGAGGACAAATGGGCGAGGACCGGAGAACAACTACAGACACCGCTCCCGTG 840
Db 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnLysThrLysThrProProVal 280
QY 841 CTGGACTCCCGCGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 281 LeuAspSerAspGlySerPheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300
QY 901 CAGCAGGGGAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
Db 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320
QY 961 CAGAAGAGCCTCTCCCTGTCTCTCCGGTAAA 990
Db 321 GlnLysSerLeuSerLeuSerProGlyLys 330
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RESULT 14

US-11-022-289-5  
; Sequence 5, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: PC POLYPEPTIDES WITH NOVEL PC LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 5  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-5  
Alignment Scores:  
Pred. No.: 1,37e-114 Length: 557  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-022-289-5 (1-557)  
QY 1 GCCTCCACAAAGGCGCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGG 60  
DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20  
QY 61 GGCACAGGGCGCTGGGCTGCTGCTCAAGGACTACTTCCCGCAACCCGGTGAGGTGCG 120  
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 121 TGGAACTCAGGCGCTGACAGCGCGTGACACCTTCCCGGTGTCTCAGTCCCTCA 180  
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGAGCTTGGGACCCAGACC 240  
DB 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80  
QY 241 TACATCTGCAAGCTGAATCACAAGCCCAAGCCACCAAGGTGGACAAAGATTGAGCCC 300  
DB 81 TyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysValGluPro 100  
QY 301 AAATCTGTGACAAACTCACAATGCCCGCCCGTCCCGACCTGAACTCCGGGGGCA 360  
DB 101 LysSerCysAspLysThrHisThrCysProProCysProAlaProGluLeuLeuGly 120  
QY 361 CCGTCAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCT 420  
DB 121 ProSerValPheLeuPheProProlsProlsAspThrLeuWetIleSerArgThrPro 140  
QY 421 GAGGTCAATGCGTGGTGTGAGTGTGACCAAGACCCCTGAGGTCAAGTTCAACTGG 480  
DB 141 GluValThrCysValValValAspValSerHisGluAspProGluValLysPheAsnTrp 160  
QY 481 TACGTGGAGCGGTGGAGGTGCATATGCCAAGACAAAGCCCGGAGAGCAGTACAC 540  
DB 161 TyrValAspGlyValGluValHisAsnAlaLysThrLysProArgGluGluGlnTyrAsn 180  
QY 541 AGCAGTACCGTGTGGTGTGAGTGTCTCAGCGTCTGACACAGACTGTGCTGAATGGCAAG 600  
DB 181 SerThrTyrArgValValSerValLeuThrValLeuHisGlnAspTrpLeuAsnGlyLys 200  
QY 601 GAGTCAAGTGAAGGTCTCCAAACAAAGCCCTTCCAGGCCCTCCAGCAACCAATCTCC 660

DB 201 GluTyrLysCysLysValSerAsnLysAlaLeuProAlaProIleGluLysThrIleSer 220  
QY 661 AAAGCCAAAGSGCAGCCCGGAGAACACAGAGTGATACACCTGCGCCCATCCCGGATGAG 720  
DB 221 LysAlaLysGlyGlnProArgGluProGlnValTyrThrLeuProProSerArgAspGlu 240  
QY 721 CTGACCAAGAACCCAGGTCAGCTGACCTGCGCTCAAGGCTTCAAGGCTTATCCCAAGCACATC 780  
DB 241 LeuThrLysAsnGlnValSerLeuThrCysLeuValLysGlyPheTyrProSerAspIle 260  
QY 781 GCCGTGGAGTGGAGAGCAATGGCGAGCGCGAGAGAACTACACAGACACACCGCTCCCGTG 840  
DB 261 AlaValGluTrpGluSerAsnGlyGlnProGluAsnAsnTyrLysThrThrProVal 280  
QY 841 CTGGACTCCGACGGCTCTTCTTCTTCTACAGCAAGCTCACGAGAGAGAGAGTGG 900  
DB 281 LeuAspSerAspGlySerPhePheLeuTyrSerLysLeuThrValAspLysSerArgTrp 300  
QY 901 CAGCAGGGGAACGTCTTCTCATGTCTTCTGATGATGATGAGGCTCTGCACAACCACTACAG 960  
DB 301 GlnGlnGlyAsnValPheSerCysSerValMetHisGluAlaLeuHisAsnHisTyrThr 320  
QY 961 CAGAAGACCT 990  
DB 321 GlnLysSerLeuSerLeuSerProGlyLys 330  
RESULT 15  
US-11-022-289-6  
; Sequence 6, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: PC POLYPEPTIDES WITH NOVEL PC LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 6  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-6  
Alignment Scores:  
Pred. No.: 1,37e-114 Length: 557  
Score: 1756.00 Matches: 328  
Percent Similarity: 99.39% Conservative: 0  
Best Local Similarity: 99.39% Mismatches: 2  
Query Match: 97.72% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-111 (1-990) x US-11-022-289-6 (1-557)  
QY 1 GCCTCCACAAAGGCGCCATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACCTCTCTGGG 60  
DB 1 AlaserThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGly 20  
QY 61 GGCACAGGGCGCTGGGCTGCTGCTCAAGGACTACTTCCCGCAACCCGGTGAGGTGCG 120  
DB 21 GlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluProValThrValSer 40  
QY 121 TGGAACTCAGGCGCTGACAGCGCGTGACACCTTCCCGGTGTCTCAGTCCCTCA 180  
DB 41 TrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaValLeuGlnSerSer 60  
QY 181 GGACTCTACTCTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGAGCTTGGGACCCAGACC 240  
DB 61 GlyLeuTyrSerLeuSerSerValThrValProSerSerSerLeuGlyThrGlnThr 80

Qy	241	TACATCTCGAAGCTGAATCA	CAAGCCCAAGCAACA	CAAGGTGGACAAGAAAGTTGAGCCC	300
Db	81	TyrIleCyseAsnValAsnHis	LyseProSerAsnThrLyseVal	AspLyseValGluPro	100
Qy	301	AAATCTTGACAAACCTCAC	ATGATGCCACCGTCCCGAC	CACTGAACCTCCGGGGGCA	360
Db	101	LyseCyseAspLyseThrHis	ThrCyseProCyseProAla	ProGluLeuLeuGlyGly	120
Qy	361	CCGTCAAGTCTTCTCTT	CCCCCAAAACCAAGGAC	CACCTCATGATCTCCCGGACCCCT	420
Db	121	ProSerValPheLeuPhePro	ProLyseProLyseAspThr	LeuMetIleSerArgThrPro	140
Qy	421	GAGGTCAATGGTGGTGG	ACTGAGCCACGAAGACCT	TGAGGTCAAGTTCAACTGG	480
Db	141	GluValThrCyseValVal	ValAspValSerHisGlu	AspProGluValLysePheAsnTrp	160
Qy	481	TACGTGGACGGCTGGAG	GTGCATATGCCAGACAA	AGCCGCGGNGAGGACGATCAAC	540
Db	161	TyrValAspGlyValGlu	ValHisAsnAlaLyseThr	LyseProArgGluGluGlnTrpAsn	180
Qy	541	AGCAGTACCGTGTGGT	CAGGCTCTCACCGTCT	CGACACGAGACTGGCTGAATGGCAAG	600
Db	181	SerThrTyArgValVal	SerValLeuThrValLeu	HisGlnAspTrpLeuAsnGlyLyse	200
Qy	601	GAGTCAAAGTCAAGGT	CTTCCAACAAAGCCCT	TCCAGCCCCCATCGAGAAAACCACTCC	660
Db	201	GluTyLyseCyseVal	SerAsnLyseAlaLeu	ProAlaProIleGluLyseThrIleSer	220
Qy	661	AAAGCCAAAGGGCAGC	CCCGAGAACCAAGGT	TACACCTGCGCCCATCCCGGATGAG	720
Db	221	LyseAlaLyseGlyGln	ProArgGluProGlnVal	TyThrLeuProProSerArgAspGlu	240
Qy	721	CTGACCAAAGAAC	CAGGTGAGCTGACCT	CGCTCGGTCAAAGGCTTCTATCCCAAGCACATC	780
Db	241	LeuThrLyseAsnGln	ValSerLeuThrCyse	LeuValLyseGlyPheTyProSerAspIle	260
Qy	781	GCCGTGGAGTGGAG	AGCAATGGCAGCCGAG	AACAACTACAAGACCAACGCTCCCCGTG	840
Db	261	AlaValGluTrpGlu	SerAsnGlyGlnPro	GluAsnAsnTyLyseThrThrProProVal	280
Qy	841	CTGGACTCCGAGCG	CTCTTCTCTACAGCA	AGCTCACCGTGGACAAGGACGAGTGG	900
Db	281	LeuAspSerAspGly	SerPheLeuTySerLyse	LeuThrValAspLyseSerArgTrp	300
Qy	901	CAGCAGGGGAAGCT	CTTCTCATGCTCCGT	GATGATGAGGCTCTGCACAACCACTACACG	960
Db	301	GlnGlnLyseVal	IlePheSerCyseSer	ValMetHisGluAlaLeuHisAsnHisTyThr	320
Qy	961	CAGAAAGACCTCT	CCCTGTCTCCGGGTAAA		990
Db	321	GlnLyseSerLeu	SerLeuSerProGlyLyse		330

Search completed: January 28, 2006, 09:32:24  
Job time : 22.6351 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 08:49:08 ; Search time 56.0706 Seconds  
(without alignments)  
838.471 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPFPDSQLK.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	2	Aaw40578 Human Kap
2	553	100.0	107	2	Aay50152 Human Kap
3	553	100.0	107	2	Aay92425 Human Kap
4	553	100.0	107	2	Aay08745 Human Kap
5	553	100.0	107	3	Aab27000 Human Kap
6	553	100.0	107	5	Abg31883 Human Kap
7	553	100.0	107	6	Abb98755 Human Kap
8	553	100.0	107	6	Abx42732 Anti-ties
9	553	100.0	107	6	Abx42734 Anti-ties
10	553	100.0	107	6	Abr55835 Anti-Ang
11	553	100.0	107	7	Adj94622 Human Kap
12	553	100.0	107	8	Adf77161 Anti-VAP-
13	553	100.0	107	8	Adl35096 Human Igg
14	553	100.0	107	8	Adl35094 Human Igg
15	553	100.0	107	8	Adm41539 Anti-inte
16	553	100.0	107	8	Adk18336 Amino aci
17	553	100.0	107	8	Adn97487 Human Kap
18	553	100.0	107	8	Adq89334 Artificialia
19	553	100.0	107	8	Adg87911 Human Imm
20	553	100.0	107	8	Adt87911 Anti-IFN-
21	553	100.0	107	8	Adt88871 Anti-IFN-
22	553	100.0	107	8	Adt88871 Human Igg
23	553	100.0	107	8	Adt51583 Light cha
24	553	100.0	107	9	Adw08870 IGF-IR ant

25	553	100.0	107	9	Adw07454 Human kap
26	553	100.0	107	9	Adw24748 Variable
27	553	100.0	107	9	Adw24790 Variable
28	553	100.0	107	9	Adx98272 Human ant
29	553	100.0	107	9	Ady26693 Human ant
30	553	100.0	107	9	Ady74804 Human lig
31	553	100.0	107	9	Adz08815 Mammalian
32	553	100.0	107	9	Adz08946 Amyloid a
33	553	100.0	107	9	Adz44472 Human Imm
34	553	100.0	107	9	Aea25951 Human Imm
35	553	100.0	107	9	Aea16547 Human MCP
36	553	100.0	107	9	Aea45321 Apolipopr
37	553	100.0	107	9	Aea45323 Apolipopr
38	553	100.0	107	9	Aea37411 Anti-huma
39	553	100.0	107	9	Aea37415 Anti-huma
40	553	100.0	107	9	Aeb09607 Human C k
41	553	100.0	107	9	Aeb72782 Anti-Ltal
42	553	100.0	108	8	Adl22765 Human ant
43	553	100.0	108	9	Adw15047 Human Fab
44	553	100.0	108	9	Aea52525 Human ant
45	553	100.0	109	8	Adj95916 Human kap

ALIGNMENTS

RESULT 1					
ID	AAW40578	standard; protein; 107 AA.			
XX	AAW40578;				
DT	21-JUL-1998	(first entry)			
DE	Human kappa CL domain protein fragment.				
XX	Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;				
KW	disorder; salvage receptor binding epitope; cell adherence interaction;				
KW	lymphocyte; T cell inflammatory response.				
XX	Homo sapiens.				
XX	US5739277-A.				
XX	14-APR-1998.				
PD	14-APR-1998.				
PF	14-APR-1995;	95US-00422101.			
XX	14-APR-1995;	95US-00422101.			
PR	14-APR-1995;	95US-00422101.			
XX	(GETH ) GENENTECH INC.				
XX	Snedecor BR, Presta LG;				
XX	WPI; 1998-250490/22.				
PT	Polypeptide(s) that are not Fc fragments and have an increased half-life				
PT	- are useful for the treatment of LFA-1 mediated disorders.				
XX	Disclosure; Fig 2; 38pp; English.				

This protein fragment is derived from a human immunoglobulin kappa CL domain and is used to describe a novel method to produce polypeptides which contain an epitope from the Fc region of an Igg molecule and a mutated salvage receptor binding epitope. They are useful for the treatment of LFA-1 mediated disorders. These are conditions caused by cell adherence interactions involving the LFA-1 receptor on lymphocytes, e.g. T cell inflammatory responses. The mutated salvage receptor sequence in the polypeptides means that they have increased in vivo circulatory half-lives when compared to normal Fc regions of Igg molecules

Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEKKYKVVACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYEKKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2  
AAV50152  
ID AAV50152 standard; protein; 107 AA.  
AC AAV50152;  
XX  
XX  
DT 31-JAN-2000 (first entry)  
XX Human kappa light chain constant region.  
DE  
XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanization; complementarity determining region; CDR; CDR grafting;  
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; light chain.  
XX  
XX Homo sapiens.  
XX EP953639-Al.  
XX  
XX 03-NOV-1999.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX 30-APR-1998; 98EP-00107925.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
XX Rettig WJ;  
XX  
XX WPI; 1999-621833/54.  
XX  
XX N-PSDB; AAZ32777.  
XX  
XX New antibody protein, useful for treating cancer and for imaging presence  
XX of activated stromal fibroblasts in healing wound or inflamed skin.  
XX  
XX Disclosure; Fig 20; 143pp; English.

This sequence represents a human kappa light chain, the cDNA of which was used in the construction of a nucleotide encoding the light chain of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAP). FAP is a cell surface molecule of reactive stromal fibroblasts, and its induction is a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. The novel human reshaped F19 was humanised by grafting the murine complementarity determining regions (CDRs) of F19 onto human variable region framework sequences, and then joining these "reshaped human" variable regions to human constant regions. These modifications also result in the improved producibility in eukaryotic cell culture systems as compared to a chimeric antibody having the entire variable regions of F19 joined to a human constant regions. The human reshaped F19 antibody has low immunogenicity for humans and is useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast

CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder  
CC cancers, pancreatic cancers and metastatic cancers. It is also useful for  
CC the detection of activated stromal fibroblasts in a healing wound,  
XX inflamed skin or a tumour in a human patient  
XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTLSKADYEKKYKVVACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYEKKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3  
AAW92425  
ID AAW92425 standard; peptide; 107 AA.  
XX  
XX AAW92425;  
XX  
XX 23-APR-1999 (first entry)  
XX Human Kappa protein CL domain.  
XX  
XX Antibody; salvage receptor binding epitope; Fab; F(ab')<sub>2</sub>; immunoglobulin;  
KW CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IgG;  
KW kappa protein; renal clearance rate; circulatory half-life.  
XX  
XX Homo sapiens.  
XX  
XX US5869046-A.  
XX  
XX 09-FEB-1999.  
XX  
XX 14-APR-1995; 95US-00422092.  
XX  
XX 14-APR-1995; 95US-00422092.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Presta LG, Snedecor BR;  
XX  
XX WPI; 1999-152694/13.  
XX  
XX Production of antibody fragments with reduced renal clearance - by  
XX introducing salvage receptor binding epitope into CH1 or CL region.  
XX  
XX Disclosure; Col 55-58; 38pp; English.

This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub> polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleared from the kidneys and does not contain an IGG Fc region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an IGG Fc region. The polypeptides have a reduced renal clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the invention

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107

RESULT 4  
AA08745  
ID AAY08745 standard; protein; 107 AA.  
AC AAY08745;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human Kappa-CL domain.  
XX  
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;  
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
KW antibody.  
XX  
OS Homo sapiens.  
XX  
FN US914112-A.  
XX  
PD 22-JUN-1999.  
XX  
PF 22-JAN-1997; 97US-00788800.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
XX  
PA (GETH ) GENENTECH INC.  
XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
FI Thomas GR, Bednar MM, Gross CE;  
XX  
DR WPI; 1999-370483/31.  
XX  
XX Anti-CD18 antibodies in stroke.  
XX  
PS Disclosure; Fig 4A-B; 25pp; English.

This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 to bind to endothelium, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD11b/CD18 complex. This sequence represents the human Kappa-CL domain which is used to illustrate the method of the invention

Query Match 100.0%; Score 553; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107

RESULT 5  
AAB27000  
ID AAB27000 standard; protein; 107 AA.  
XX  
AC AAB27000;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Human kappa CL domain.  
XX  
KW Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;  
KW mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;  
KW psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;  
KW inflammation; vaccine.  
XX  
OS Homo sapiens.  
XX  
FN US6121022-A.  
XX  
PD 19-SEP-2000.  
XX  
PF 14-APR-1995; 95US-00422112.  
XX  
PR 14-APR-1995; 95US-00422112.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Preeta LG, Snedecor BR;  
XX  
DR WPI; 2000-610925/58.  
XX  
PT New nucleic acid encoding new modified polypeptides with increased  
PT circulatory half-life useful for preventing/treating LFA-1-mediated  
PT disorders, e.g. reducing inflammatory responses or inducing tolerance to  
PT immunostimulants.  
XX  
PS Disclosure; Fig 2; 38pp; English.

The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an Fc region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107  
Db 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSPNRGEC 107

RESULT 6  
ABG31883  
ID ABG31883 standard; protein; 107 AA.  
XX  
AC ABG31883;



XX DT 05-NOV-2002 (first entry)  
 XX DE Human kappa CL domain.  
 XX KW Human; kappa CL domain; cerebral blood flow; infarct size;  
 KW focal ischaemic stroke; main cerebral artery;  
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.  
 XX OS Homo sapiens.  
 XX OS US2002081294-A1.  
 XX PN 27-JUN-2002.  
 XX PD 20-DEC-2000; 2000US-00811384.  
 XX PF 23-JAN-1996; 96US-0093038P.  
 XX PR 22-JAN-1997; 97US-00788800.  
 XX PR 17-FEB-1999; 99US-00251652.  
 XX XX (GETH ) GENENTECH INC.  
 XX PA Bednar MM, Gross CE, Thomas GR, Gross LJ;  
 XX PI WPI; 2002-626528/67.  
 XX DR Increasing cerebral blood flow and/or reducing infarct size in focal  
 PT ischemic stroke using anti-CD18 antibody and tissue plasminogen activator  
 PT is useful to improve clinical outcome in acute ischemic stroke.  
 XX XX Disclosure; Fig 4; 27pp; English.  
 XX CC The invention relates to a method of increasing cerebral blood flow and/  
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction  
 CC of a main cerebral artery in a human, comprising co-administering tissue  
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the  
 CC stroke. The method is used to improve the clinical outcome in acute  
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy  
 CC for treating thromboembolic stroke, particularly where thrombolytic  
 CC therapy has been unsuccessful or is contra-indicated. The present  
 CC sequence represents the human kappa CL domain used in the method of the  
 CC invention  
 XX SQ  
 Query Match 100.0%; Score 553; DB 5; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Qy 61 SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107  
 RESULT 7  
 ABB98755  
 ID ABB98755 standard; protein; 107 AA.  
 XX AC ABB98755;  
 XX XX 23-JAN-2003 (first entry)  
 XX DE Human kappa light constant chain.  
 XX KW Human; cytostatic; antitumour; immunosuppressive; antiallergic;  
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;  
 KW cancer; monoclonal antibody F19; colorectal cancer;

KW non-small cell lung carcinoma; breast cancer; pancreatic cancer; tumour;  
 KW systemic autoimmune disease; allergy; light chain; constant region.  
 XX OS Homo sapiens.  
 XX PN WO200283171-A2.  
 XX PD 24-OCT-2002.  
 XX PF 11-APR-2002; 2002WO-EP004041.  
 XX PR 12-APR-2001; 2001US-0283868P.  
 XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 XX PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.  
 XX PI Amelsberg A, Scott A, Tanswell P;  
 XX XX WPI; 2003-058609/05.  
 XX DR N-PSDB; ABV74601.  
 XX PT Use of a humanized antibody which specifically binds to fibroblast  
 PT activation protein alpha for manufacturing a medicament for treating  
 PT cancer.  
 XX PS Claim 7; Page 55; 57pp; English.  
 XX CC The present invention relates to the use of a humanised antibody (I),  
 CC which specifically binds to fibroblast activation protein alpha  
 CC (FAPalpha), for manufacturing a medicament for treating cancer. (I) has  
 CC the complementary determining region (CDR) of the monoclonal antibody  
 CC F19, but has framework modifications resulting in improved producibility  
 CC in host cells as compared to a chimeric antibody having the variable  
 CC regions of F19 and foreign constant regions. To generate (I), a chimeric  
 CC antibody was constructed having variable regions of the light and heavy  
 CC chains of F19 and human light and heavy constant regions. (I) is useful  
 CC for treating a patient suffering from a pathological condition  
 CC characterised by expression of FAPalpha, such as colorectal cancer, non-  
 CC small cell lung carcinoma, breast cancer, pancreatic cancer, tumours,  
 CC systemic autoimmune diseases and allergies. The present sequence is human  
 CC kappa light constant chain which was used to produce (I)  
 XX SQ  
 Sequence 107 AA;  
 Query Match 100.0%; Score 553; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Qy 61 SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 61 SKDSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107  
 RESULT 8  
 ABR42732  
 ID ABR42732 standard; protein; 107 AA.  
 XX AC ABR42732;  
 XX XX 26-AUG-2003 (first entry)  
 XX DE Anti-tissue factor humanized antibody light chain constant region.  
 XX KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;  
 KW antiinflammatory; mouse; human; hOAT.  
 XX OS Mus sp.  
 XX OS Homo sapiens.  
 XX OS Chimeric.

```
XX PN WO2003037911-A2.
XX PD
XX PP 08-MAY-2003.
XX PR 29-OCT-2002; 2002WO-US034727.
XX PR 29-OCT-2001; 2001US-0343306P.
XX PR 21-NOV-2001; 2001US-00990586.
XX PA (SUNO-) SUNOL MOLECULAR CORP.
XX PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX DR WPI; 2003-468399/44.
XX PT New humanized antibody that binds specifically to human tissue factor,
XX PT useful for in vivo diagnostic methods, or for inhibiting blood
XX PT coagulation or blood clot formation, angiogenesis, tumor metastases or
XX PT inflammation in a mammal.
XX PS Example 10; Fig 14A; 110pp; English.
XX CC The present sequence is the protein sequence of the light chain constant
XX CC region of anti-human tissue factor (TF) humanized antibody hOAT
XX CC (humanised CH36-IgG1). Humanized antibodies of the invention provide
XX CC superior anticoagulant activity by binding native human TF with high
XX CC affinity and specificity. The antibodies bind human TF, either alone or
XX CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
XX CC Factor IX) binding to TF or the complex, and thereby reducing blood
XX CC coagulation. The humanized antibodies are useful for inhibiting blood
XX CC coagulation or blood clot formation, angiogenesis, tumor metastases or
XX CC inflammation in a mammal. They are also useful as drug carriers, as
XX CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
XX CC diagnosis
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 9
ABR42734
ID ABR42734 standard; protein; 107 AA.
AC ABR42734;
DT 26-AUG-2003 (first entry)
XX Anti-tissue factor humanized antibody light chain constant region.
XX Tissue factor; humanization; antibody; anticoagulant; cytostatic;
XX antiinflammatory; mouse; human; hOAT.
XX Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX PN WO2003037911-A2.
XX PD 08-MAY-2003.
XX PR 29-OCT-2002; 2002WO-US034727.
```

```
XX PR 29-OCT-2001; 2001US-0343306P.
XX PR 21-NOV-2001; 2001US-00990586.
XX PA (SUNO-) SUNOL MOLECULAR CORP.
XX PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX DR WPI; 2003-468399/44.
XX PT New humanized antibody that binds specifically to human tissue factor,
XX PT useful for in vivo diagnostic methods, or for inhibiting blood
XX PT coagulation or blood clot formation, angiogenesis, tumor metastases or
XX PT inflammation in a mammal.
XX PS Example 10; Fig 15A; 110pp; English.
XX CC The present sequence is the protein sequence of the light chain constant
XX CC region of anti-human tissue factor (TF) humanized antibody hPAT
XX CC (humanised CH36-IgG4). Humanized antibodies of the invention provide
XX CC superior anticoagulant activity by binding native human TF with high
XX CC affinity and specificity. The antibodies bind human TF, either alone or
XX CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
XX CC Factor IX) binding to TF or the complex, and thereby reducing blood
XX CC coagulation. The humanized antibodies are useful for inhibiting blood
XX CC coagulation or blood clot formation, angiogenesis, tumor metastases or
XX CC inflammation in a mammal. They are also useful as drug carriers, as
XX CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
XX CC diagnosis
XX SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
RESULT 10
ABR55835
ID ABR55835 standard; protein; 107 AA.
XX ABR55835;
XX 02-SEP-2003 (first entry)
XX Anti-Ang-2 antibody kappa constant region.
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
XX gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
XX angiogenesis; antibody.
XX OS Homo sapiens.
XX PN WO2003030833-A2.
XX PD 17-APR-2003.
XX PF 11-OCT-2002; 2002WO-US032613.
XX PR 11-OCT-2001; 2001US-0328604P.
XX PR 10-OCT-2002; 2002US-00269805.
XX PA (AMGE-) AMGEN INC.
XX PI Oliner JD;
```

XX WPI; 2003-504963/47.  
 XX New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful  
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
 XX  
 XX Example 4; Page 96; 161pp; English.  
 XX  
 CC The invention relates to a specific binding agent, which comprises at  
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its  
 CC fragment. The binding agents are antibodies that recognize and bind to  
 CC angiopoietin-2 (Ang-2). The specific binding agent, particularly the  
 CC antibody, is useful for inhibiting undesired angiogenesis, treating  
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
 CC 2 activity, modulating vascular permeability or plasma leakage, or  
 CC treating a disease (e.g. ocular neovascular disease, obesity,  
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
 CC disease, bone-related disease, or psoriasis) in a mammal. The present  
 CC sequence represents a human kappa constant region of an anti-Ang-2  
 CC antibody  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 553; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 RESULT 11  
 ADJ94622  
 ID ADJ94622 standard; protein; 107 AA.  
 AC ADJ94622;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human kappa chain (CK) constant region.  
 XX  
 KW humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; Mab;  
 KW IVIAB variable region; B-cell lymphoma; leukaemia; autoimmune disease;  
 KW thrombocytopenia; lupus; rheumatoid arthritis; kappa chain; human; CK;  
 KW constant region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003068821-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 14-FEB-2003; 2003WO-GB000665.  
 XX  
 PR 14-FEB-2002; 2002US-0356132P.  
 PR 07-OCT-2002; 2002US-0416232P.  
 XX  
 XX (IMMU-) IMMUNOMEDICS INC.  
 PA (MCCA/) MCCA J. D.  
 XX  
 PI Hansen H, Qu Z, Goldenberg DM;  
 XX  
 DR WPI; 2003-697522/66.  
 DR N-PSDB; ADJ94621.  
 XX  
 PT New humanized anti-CD20 monoclonal antibody (Mab) that retains

PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting  
 PT of the murine anti-CD20 Mab, useful for treating B-cell lymphoma,  
 XX leukemia or an autoimmune disease.  
 XX Example 1; Fig 7B; 106pp; English.  
 XX  
 CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody  
 CC (Mab) or its antigen-binding fragment containing the complementarity  
 CC determining regions (CDRs) of at least one murine anti-CD20 Mab variable  
 CC region and the framework regions (FRs) of at least one human IVIAB  
 CC variable region. The antibodies of the invention are useful for  
 CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune  
 CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The  
 CC present amino acid sequence represents a human kappa chain (CK) constant  
 CC region.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 100.0%; Score 553; DB 7; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
 RESULT 12  
 ADF77161  
 ID ADF77161 standard; protein; 107 AA.  
 XX  
 AC ADF77161;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Anti-VAP-1 monoclonal antibody L chain constant region.  
 XX  
 KW complementarity determining region; CDR; mouse;  
 KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;  
 KW chimeric; inflammatory disorder; rheumatoid arthritis;  
 KW inflammatory bowel disease; autoimmune disease; psoriasis;  
 KW immunoscintigraphic imaging.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003093319-A1.  
 XX  
 PD 13-NOV-2003.  
 XX  
 PF 28-APR-2003; 2003WO-FI000330.  
 XX  
 PR 29-APR-2002; 2002FI-00000807.  
 XX  
 XX (BIOT-) BIOTIE THERAPIES CORP.  
 XX  
 PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;  
 XX  
 DR WPI; 2004-022642/02.  
 XX  
 PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and  
 PT encoding nucleic acid molecules, useful for diagnosing and treating  
 PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.  
 XX  
 PS Claim 18; SEQ ID NO 22; 56pp; English.  
 XX  
 CC This sequence represents the constant region of a human anti-Vascular  
 CC Adhesion Protein-1 (VAP-1) antibody light chain. This sequence may be  
 CC used in the production of a chimeric mouse-human anti-VAP-1 antibody. The  
 CC nucleic acid molecules, polypeptides or antibodies are useful in treating

CC VAP-1 mediated inflammatory disorders, such as rheumatoid arthritis,  
CC inflammatory bowel disease, autoimmune diseases or psoriasis. The  
CC chimeric VAP-1 antibody is further used for in vitro and in vivo  
CC diagnostic applications, including in vivo immunoscintigraphic imaging of  
CC inflammation sites. The chimeric MAb's of the invention have improved  
CC kinetic properties compared to the corresponding murine antibodies.

XX Sequence 107 AA;  
SQ  
Query Match 100.0%; Score 553; DB 8; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60  
DB 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60  
QY 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 13  
ADL35096  
ID ADL35096 standard; protein; 107 AA.  
XX  
AC ADL35096;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human IgG4 (hPAT) kappa light chain constant domain protein SeqID 99.  
XX  
KW antibody; variable domain; framework region; FR; huFR;  
KW immune system molecule; kappa; anti-tissue factor; hPAT; human.  
XX  
OS Homo sapiens.  
XX  
FN WO2004020579-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 06-AUG-2003; 2003WO-US024637.  
XX  
PR 29-AUG-2002; 2002US-00230880.  
XX  
PA (SUNO-) SUNOL MOLECULAR CORP.  
XX  
PI Wong HC, Stinson JR, Mosquera LA;  
XX  
DR WPI; 2004-239169/22.

PT Producing humanized antibodies for diagnostic and therapeutic purposes  
PT comprises optimizing similarity between individual antibody framework  
PT regions to help identify human framework regions suitable for making the  
PT antibodies.

PS Disclosure; SEQ ID NO 99; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
XX antibody variable (V) domain or its fragment by optimising sequence  
XX similarity between individual antibody framework regions (FRs) in order  
XX to identify suitable human FRs (huFRs). Specifically, it refers to novel  
XX immune system molecules i.e. humanised monoclonal antibodies that exhibit  
XX suitable binding affinity with reduced immunogenicity in humans. The  
XX present invention describes a method of mutagenising DNA of non-human FRs  
XX to encode humanised FRs having an amino acid sequence that is  
XX substantially identical to the selected human FR previously identified  
XX through sequence similarity searching. As such, this method provides  
XX humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
XX -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
XX products to treat and/or diagnose diseases in humans and animals.  
XX Furthermore, the method expands the number of best fit possibilities that  
XX can be generated and provides a rational basis for assembling nearly all

CC humanised immune system molecules of interest. This polypeptide sequence  
CC is the human IgG4 kappa light chain constant domain protein of the  
CC invention.

XX Sequence 107 AA;

SQ  
Query Match 100.0%; Score 553; DB 8; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-48;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60  
DB 1 RTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTRQD 60  
QY 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 14  
ADL35094  
ID ADL35094 standard; protein; 107 AA.  
XX  
AC ADL35094;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human IgG1 (hOAT) kappa light chain constant domain protein SeqID 97.  
XX  
KW antibody; variable domain; framework region; FR; huFR;  
KW immune system molecule; kappa; anti-tissue factor; hOAT; human.

XX Homo sapiens.  
XX  
FN WO2004020579-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 06-AUG-2003; 2003WO-US024637.  
XX  
PR 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.  
XX  
PI Wong HC, Stinson JR, Mosquera LA;  
XX  
DR WPI; 2004-239169/22.

PT Producing humanized antibodies for diagnostic and therapeutic purposes  
PT comprises optimizing similarity between individual antibody framework  
PT regions to help identify human framework regions suitable for making the  
PT antibodies.

PS Disclosure; SEQ ID NO 97; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
XX antibody variable (V) domain or its fragment by optimising sequence  
XX similarity between individual antibody framework regions (FRs) in order  
XX to identify suitable human FRs (huFRs). Specifically, it refers to novel  
XX immune system molecules i.e. humanised monoclonal antibodies that exhibit  
XX suitable binding affinity with reduced immunogenicity in humans. The  
XX present invention describes a method of mutagenising DNA of non-human FRs  
XX to encode humanised FRs having an amino acid sequence that is  
XX substantially identical to the selected human FR previously identified  
XX through sequence similarity searching. As such, this method provides  
XX humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
XX -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
XX products to treat and/or diagnose diseases in humans and animals.  
XX Furthermore, the method expands the number of best fit possibilities that  
XX can be generated and provides a rational basis for assembling nearly all  
XX humanised immune system molecules of interest. This polypeptide sequence  
XX is the human IgG1 kappa light chain constant domain protein of the  
XX invention.

```

XX SQ Sequence 107 AA;
Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||

QY 61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db |||||

RESULT 15
ADM41539
ID ADM41539 standard; protein; 107 AA.
XX
AC ADM41539;
XX
DT 03-JUN-2004 (first entry)
XX
DE Anti-interleukin-1 receptor type 1 antibody kappa chain constant region.
XX
KW Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW prozoocicide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW anticonvulsant; dermatological; antigen; antiparkinsonian; antidiabetic;
KW cyostatic.
XX
OS Homo sapiens.
XX
FN WO2004022718-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027978.
XX
PR 06-SEP-2002; 2002US-0408719P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Varnum B, Vezina C, Witte A, Qian X, Martin P, Huang H;
PI Elliott G;
XX
DR WPI; 2004-248462/23.
DR N-PSDB; ADM41538.
XX
PT Isolated human antibody that specifically binds interleukin-1 receptor
PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS Disclosure; SEQ ID NO 4; 179pp; English.
XX
CC The present sequence is that of a human anti-interleukin-1 receptor type
CC 1 (IL-1R1) monoclonal antibody (Mab) kappa chain constant region. Human
CC Mabs to IL-1R1 were prepared using the HCo7 strain of transgenic mice,
CC which expresses human antibody genes. These mice were immunised with
CC purified recombinant IL-1R1, and splenocytes from immunised mice were
CC fused to a mouse myeloma cell line to generate hybridomas. Hybridomas
CC which secreted a MAb that bound with high avidity to IL-1R1 were
CC selected. The Mabs inhibit IL-1 signalling by competing with IL-1beta and
CC IL-1alpha binding to IL-1R. These Mabs, as well as single chain
CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
CC and (Fab')2 antibodies derived from them, are used in methods of treating
CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
CC Clostridium associated illnesses, coronary conditions, cancer including

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CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,
CC fibromyalgia, glomerulonephritis, graft versus host disease,
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
CC ischaemia, Kawasaki's disease, learning impairment, lung disease,
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
CC septic shock, side effects of radiation therapy, temporal mandibular
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
XX surgery, infection or other disease processes.
XX
SQ Sequence 107 AA;

```

```

Query Match 100.0%; Score 553; DB 8; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.1e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db |||||
QY 61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db |||||
QY 61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db |||||

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Search completed: January 28, 2006, 09:38:16
Job time : 57.0706 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:23:14 ; Search time 10.9249 Seconds  
(without alignments)  
942.358 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPDEQLKS.....EVTHQGLSPVTKSFNRGEC 107  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues 283416  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0243	Ig kappa chain NIG
2	553	100.0	215	2 JE0244	Ig kappa chain NIG
3	553	100.0	215	2 JE0242	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-1
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 K1RTB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain V-C
13	359	64.9	106	1 K1RTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain C r
17	352	63.7	218	2 JC5810	monoclonal antibod
18	352	63.7	219	2 S52028	Ig kappa chain - m
19	352	63.7	219	2 PC4203	Ig kappa chain - m
20	352	63.7	219	2 S16112	Ig kappa chain v r
21	352	63.7	220	2 A31790	Ig kappa chain v r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 K1MS	Ig kappa chain C r
27	350	63.3	126	2 I54782	gene Pvt-Ia/Ig-Ck
28	348	62.9	225	2 JL0029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

30	321	58.0	214	2 S68212	Ig kappa chain (Ma
31	312	56.4	210	2 A56169	Ig kappa chain V r
32	308.5	55.8	106	2 G20907	Ig kappa-B4 chain
33	306.5	55.4	106	1 K4RBS	Ig kappa-2 chain C
34	277.5	50.2	229	2 A20969	Ig kappa chain pre
35	257.5	46.6	103	1 K4RB	Ig kappa-B4 chain
36	256	46.3	104	2 F53275	Ig kappa-1 chain C
37	246.5	44.6	104	1 K9RB	Ig kappa-B9 chain
38	245	44.3	238	2 A49633	Ig lambda-like cha
39	241	43.6	104	1 K5RBV	Ig kappa chain C r
40	237	42.9	118	2 A46518	Ig li chain J-C re
41	231	41.8	103	2 B26167	Ig lambda chain C
42	231	41.8	213	2 A21177	Ig light chain pre
43	225	40.7	108	1 K3FG	Ig light chain C r
44	223.5	40.4	103	1 K5RB	Ig kappa-B5 chain
45	222	40.1	197	2 S29593	Ig kappa chain (WM

ALIGNMENTS

RESULT 1

JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, P.; Yamaki, H.; T  
Submitted to JFID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>

A:CROSS-references: UNIPARC:UPI0000176984  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
DB	109	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 168
QY	61	SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107
DB	169	SKDSTYSLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, P.; Yamaki, H.; T  
Submitted to JFID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>

A:CROSS-references: UNIPARC:UPI0000176982  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
----	---	--

Db 109 RTVAAPSVFI... 168

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107

Db 169 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 215

RESULT 3

JG kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: J0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T. submitted to JGPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul

A:Reference number: J0241

A:Accession: J0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

A:Cross-references: UNIPARC:UPI0000176983

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.6e-46;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI... 168

Db 109 RTVAAPSVFI... 168

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107

Db 169 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 215

RESULT 4

S52059

JC-kappa protein - human

C:Species: Homo sapiens (man)

C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Sep-2000

C:Accession: S52059

R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.; EMBO J. 13, 5937-5943, 1994

A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c

A:Reference number: S52059; MUID:95112804; PMID:7813432

A:Accession: S52059

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <FRA>

A:Cross-references: UNIPARC:UPI00001184D0

C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 99.5%; Score 550; DB 2; Length 135;

Best Local Similarity 99.1%; Pred. No. 1.8e-46;

Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI... 60

Db 29 RTVAAPSVFI... 88

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 107

Db 89 SKDSTYSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 135

RESULT 5

K3HU

Ig kappa chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 09-Jul-2004

C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02;

R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.

Biochemistry 9, 3155-3161, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequence

A:Reference number: A90562; MUID:71064023; PMID:5489770

A:Contents: myeloma protein Eu

A:Accession: B90562

A:Molecule type: protein

A:Residues: 1-106 <GOT>

A:Cross-references: UNIPROT:P01834; UNIPARC:UPI000002F106

A>Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; Eu, disulfide bonds

R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972

A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub

A:Reference number: A91651; MUID:72188439; PMID:5027703

A:Contents: Bence Jones protein Ti

A:Accession: A91651

A:Molecule type: protein

A:Residues: 1-106 <SUT>

A:Cross-references: UNIPARC:UPI000002F106

R:Hietzer, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.

Cell 22, 197-207, 1980

A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserve

A:Reference number: A90806; MUID:81042304; PMID:6775818

A:Accession: A90806

A:Molecule type: DNA

A:Residues: 1-106 <HIE>

A:Cross-references: UNIPARC:UPI000002F106; GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g

A>Note: the sequence was determined from the germline gene

R:Hilchmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, N.

In Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, 1

A:Reference number: A94417

A:Contents: Bence Jones protein Roy

A:Accession: A94417

A:Molecule type: protein

A:Residues: 1-44,'A','46-56','Q','58-82','L','84-106 <HIL>

A:Cross-references: UNIPARC:UPI000017376D

A>Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu

R:Hilchmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967

A:Title: Die voltaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).

A:Reference number: A91639; MUID:68242259; PMID:5586923

A:Contents: Bence Jones protein Cum

A:Accession: A91639

A:Molecule type: protein

A:Residues: 1-56,'Q','58-106 <HI2>

A:Cross-references: UNIPARC:UPI000017376E

R:Titani, K.; Shinoda, T.; Putnam, F.W.

J. Biol. Chem. 244, 3550-3560, 1969

A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete s

A:Reference number: A92047; MUID:6924734; PMID:4893682

A:Contents: Bence Jones protein Ag

A:Accession: A92047

A:Molecule type: protein

A:Residues: 1-13,'N','15-106 <TIT>

A:Cross-references: UNIPARC:UPI000017376F

R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.

Science 169, 56-59, 1970

A:Title: Macroglobulin structure: variable sequence of light and heavy chains.

A:Reference number: A94242; MUID:70201507; PMID:5447531

A:Contents: Waldenstrom's macroglobulin Ou

A:Accession: A94242

A:Molecule type: protein

A:Residues: 1-13,'N','15-106 <KOH>

A:Cross-references: UNIPARC:UPI000017376F

R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.

Am. J. Hum. Genet. 48, 613-620, 1991

A:Title: Km typing with PCR: application to population screening.



A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Cross-references: UNIPARC:UPI0000173770  
A>Note: allotype inv(3)  
R:Steiner, V.; Chang, J.Y.  
PDBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Genetics:

A:Gene: GDB:IGKC  
A:Cross-references: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into larger chain disulfide bonds; immunoglobulin C region; immunoglobulin homology  
C:Superfamily: immunoglobulin C region; immunoglobulin  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:126-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.1e-46;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
DB 1 TVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 KDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
A:Accession: J80241  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JTPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: J80241  
A:Accession: J80241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
A:Cross-references: UNIPARC:UPI0000176981  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:116-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;  
Best Local Similarity 97.2%; Pred. No. 5.7e-45;  
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 110 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 170 SKDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
A:Accession: A23746

R:Leoni, J.; Ghiso, J.; Goni, P.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: A23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
A:Cross-references: UNIPARC:UPI0000176985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:116-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;  
Best Local Similarity 98.1%; Pred. No. 2.6e-43;  
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 109 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
DB 169 SKDSYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8  
A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
A:Accession: A37927  
R:Kuth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: A37927  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
A:Cross-references: UNIPARC:UPI0000176ED6  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:112-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;  
Best Local Similarity 99.0%; Pred. No. 5e-43;  
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL 68  
DB 1 FIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL 60

QY 69 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9  
S26653  
Ig kappa chain C region - chimpanzee (fragment)  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
A:Accession: S26653  
R:Erlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybrids 1, 23-26, 1990  
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies: r  
A:Reference number: S26652; MUID:91355693; PMID:2129418  
A:Accession: S26653  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-99 <EHR>  
A:Cross-references: UNIPARC:UPI0000176ED5; EMBL:X65287

C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.9e-42;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 TVAAPSVFIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
Db 1 TVAAPSVFIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
  
Qy 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTK 100  
Db 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTK 99

RESULT 10  
S06084  
Ig kappa chain precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C;Accession: S06084  
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
A;Reference number: S06084; MUID:90016888; PMID:2508067  
A;Accession: S06084  
A;Molecule type: mRNA  
A;Residues: 1-240 <CR>  
C;Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-240/Product: Ig kappa chain #status predicted <MAT>  
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 372; DB 2; Length 240;  
Best Local Similarity 65.4%; Pred. No. 7.4e-29;  
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 134 RADAAPTYSIFPPSTEQLATGASVVCCLMNNFYPRDISVKWKIDGTERRDGLDVSVDQD 193  
  
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 194 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 240

RESULT 11  
KIRTB  
Ig kappa chain C region (allele b) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C;Accession: A93901; A92807; A02117  
R;Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le  
A;Reference number: A93901; MUID:82082587; PMID:6273908  
A;Accession: A93901  
A;Molecule type: DNA  
A;Residues: 1-106 <SHE>  
C;Cross-references: UNIPROT:P01835; UNIPARC:UPI000012DB83; GB:V01241; GB:J00745; GB:J025  
A;Experimental source: strain LOU  
R;Starace, V.; Querinjean, P.  
J. Immunol. 115, 59-62, 1975  
A;Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation  
A;Reference number: A92807; MUID:75212236; PMID:807630  
A;Contents: Bence Jones protein S211  
A;Accession: A92807  
A;Molecule type: protein  
A;Residues: 1,'N',3-29,'K',31-47,49-78,'Q',80-86,'Q',88-98,'W',99,'N',101-106 <STA>

A;Cross-references: UNIPARC:UPI0000173771  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;19-88/Domain: immunoglobulin homology <IMM>  
F;26-86/Disulfide bonds: #status predicted  
F;106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 66.4%; Score 367; DB 1; Length 106;  
Best Local Similarity 65.4%; Pred. No. 8.7e-29;  
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;  
  
Qy 4 AAPSVFIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 63  
Db 3 AAPTYSIFPPSTEQLATGASVVCCLMNNFYPRDISVKWKIDGTERRDGLDVSVDQDSK 62  
  
Qy 64 STYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 63 STYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 106

RESULT 12  
PT0219  
Ig kappa chain V-C region (PLC18) - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jan-2000  
C;Accession: PT0219  
R;Lammere, B.M.; Beaman, K.D.; Kim, Y.B.  
Mol. Immunol. 28, 877-880, 1991  
A;Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.  
A;Reference number: PT0219; MUID:91342694; PMID:1715030  
A;Accession: PT0219  
A;Molecule type: mRNA  
A;Residues: 1-178 <LAM>  
A;Cross-references: UNIPARC:UPI00001151A1; GB:M59321; NID:G164508; PIDN:AAA03520.1; PID:  
A;Experimental source: spleen, strain Minnesota Miniature  
A;Note: the authors translated the codon CTC for residue 141 as Ser  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-70/Domain: V region (fragment) <VRG>  
F;12-18/Region: complementarity-determining 1  
F;19-51/Region: framework 1  
F;52-60/Region: complementarity-determining 2  
F;61-70/Region: framework 2  
F;71-178/Domain: C region <CRG>  
F;96-156/Disulfide bonds: #status predicted  
F;176/Disulfide bonds: interchain #status predicted

Query Match 66.2%; Score 366; DB 2; Length 178;  
Best Local Similarity 64.5%; Pred. No. 2e-28;  
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 70 RADAKPSVFIPPSPDEQLATPTVSVCLNNFYPRDISVKWKIDGTERRDGLDVSVDQD 129  
  
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
Db 130 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 176

RESULT 13  
KIRTA  
Ig kappa chain C region (allele a) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1982 #sequence\_revision 10-Sep-1982 #text\_change 09-Jul-2004  
C;Accession: A02118  
R;Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A;Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le  
A;Reference number: A93901; MUID:82082587; PMID:6273908  
A;Accession: A02118



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:21:24 ; Search time 56.7132 Seconds  
(without alignments)  
1331.110 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPFPSEDLKLS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	553	100.0	120	2	Q6P5R5 HUMAN	Q6P5R5 homo sapien
2	553	100.0	234	2	Q5E9E6 HUMAN	Q5E9E6 homo sapien
3	553	100.0	234	2	Q72473 HUMAN	Q72473 homo sapien
4	553	100.0	235	2	Q6GMV9 HUMAN	Q6GMV9 homo sapien
5	553	100.0	235	2	Q6GMW0 HUMAN	Q6GMW0 homo sapien
6	553	100.0	235	2	Q6EUF2 HUMAN	Q6EUF2 homo sapien
7	553	100.0	236	2	Q6GMX0 HUMAN	Q6GMX0 homo sapien
8	553	100.0	236	2	Q6P5S8 HUMAN	Q6P5S8 homo sapien
9	553	100.0	236	2	Q6PIH4 HUMAN	Q6PIH4 homo sapien
10	553	100.0	236	2	Q6PIL8 HUMAN	Q6PIL8 homo sapien
11	553	100.0	236	2	Q6PIT5 HUMAN	Q6PIT5 homo sapien
12	553	100.0	236	2	Q723Y4 HUMAN	Q723Y4 homo sapien
13	553	100.0	236	2	Q6PIH7 HUMAN	Q6PIH7 homo sapien
14	553	100.0	236	2	Q6GMX9 HUMAN	Q6GMX9 homo sapien
15	553	100.0	236	2	Q6GMX8 HUMAN	Q6GMX8 homo sapien
16	553	100.0	236	2	Q6GMW1 HUMAN	Q6GMW1 homo sapien
17	553	100.0	236	2	Q502W4 HUMAN	Q502W4 homo sapien
18	553	100.0	239	2	Q6P491 HUMAN	Q6P491 homo sapien
19	553	100.0	239	2	Q8TCD0 HUMAN	Q8TCD0 homo sapien
20	553	100.0	240	2	Q6PIH6 HUMAN	Q6PIH6 homo sapien
21	549	99.3	239	2	Q8NEK0 HUMAN	Q8NEK0 homo sapien
22	548	99.1	106	1	KAC HUMAN	P01834 homo sapien
23	548	99.1	234	2	Q5G9I9 HUMAN	Q5G9I9 homo sapien
24	369	66.7	234	2	Q4KM66 RAT	Q4KM66 rattus norv
25	369	66.7	234	2	Q5M838 RAT	Q5M838 rattus norv
26	367	66.4	106	1	KACB RAT	P01835 rattus norv
27	359	64.9	106	1	KACA RAT	P01836 rattus norv
28	358	64.7	219	2	Q5SZC0 MOUSE	Q5SZC0 mus musculus
29	352	63.7	234	2	Q5XK94 MOUSE	Q5XK94 mus musculus
30	352	63.7	235	2	Q5XFY8 MOUSE	Q5XFY8 mus musculus
31	352	63.7	235	2	Q58EV6 MOUSE	Q58EV6 mus musculus

RESULT 1						
Q6P5R5	HUMAN					
ID	Q6P5R5_HUMAN	PRELIMINARY;		PRT;	120 AA.	
AC	Q6P5R5					
DT	05-JUL-2004	(Tremblrel. 27, Created)				
DT	05-JUL-2004	(Tremblrel. 27, Last sequence update)				
DT	05-JUL-2004	(Tremblrel. 27, Last annotation update)				
DE	IGKC protein.					
GN	Name=IGKC;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Glandular pool- thyroid;					
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,					
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Kravinsky M.I., Skalska U., Smailus D.E.,					
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences."					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RL	[2]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Glandular pool- thyroid;					
RG	NIH MGC Project;					
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.					
CC	-I- FUNCTION: Beta-2-microglobulin is the beta-chain of major					
CC	histocompatibility complex class I molecules (by similarity).					
CC	-I- SUBCELLULAR LOCATION: Secreted (by similarity).					
DR	EMBL; BC062732; AAHG2732.1; -; mRNA.					
DR	HSSP; P01837; 1KCU.					
DR	SMR; Q6P5R5; 3-120.					
DR	Ensembl; ENSG00000163245; Homo sapiens.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig.cl.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	Pfam; PF07654; C1-set; I.					

Q7L898	mus musculus
Q52195	mus musculus
Q569Y8	mus musculus
Q6J187	mus musculus
Q58EU4	mus musculus
Q58EU8	mus musculus
Q52164	mus musculus
Q63ZX4	mus musculus
P01837	mus musculus
P01839	oryctolagus
Q569I7	homo sapien
Q61EJ1	oryctolagus
Q61EJ2	oryctolagus
P01840	oryctolagus

```
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immune response; Immunoglobulin domain; MHC I.
SQ SEQUENCE 120 AA; 13153 MW; B42FA2928C5C8F1F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 14 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 73

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 74 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 120

RESULT 2
QSEF66 HUMAN
ID Q5BFE6 HUMAN PRELIMINARY; PRT; 234 AA.
AC Q5BFE6
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 kappa light chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW8207.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light
FT CHAIN chain.
SQ SEQUENCE 234 AA; 25698 MW; 866DDC01E4FDD7D5EA CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 3
Q72473 HUMAN
ID Q72473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q72473
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW8207.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light
FT CHAIN chain.
SQ SEQUENCE 234 AA; 25698 MW; 866DDC01E4FDD7D5EA CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 4
Q6GMV9 HUMAN
ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

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AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW8207.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 128 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 188 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 4
Q6GMV9 HUMAN
ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073793; AAH73793.1; -; mRNA.  
 DR SMR; O6GMW9; 21-235.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCILNPFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 129 RTVAAPSVFIPPPDEQLKSGTASVVCILNPFYPREAKVQWKVDNALQSGNSQESVTEQD 188  
  
 QY 61 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 189 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 235  
  
 RESULT 5  
 Q6GMW0 HUMAN  
 ID Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6GMW0;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE IGKV1-5 protein.  
 GN Name=IGKV1-5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Director MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073792; AAH73792.1; -; mRNA.  
 DR SMR; O6GMW0; 21-233.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG.cl.  
 DR InterPro; IPR003006; IG.MHC.  
 DR InterPro; IPR003596; IG.v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
 SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCILNPFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 DB 129 RTVAAPSVFIPPPDEQLKSGTASVVCILNPFYPREAKVQWKVDNALQSGNSQESVTEQD 188  
  
 QY 61 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
 DB 189 SKDSTYLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 235  
  
 RESULT 6  
 Q6PJF2 HUMAN  
 ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.  
 AC Q6PJF2;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)



Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strauberg R.;  
 RL EMBL; BC016380; AAH16380.1; -; mRNA.  
 DR HSP; P01837; 1KTU.  
 DR SMR; O6PJP2; 21-235.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;  
 Query Match 100.0%; Score 553; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 129 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 188  
 Qy 61 SKDSTYSLSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 107  
 Db 189 SKDSTYSLSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 235

RESULT 7  
 Q6GKX0 HUMAN  
 ID Q6GKX0\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6GKX0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Spleen;  
 RA Strauberg R.;  
 RL EMBL; BC073775; AAH73775.1; -; mRNA.  
 DR SMR; O6GMX0; 23-236.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
 Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189  
 Qy 61 SKDSTYSLSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 107  
 Db 190 SKDSTYSLSTLTLSKADYKHKYKVCVTHQGLSSPVTKSFNRGEC 236

RESULT 8  
 Q6P5S8 HUMAN  
 ID Q6P5S8\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6P5S8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -; mRNA.
DR HSSP; P01837; 1KCX.
DR SMR; Q6P598; 21-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBB4FF5F27 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 190 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 9
ID Q6PIH4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -; mRNA.
DR HSSP; P01607; 1AE2.
DR SMR; Q6PIH4; 23-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 190 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 10
ID Q6PIL8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032451; AAH2451.1; -, mRNA.  
 DR HSSP; P01837; IKCU.  
 DR SMR; Q6PIL8; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60  
 Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 189  
  
 Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 190 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 236  
  
 RESULT 11  
 ID Q6PIT5 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIT5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC029444; AAH29444.1; -, mRNA.  
 DR HSSP; P01607; IAR2.  
 DR SMR; Q6PIT5; 26-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;  
  
 Query Match 100.0%; Score 553; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60  
 Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 189  
  
 Qy 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
 Db 190 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 236  
  
 RESULT 12  
 ID Q7Z3Y4 HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q7Z3Y4;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.

```

[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC TISSUE=Skeletal Muscle;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED21084BC6 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNPFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNPFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSPNRGEC 107
DB 190 SKDSTYLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSPNRGEC 236

RESULT 13
Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC TISSUE=Skeletal Muscle;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNPFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 130 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNPFYPREAKVQWKVDNALQSGNSQESVTEQD 189

QY 61 SKDSTYLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSPNRGEC 107
DB 190 SKDSTYLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSPNRGEC 236

RESULT 14
Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -; mRNA.
DR SMR; Q6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF77 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 190 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 15
Q6GMX8 HUMAN
ID Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS0290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 100.0%; Score 553; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 130 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 189

Qy 61 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 190 SKDSTYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 236

Search completed: January 28, 2006, 09:44:19
Job time : 56.7132 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 09:31:34 ; Search time 15.7447 Seconds  
(without alignments)  
561.857 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPSDEQLKS.....EVTHQGLSSPTVKFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA\*  
1: /cgm2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgm2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgm2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgm2\_6/ptodata/1/iaa/PCITUS COMB.pep.\*  
5: /cgm2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	1	US-08-422-101-8
2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	1	US-08-422-092-8
4	553	100.0	107	1	US-08-788-800-5
5	553	100.0	107	2	US-08-422-093-8
6	553	100.0	107	2	US-08-422-112-8
7	553	100.0	107	2	US-09-301-593-20
8	553	100.0	212	2	US-10-011-125A-5
9	553	100.0	213	2	US-08-630-820-6
10	553	100.0	213	2	US-08-397-411-12
11	553	100.0	213	2	US-09-273-453-6
12	553	100.0	213	2	US-09-996-288-209
13	553	100.0	213	2	US-09-996-288-211
14	553	100.0	213	2	US-09-996-288-213
15	553	100.0	213	2	US-09-996-288-215
16	553	100.0	213	2	US-09-996-288-217
17	553	100.0	213	2	US-09-996-288-219
18	553	100.0	213	2	US-09-996-288-221
19	553	100.0	213	2	US-09-996-288-223
20	553	100.0	213	2	US-09-996-288-225
21	553	100.0	213	2	US-09-996-288-227
22	553	100.0	213	2	US-09-996-288-229
23	553	100.0	213	2	US-09-996-288-231
24	553	100.0	213	2	US-09-996-288-233
25	553	100.0	213	2	US-09-996-288-235
26	553	100.0	213	2	US-09-996-288-237
27	553	100.0	213	2	US-09-996-288-239

28	553	100.0	213	2	US-09-996-288-241	Sequence 241, App
29	553	100.0	213	2	US-09-996-288-243	Sequence 243, App
30	553	100.0	213	2	US-09-996-288-245	Sequence 245, App
31	553	100.0	213	2	US-09-996-288-247	Sequence 247, App
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33	553	100.0	213	2	US-09-996-288-253	Sequence 253, App
34	553	100.0	213	2	US-09-996-288-255	Sequence 255, App
35	553	100.0	213	2	US-09-996-288-257	Sequence 257, App
36	553	100.0	213	2	US-09-996-265-209	Sequence 209, App
37	553	100.0	213	2	US-09-996-265-211	Sequence 211, App
38	553	100.0	213	2	US-09-996-265-213	Sequence 213, App
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41	553	100.0	213	2	US-09-996-265-219	Sequence 219, App
42	553	100.0	213	2	US-09-996-265-221	Sequence 221, App
43	553	100.0	213	2	US-09-996-265-223	Sequence 223, App
44	553	100.0	213	2	US-09-996-265-225	Sequence 225, App
45	553	100.0	213	2	US-09-996-265-227	Sequence 227, App

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5739277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,101  
; FILING DATE: 14-Apr-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 5.7e-57;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSQTASVVCLLNNFYPREAKVQMKVONALSGNSQSVTEQD 60  
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Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-08-422-091-8
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Preeto
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-091-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Preeto
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997

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; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-092-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Qy      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997

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; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-788-800-5

Query Match      100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
   |||||
DB 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
   |||||

RESULT 5
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,093
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-093-8

Query Match      100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
   |||||
DB 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
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RESULT 6
US-08-422-112-8
; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,112
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-112-8

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||
DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
   |||||

QY 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
   |||||
DB 61 SKDSTYSLSSLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
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RESULT 7
US-09-301-593-20
; Sequence 20, Application US/09301593A
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; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-20

Query Match      100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.7e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-011-125A-5
; Sequence 5, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-5

Query Match      100.0%; Score 553; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 9
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US-08-630-820-6
; Sequence 6, Application US/08630820
; Patent No. 6008023
; GENERAL INFORMATION:
; APPLICANT: Oppper, Martin
; APPLICANT: BOSSLET, Klaus
; APPLICANT: CZECH, Joerg
; TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
; TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; NUMBER OF SEQUENCES: 7
; TITLE OF INVENTION: IN E. COLI
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,820
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19513676.4
; FILING DATE: 11-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-820-6

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
```

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/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/397,411
/ FILING DATE: 01-MAR-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/859,583
/ FILING DATE: 27-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 011823-004901
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 213 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-397-411-12

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 11
US-09-273-453-6
/ Sequence 6, Application US/09273453
/ Patent No. 6602688
/ GENERAL INFORMATION:
/ APPLICANT: OPPER, Martin
/ BOSSLER, Klaus
/ CZECH, Joerg
/ TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
/ ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
/ IN E. COLI
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/273,453
/ FILING DATE: 22-Mar-1999
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: 08/630,820
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: GRANADOS, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 18748/306
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 213 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
/ US-09-273-453-6

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 12
US-09-996-288-209
/ Sequence 209, Application US/09996288
/ Patent No. 6818216
/ GENERAL INFORMATION:
/ APPLICANT: Young, James
/ APPLICANT: Scott, Koenig
/ APPLICANT: Leelie, Johnson
/ TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
/ TITLE OF INVENTION: and Treatment
/ FILE REFERENCE: 10271-047-999
/ CURRENT APPLICATION NUMBER: US/09/996,288
/ CURRENT FILING DATE: 2001-11-28
/ NUMBER OF SEQ ID NOS: 259
/ SOFTWARE: Patent In version 3.1
/ SEQ ID NO 209
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-996-288-209

Query Match 100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13
US-09-996-288-211
/ Sequence 211, Application US/09996288
/ Patent No. 6818216
/ GENERAL INFORMATION:
/ APPLICANT: Young, James
/ APPLICANT: Scott, Koenig
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; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-211

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-09-996-288-213
; Sequence 213, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-213

Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-09-996-288-215
; Sequence 215, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
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; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-215
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Query Match      100.0%; Score 553; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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Search completed: January 28, 2006, 09:47:29  
Job time : 15.7447 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:44:35 ; Search time 45.6276 Seconds  
(without alignments)  
979.839 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPPDEQLKS.....EVTHQGLSPVTKSFNRGEC 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_Main:  
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2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	553	100.0	107	3	US-09-811-384-5
3	553	100.0	107	3	US-09-990-586-97
4	553	100.0	107	3	US-09-990-586-99
5	553	100.0	107	4	US-10-121-464-18
6	553	100.0	107	4	US-10-269-805-67
7	553	100.0	107	4	US-10-159-006-20
8	553	100.0	107	4	US-10-310-113-166
9	553	100.0	107	4	US-10-310-113-168
10	553	100.0	107	4	US-10-230-880-97
11	553	100.0	107	4	US-10-230-880-99
12	553	100.0	107	4	US-10-366-709-54
13	553	100.0	107	4	US-10-404-286-5
14	553	100.0	107	4	US-10-656-769-4
15	553	100.0	107	4	US-10-679-620-60
16	553	100.0	107	4	US-10-733-563-112
17	553	100.0	107	5	US-10-815-449-10
18	553	100.0	107	5	US-10-684-957-4
19	553	100.0	107	5	US-10-886-838-8
20	553	100.0	107	5	US-10-822-300-9
21	553	100.0	107	5	US-10-687-118-9
22	553	100.0	107	5	US-10-873-932A-41
23	553	100.0	107	5	US-10-891-658-8
24	553	100.0	107	5	US-10-937-596-29
25	553	100.0	107	5	US-10-893-576-44
26	553	100.0	107	5	US-10-810-881A-40
27	553	100.0	107	5	US-10-981-936-40

28	553	100.0	107	6	US-11-001-980-4	Sequence 4, Appli
29	553	100.0	107	6	US-11-001-980-8	Sequence 8, Appli
30	553	100.0	107	6	US-11-132-143-60	Sequence 60, Appli
31	553	100.0	107	6	US-11-102-403-23	Sequence 23, Appli
32	553	100.0	109	4	US-10-272-899A-12	Sequence 12, Appli
33	553	100.0	109	4	US-10-733-563-116	Sequence 116, Appli
34	553	100.0	134	4	US-10-272-899A-66	Sequence 66, Appli
35	553	100.0	212	4	US-10-011-125-5	Sequence 5, Appli
36	553	100.0	212	4	US-10-320-231A-77	Sequence 77, Appli
37	553	100.0	212	5	US-10-867-506-77	Sequence 77, Appli
38	553	100.0	213	3	US-09-796-848A-38	Sequence 38, Appli
39	553	100.0	213	3	US-09-796-848A-40	Sequence 40, Appli
40	553	100.0	213	3	US-09-796-848A-42	Sequence 42, Appli
41	553	100.0	213	3	US-09-796-848A-44	Sequence 44, Appli
42	553	100.0	213	3	US-09-796-848A-46	Sequence 46, Appli
43	553	100.0	213	3	US-09-796-848A-48	Sequence 48, Appli
44	553	100.0	213	3	US-09-796-848A-50	Sequence 50, Appli
45	553	100.0	213	3	US-09-796-848A-52	Sequence 52, Appli

ALIGNMENTS

RESULT 1  
US-09-301-593-20  
; Sequence 20, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Retig, Wolfgang J.  
; TITLE OF INVENTION: PAD-Specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 107  
; TYPE: PRI  
; ORGANISM: Homo sapiens  
US-09-301-593-20

Query Match	100.0%	Score 553;	DB 3;	Length 107;
Best Local Similarity	100.0%	Pred. No. 1.7e-51;	Mismatches 0;	Indels 0;
Matches 107;	Conservative	0;		Gaps 0;
QY	1	RTVAAPSVFIPPPDEQLKSGTASVVC	LNFPY	PREAKVQWKVDNALQSGNSQESVTEQD 60
Db	1	RTVAAPSVFIPPPDEQLKSGTASVVC	LNFPY	PREAKVQWKVDNALQSGNSQESVTEQD 60
QY	61	SKDSTYLSLSTLTLSKADYEHKHYK	VACVTHQGLSSPVTKSFNRGEC	107
Db	61	SKDSTYLSLSTLTLSKADYEHKHYK	VACVTHQGLSSPVTKSFNRGEC	107

RESULT 2  
US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genentech, Inc.  
;; STREET: 1 DNA Way  
;; CITY: South San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94080  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WinPatIn (Genentech)  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/811,384  
;; FILING DATE: 20-Dec-2000  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/251652  
;; FILING DATE: 17-FEB-2000  
;; APPLICATION NUMBER: 08/788800  
;; FILING DATE: 22-JAN-1997  
;; APPLICATION NUMBER: 60/093038  
;; FILING DATE: 23-JAN-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Love, Richard B.  
;; REGISTRATION NUMBER: 34,659  
;; REFERENCE/DOCKET NUMBER: P1729C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-5530  
;; TELEFAX: 650/952-9881  
;;  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-811-384-5

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
  
Qy 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3  
US-09-990-586-97  
; Sequence 97, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: Description of Artificial Sequence: Antibody  
US-09-990-586-97

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
  
Qy 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4  
US-09-990-586-99  
; Sequence 99, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 99  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-99

Query Match 100.0%; Score 553; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
  
Qy 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
Db 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5  
US-10-121-464-18  
; Sequence 18, Application US/10121464  
; Publication No. US20030103968A1  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim International GmbH  
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies  
; FILE REFERENCE: 1-1203ff  
; CURRENT APPLICATION NUMBER: US/10/121,464  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/283,868  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Antibody  
US-10-121-464-18

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 6

US-10-269-805-67

; Sequence 67, Application US/10269805

; Publication No. US20030124129A1

; GENERAL INFORMATION:

; APPLICANT: OLINER, JONATHAN D.

; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

; FILE REFERENCE: A-722

; CURRENT APPLICATION NUMBER: US/10/269,805

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/328,604

; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-269-805-67

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 7

US-10-159-006-20

; Sequence 20, Application US/10159006

; Publication No. US20030143229A1

; GENERAL INFORMATION:

; APPLICANT: Park, John B.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652-1890002

; CURRENT APPLICATION NUMBER: US/10/159,006

; CURRENT FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 09/301,593

; PRIOR FILING DATE: 1999-04-29

; PRIOR APPLICATION NUMBER: EP 98107925.4

; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: US 60/086,049

; PRIOR FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-159-006-20

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 8

US-10-310-113-166

; Sequence 166, Application US/10310113

; Publication No. US20030176664A1

; GENERAL INFORMATION:

; APPLICANT: JIAO, JIN-AN

; APPLICANT: WONG, HING C.

; APPLICANT: NIEVES, ESPERANZA LILIANA

; APPLICANT: MOSQUERA, LUIS A.

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

; FILE REFERENCE: 58122(71758)

; CURRENT APPLICATION NUMBER: US/10/310,113

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 09/990,586

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/343,306

; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: 09/293,854

; PRIOR FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: 08/814,806

; NUMBER OF SEQ ID NOS: 169

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 166

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-310-113-166

Query Match 100.0%; Score 553; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-51;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

DB 1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTTQD 60

QY 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

## RESULT 9

US-10-310-113-168

; Sequence 168, Application US/10310113

; Publication No. US20030176664A1

; GENERAL INFORMATION:

; APPLICANT: JIAO, JIN-AN

; APPLICANT: WONG, HING C.

; APPLICANT: NIEVES, ESPERANZA LILIANA

; APPLICANT: MOSQUERA, LUIS A.

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

; FILE REFERENCE: 58122(71758)

; CURRENT APPLICATION NUMBER: US/10/310,113

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 09/990,586

; PRIOR FILING DATE: 2001-11-21



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; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 10
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 11
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
```

```
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 12
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Query Match      100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 13
US-10-404-286-5
; Sequence 5, Application US/10404286
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Publication No. US20040057951A1  
GENERAL INFORMATION:  
APPLICANT: Bednar, Martin M.  
Thomas, G. Roger  
Gross, Cordell E.  
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/404,286  
FILING DATE: 31-Mar-2006  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/811384  
FILING DATE: 20-DEC-2000  
APPLICATION NUMBER: 09/251652  
FILING DATE: 17-FEB-2000  
APPLICATION NUMBER: 08/788800  
FILING DATE: 22-JAN-1997  
APPLICATION NUMBER: 60/093038  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, David W.  
REGISTRATION NUMBER: NONE  
REFERENCE/DOCKET NUMBER: P1729C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1739  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-404-286-5

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 14  
US-10-656-769-4  
Sequence 4, Application US/10656769  
Publication No. US20040097712A1  
GENERAL INFORMATION:  
APPLICANT: Varnum, Brian  
APPLICANT: Witte, Allison  
APPLICANT: Vezina, Chris  
APPLICANT: Wong, Lu Min  
APPLICANT: Qian, Xueming  
TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody  
FILE REFERENCE: 01,1554  
CURRENT APPLICATION NUMBER: US/10/656,769

CURRENT FILING DATE: 2003-09-05  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-656-769-4

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 15  
US-10-679-620-60  
Sequence 60, Application US/10679620  
Publication No. US20040110930A1  
GENERAL INFORMATION:  
APPLICANT: Large Scale Biology  
APPLICANT: Reiml, Stephen J.  
APPLICANT: Edwards, Patricia C.  
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
FILE REFERENCE: 34150-004A  
CURRENT APPLICATION NUMBER: US/10/679,620  
CURRENT FILING DATE: 2003-10-03  
PRIOR APPLICATION NUMBER: 60/415,940  
PRIOR FILING DATE: 2002-10-03  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 60  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: huscFabmlA6, see Example 15  
US-10-679-620-60

Query Match 100.0%; Score 553; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
DB 1 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
DB 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

Search completed: January 28, 2006, 10:11:23  
Job time : 45.6276 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 09:45:45 ; Search time 6.42643 Seconds  
(without alignments)  
180.304 Million cell updates/sec

Title: US-10-733-563-112  
Perfect score: 553  
Sequence: 1 RTVAAPSVFIPPSDEQLKS.....EVTHQGLSSPVTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	6	US-10-999-866-40
2	553	100.0	107	6	US-10-886-383-8
3	553	100.0	107	6	US-10-988-207-21
4	553	100.0	107	7	US-11-025-712-5
5	553	100.0	107	7	US-11-075-351-61
6	553	100.0	107	7	US-11-061-821-40
7	553	100.0	107	7	US-11-102-621-9
8	553	100.0	110	7	US-11-024-251-27
9	553	100.0	213	7	US-11-172-320-8
10	553	100.0	213	7	US-11-172-320-8
11	553	100.0	213	7	US-11-174-186-42
12	553	100.0	213	7	US-11-120-338-13
13	553	100.0	213	7	US-11-120-338-16
14	553	100.0	213	7	US-11-173-969-4
15	553	100.0	213	7	US-11-173-969-8
16	553	100.0	213	7	US-11-102-621-118
17	553	100.0	213	7	US-11-102-621-135
18	553	100.0	213	7	US-11-107-028-31
19	553	100.0	213	7	US-11-107-028-44
20	553	100.0	213	7	US-11-106-820-24
21	553	100.0	213	7	US-11-106-820-29
22	553	100.0	213	7	US-11-106-820-44
23	553	100.0	213	7	US-11-158-505-34
24	553	100.0	214	7	US-11-025-712-11
25	553	100.0	214	7	US-11-094-625-9

26	553	100.0	214	7	US-11-102-621-129	Sequence 129, App
27	553	100.0	214	7	US-11-128-900-71	Sequence 71, Appl
28	553	100.0	214	7	US-11-154-337-14	Sequence 14, Appl
29	553	100.0	214	7	US-11-154-337-16	Sequence 16, Appl
30	553	100.0	215	7	US-11-102-621-141	Sequence 141, App
31	553	100.0	215	7	US-11-166-906-2	Sequence 2, Appl
32	553	100.0	218	6	US-10-923-327-6	Sequence 6, Appl
33	553	100.0	218	6	US-10-923-327-8	Sequence 8, Appl
34	553	100.0	218	6	US-10-923-327-10	Sequence 10, Appl
35	553	100.0	218	6	US-10-923-327-12	Sequence 12, Appl
36	553	100.0	218	6	US-10-923-327-17	Sequence 17, Appl
37	553	100.0	218	7	US-11-084-554-11	Sequence 11, Appl
38	553	100.0	218	7	US-11-158-505-4	Sequence 4, Appl
39	553	100.0	218	7	US-11-158-505-28	Sequence 28, Appl
40	553	100.0	218	7	US-11-004-590-229	Sequence 229, App
41	553	100.0	219	7	US-11-080-587-8	Sequence 8, Appl
42	553	100.0	232	7	US-11-106-820-23	Sequence 23, Appl
43	553	100.0	233	7	US-11-128-900-15	Sequence 15, Appl
44	553	100.0	233	7	US-11-128-900-67	Sequence 67, Appl
45	553	100.0	234	7	US-11-128-900-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-10-999-866-40  
; Sequence 40, Application US/10999866  
; Publication No. US20050266004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CEN5042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 40  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(107)  
; OTHER INFORMATION: Light chain kappa constant region (IgKc)  
US-10-999-866-40

Query Match	100.0%	Score 553;	DB 6;	Length 107;
Best Local Similarity	100.0%	Pred. No. 1.3e-51;		
Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	RTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEQD	60	
Db	1	RTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALSGNSQESVTEQD	60	
QY	61	SKDSTYSLSSTLTLSKADYERKHVYACVTHQGLSSPVTKSPNRGEC	107	
Db	61	SKDSTYSLSSTLTLSKADYERKHVYACVTHQGLSSPVTKSPNRGEC	107	

RESULT 2  
US-10-886-383-8  
; Sequence 8, Application US/10886383  
; Publication No. US20060005571A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffmann-La Roche Inc.  
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses  
; FILE REFERENCE: 21695  
; CURRENT APPLICATION NUMBER: US/10/886,383  
; CURRENT FILING DATE: 2004-07-08

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; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-8

Query Match      100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107

RESULT 3
US-10-988-207-21
; Sequence 21, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988.207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 21
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab TGN1412 constant region light chain
US-10-988-207-21

Query Match      100.0%; Score 553; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107

RESULT 4
US-11-025-712-5
; Sequence 5, Application US/11025712
; Publication No. US2005025108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-DEC-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-025-712-5

Query Match      100.0%; Score 553; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107

RESULT 5
US-11-075-351-61
; Sequence 61, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-61

Query Match      100.0%; Score 553; DB 7; Length 107;
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Best Local Similarity 100.0%; Pred. No. 1.3e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPRKAYQWKVDNALQSGNSQESVTEQD 60  
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Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPRKAYQWKVDNALQSGNSQESVTEQD 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 SKDSTYSLSSLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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Db 61 SKDSTYSLSSLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 6  
US-11-061-821-40  
; Sequence 40, Application US/11061821  
; Publication No. US20050266005A1  
; GENERAL INFORMATION:  
; APPLICANT: Heavtex, George; Li, Li; Oneil, Karyn  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES  
; FILE REFERENCE: CEN5048 NP  
; CURRENT APPLICATION NUMBER: US/11/061,821  
; PRIOR FILING DATE: 2005-02-18  
; PRIOR APPLICATION NUMBER: 60/549,648  
; PRIOR FILING DATE: 2004-02-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver 3.3  
; SEQ ID NO 40  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(107)  
; OTHER INFORMATION: Light chain kappa constant region (IgKc)

US-11-061-821-40

Query Match 100.0%; Score 553; DB 7; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.3e-51;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RTVAAPSVFIPPPSDEQLKSGTASVVCILNNFYPRKAYQWKVDNALQSGNSQESVTEQD 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 SKDSTYSLSSLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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Db 61 SKDSTYSLSSLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 7  
US-11-102-621-9  
; Sequence 9, Application US/11102621  
; Publication No. US20050276799A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs, Inc.  
; APPLICANT: Hinton, Paul R.  
; APPLICANT: Teurushita, Naoya  
; APPLICANT: Tec, J. Yun  
; APPLICANT: Vasquez, Maximiliano  
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF  
; FILE REFERENCE: ANTIBODIES BY MUTAGENESIS  
; CURRENT APPLICATION NUMBER: US/11/102,621  
; PRIOR FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: US 10/822,300  
; PRIOR FILING DATE: 2004-04-09  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-11-172-320-4

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 10
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172.320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-11-172-320-8

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
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; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 12
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-13

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 213

RESULT 13
US-11-120-338-16
; Sequence 16, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
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; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-16

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
US-11-173-969-4
; Sequence 4, Application US/11/173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-11-173-969-4

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-11-173-969-8
; Sequence 8, Application US/11/173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates

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; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: 8
US-11-173-969-8

Query Match      100.0%; Score 553; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: January 28, 2006, 10:12:15
Job time : 6.42643 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p\_model

Run on: January 28, 2006, 08:12:21 ; Search time 50.1261 seconds  
(without alignments)  
5627.428 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564  
Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1.624 @runat\_27012006\_180005\_4773 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 21.\*

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2: Geneseqp1990a:\*  
3: Geneseqp2000a:\*  
4: Geneseqp2001a:\*  
5: Geneseqp2002a:\*  
6: Geneseqp2003a:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004a:\*  
9: Geneseqp2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	553	98.0	107	2 AAW40578	Human kap
2	553	98.0	107	2 AAY50152	Human kap
3	553	98.0	107	2 AAW92425	Human kap
4	553	98.0	107	2 AAY08745	Human kap
5	553	98.0	107	3 AAB27000	Human kap
6	553	98.0	107	5 AAG31883	Human kap
7	553	98.0	107	6 ABB98755	Human kap
8	553	98.0	107	6 ABR42732	Anti-tiss
9	553	98.0	107	6 ABR42734	Anti-tiss

10	553	98.0	107	6 ABR55835	Anti-Ang-
11	553	98.0	107	7 ADJ94622	Human kap
12	553	98.0	107	8 ADJ77161	Anti-VAP-
13	553	98.0	107	8 ADL35096	Human IGG
14	553	98.0	107	8 ADL35094	Human IGG
15	553	98.0	107	8 ADM41539	Anti-inte
16	553	98.0	107	8 ADK18336	Amino aci
17	553	98.0	107	8 ADN97487	Artificia
18	553	98.0	107	8 ADQ89334	Human inm
19	553	98.0	107	8 ADS87911	Anti-IFN-
20	553	98.0	107	8 ADS94908	Anti-IFN-
21	553	98.0	107	8 ADT88871	Human IGG
22	553	98.0	107	8 ADT51583	Light cha
23	553	98.0	107	8 ADU68013	Mouse ant
24	553	98.0	107	9 ADW08870	IGF-IR an
25	553	98.0	107	9 ADW07454	Human kap
26	553	98.0	107	9 ADW24748	Variable
27	553	98.0	107	9 ADW24790	Variable
28	553	98.0	107	9 ADX98272	Human ant
29	553	98.0	107	9 ADY26693	Human ant
30	553	98.0	107	9 ADY74804	Human lig
31	553	98.0	107	9 ADZ08815	Mammalian
32	553	98.0	107	9 ADZ08946	Amyloid a
33	553	98.0	107	9 ADZ44472	Human inm
34	553	98.0	107	9 AEA25951	Human inm
35	553	98.0	107	9 AEA16547	Human MCP
36	553	98.0	107	9 AEA45321	Apolipop
37	553	98.0	107	9 AEA45323	Apolipop
38	553	98.0	107	9 AEA37411	Anti-huma
39	553	98.0	107	9 AEA37415	Anti-huma
40	553	98.0	107	9 AEB09607	Human C k
41	553	98.0	107	9 AEB2782	Anti-Ltal
42	553	98.0	108	8 ADL22765	Human ant
43	553	98.0	108	8 ADW15047	Human fab
44	553	98.0	108	9 AEA52525	Human ant
45	553	98.0	109	8 ADJ95916	Human kap

ALIGNMENTS

RESULT 1

AAW40578

ID AAW40578 standard; protein; 107 AA.

XX AAW40578;

XX 21-JUL-1998 (first entry)

XX Human kappa CL domain protein fragment.

XX Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;  
XX disorder; salvage receptor binding epitope; cell adherence interaction;  
XX lymphocyte; T cell inflammatory response.

XX Homo sapiens.

XX US5739277-A.

XX 14-APR-1998.

XX 14-APR-1995; 95US-00422101.

XX 14-APR-1995; 95US-00422101.

XX (GETH ) GENENTECH INC.

XX Snedecor BR, Presta LG;

XX WPI; 1998-250490/22.

XX Polypeptide(s) that are not Fc fragments and have an increased half-life  
XX - are useful for the treatment of LFA-1 mediated disorders.

PS Disclosure; Fig 2; 38pp; English.

XX This protein fragment is derived from a human immunoglobulin kappa CL  
CC domain and is used to describe a novel method to produce polypeptides  
CC which contain an epitope from the FC region of an IgG molecule and a  
CC mutated salvage receptor binding epitope. They are useful for the  
CC treatment of LPA-1 mediated disorders. These are conditions caused by  
CC cell adherence interactions involving the LPA-1 receptor on lymphocytes,  
CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence  
CC in the polypeptides means that they have increased in vivo circulatory  
CC half-lives when compared to normal FC regions of IgG molecules  
XX  
SQ Sequence 107 AA;

Alignment Scores:  
Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x AAW40578 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACGAGTTGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAAsnAAsnPheTyProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATACCGCTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 41 TrpLysValAspAAsnAlaLeuGlnSerGlyAAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGCACCCTACAGCTCAGCAGCAGCCCTGAGCAAGAGCAGCTACAGAG 240  
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 80  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 2

AA50152  
ID AAY50152 standard; protein; 107 AA.

XX  
AC AAY50152;  
XX  
XX  
DT 31-JAN-2000 (first entry)  
XX  
DE Human kappa light chain constant region.

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
KW humanisation; complementarity determining region; CDR; CDR grafting;  
KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;  
KW immune response; framework sequence; constant region; variable region;  
KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;  
KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;  
KW skin inflammation; tumour; immunogenicity; light chain.

OS Homo sapiens.

XX EP953639-A1.

XX 03-NOV-1999.

XX 30-APR-1998; 98EP-00107925.

XX  
PR 30-APR-1998; 98EP-00107925.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
PI Park JB, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
PI Rettig WJ;  
XX  
DR WPI; 1999-621833/54.  
DR N-PSDB; AAZ32777.  
XX  
PT New antibody protein, useful for treating cancer and for imaging presence  
PT of activated stromal fibroblasts in healing wound or inflamed skin.  
XX  
PS Disclosure; Fig 20; 143pp; English.

XX This sequence represents a human kappa light chain, the cDNA of which was  
CC used in the construction of a nucleotide encoding the light chain of a  
CC human reshaped monoclonal antibody F19. F19 (ATCC Accession number HB  
CC 8259) is a murine monoclonal antibody against fibroblast activation  
CC protein alpha (FAP). FAP is a cell surface molecule of reactive stromal  
CC fibroblasts, and its induction is a highly consistent molecular trait of  
CC the reactive stroma of many types of epithelial cancer. Although F19 may  
CC be useful in vitro, e.g., for diagnosis, its applications for in vivo use  
CC in humans are problematic as it elicits a human anti-mouse response which  
CC reduces the efficacy of the antibody in patients and impairs continued  
CC administration. The novel human reshaped F19 was humanised by grafting  
CC the murine complementarity determining regions (CDRs) of F19 onto human  
CC variable region framework sequences, and then joining these "reshaped  
CC human" variable regions to human constant regions. These modifications  
CC also result in the improved producibility in eukaryotic cell culture  
CC systems as compared to a chimeric antibody having the entire variable  
CC regions of F19 joined to a human constant regions. The human reshaped F19  
CC antibody has low immunogenicity for humans and is useful for treating  
CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast  
CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder  
CC cancers, pancreatic cancers and metastatic cancers. It is also useful for  
CC the detection of activated stromal fibroblasts in a healing wound,  
CC inflamed skin or a tumour in a human patient  
XX

SQ Sequence 107 AA;

Alignment Scores:

Pred. No.: 4.93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x AAY50152 (1-107)

Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGACGAGTTGAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAAsnAAsnPheTyProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATACCGCTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 41 TrpLysValAspAAsnAlaLeuGlnSerGlyAAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGCACCCTACAGCTCAGCAGCAGCCCTGAGCAAGAGCAGCTACAGAG 240  
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 80  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGAGAGTGT 321

Db 101 SerPheAsnArgGlyGluCys 107  
|||||  
RESULT 3  
AAW92425  
ID AAW92425 standard; peptide; 107 AA.  
XX  
AC AAW92425;  
XX  
DT 23-APR-1999 (first entry)  
XX  
DE Human Kappa protein CL domain.  
XX  
KW Antibody; salvage receptor binding epitope; Fab; F(ab')<sub>2</sub>; immunoglobulin;  
KW CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IgG;  
KW kappa protein; renal clearance rate; circulatory half-life.  
XX  
OS Homo sapiens.  
XX  
PN US5869046-A.  
XX  
PD 09-FEB-1999.  
XX  
PF 14-APR-1995; 95US-00422092.  
XX  
PR 14-APR-1995; 95US-00422092.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Presta LG, Snedecor BR;  
XX  
DR WPI; 1999-152694/13.  
XX  
PT Production of antibody fragments with reduced renal clearance - by  
PT introducing salvage receptor binding epitope into CH1 or CL region.  
XX  
PS Disclosure; Col 55-58; 38pp; English.  
XX  
CC This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub>  
CC polypeptide having increased half-life in vivo, where the polypeptide  
CC contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is  
CC cleared from the kidneys and does not contain an IgG Fc region. The  
CC method involves altering the polypeptide within the CH1 or CL region to  
CC incorporate a salvage receptor binding epitope taken from two loops of a  
CC CH2 domain of an IgG Fc region. The polypeptides have a reduced renal  
CC clearance rate and an increased circulatory half-life. This sequence  
CC represents a human kappa protein CL domain used in the method of the  
CC invention  
XX  
SQ Sequence 107 AA;  
Alignment Scores:  
Pred. No.: 4,930-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x AAW92425 (1-107)  
Qy 1 CGTAGCGTGCTGCACCATCTGTCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAATGCTCTGTGTGTGCTGTGATTAATCTTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 40  
Qy 121 TGGAGGTGGATTAACGCTCCATCCGTTAACTCCAGGAGAGTGTCACAGAGCAGAC 180  
Db 41 TrpLysValAspAsnAlaGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60

Qy 181 AGCAAGGACAGCAGCCTACAGCCTCAGCAGCAGCCCTGACCTGAGCAAGAGCAGCAGTACGAG 240  
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 80  
Qy 241 AAACACAAAGTCTAGCCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300  
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107  
RESULT 4  
AAW08745  
ID AAW08745 standard; protein; 107 AA.  
XX  
AC AAW08745;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human Kappa-CL domain.  
XX  
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;  
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
KW antibody.  
XX  
OS Homo sapiens.  
XX  
PN US5914112-A.  
XX  
PD 22-JUN-1999.  
XX  
PF 22-JAN-1997; 97US-00788800.  
XX  
PR 23-JAN-1996; 96US-0093038P.  
XX  
PA (GETH ) GENENTECH INC.  
PA (UYVB-) UNIV VERMONT & STATE AGRIC COLLEGE.  
XX  
PI Thomas GR, Bednar MM, Gross CB;  
XX  
DR WPI; 1999-370483/31.  
XX  
PT Anti-CD18 antibodies in stroke.  
XX  
PS Disclosure; Fig 4A-B; 25pp; English.  
XX  
CC This invention describes a method for improving the clinical outcome in  
CC focal ischaemic stroke by administering novel anti-CD18 antibody which  
CC has cerebroprotective properties. The invention particularly describes a  
CC method of treating focal ischaemic stroke caused by the obstruction of a  
CC main cerebral artery which comprises administering an anti-CD18 antibody  
CC to increase the blood flow or reduce the infarct size, where: (1) the  
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
CC antibody dissociates CD18/CD18 complex. This sequence represents the  
CC human Kappa-CL domain which is used to illustrate the method of the  
CC invention  
XX  
SQ Sequence 107 AA;  
Alignment Scores:  
Pred. No.: 4,930-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x AAW08745 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGACGAGTTCGAATCT 60  
 Db |||||  
 QY 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
 Db |||||  
 QY 61 GGAACCTGCCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db |||||  
 QY 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
 Db |||||  
 QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
 Db |||||  
 QY 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 Db |||||  
 QY 181 AGCAAGGACAGACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGCAGATACGAG 240  
 Db |||||  
 QY 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
 Db |||||  
 QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGSCCTGAGCTCCGCCGTCCACAAG 300  
 Db |||||  
 QY 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 Db |||||  
 QY 301 AGCTTCAACAGGGGAGAGTGT 321  
 Db |||||  
 QY 101 SerPheAsnArgGlyGluCys 107  
 Db |||||

RESULT 5  
 AAB27000  
 ID AAB27000 standard; protein; 107 AA.  
 XX  
 AC AAB27000;  
 XX  
 DT 25-JAN-2001 (first entry)  
 XX  
 DE Human kappa CL domain.  
 XX  
 KW Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;  
 KW mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;  
 KW psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;  
 KW inflammation; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6121022-A.  
 XX  
 PD 19-SEP-2000.  
 XX  
 PF 14-APR-1995; 95US-00422112.  
 XX  
 PR 14-APR-1995; 95US-00422112.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Presta LG, Snedecor BR;  
 XX  
 DR WPI; 2000-610925/58.  
 XX  
 FT New nucleic acid encoding new modified polypeptides with increased  
 FT circulatory half-life useful for preventing/treating LFA-1-mediated  
 FT disorders, e.g. reducing inflammatory responses or inducing tolerance to  
 FT immunostimulants.  
 XX  
 PS Disclosure; Fig 2; 38pp; English.  
 XX

The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an Fc region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They

CC may also be used in diagnostic assays. The nucleic acids and modified  
 CC polypeptides are useful for the passive immunisation of patients, as well  
 CC as for affinity purification of an antigen from recombinant cell culture  
 CC or natural sources  
 XX  
 SQ Sequence 107 AA;  
 Alignment Scores:  
 Pred. No.: 4.93e-55 Length: 107  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: Gaps: 0  
 US-10-733-563-113 (1-321) x AAB27000 (1-107)  
 QY 1 CGTACGGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGACGAGTTCGAATCT 60  
 Db |||||  
 QY 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
 Db |||||  
 QY 61 GGAACCTGCCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 Db |||||  
 QY 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
 Db |||||  
 QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
 Db |||||  
 QY 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
 Db |||||  
 QY 181 AGCAAGGACAGACCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGAGCAGATACGAG 240  
 Db |||||  
 QY 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
 Db |||||  
 QY 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCATCAGGSCCTGAGCTCCGCCGTCCACAAG 300  
 Db |||||  
 QY 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 Db |||||  
 QY 301 AGCTTCAACAGGGGAGAGTGT 321  
 Db |||||  
 QY 101 SerPheAsnArgGlyGluCys 107  
 Db |||||

RESULT 6  
 ABG31883  
 ID ABG31883 standard; protein; 107 AA.  
 XX  
 AC ABG31883;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Human kappa CL domain.  
 XX  
 KW Human; kappa CL domain; cerebral blood flow; infarct size;  
 KW focal ischaemic stroke; main cerebral artery;  
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;  
 KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002081294-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 20-DEC-2000; 2000US-00811384.  
 XX  
 PR 23-JAN-1996; 96US-0093038P.  
 XX  
 PR 22-JAN-1997; 97US-00788800.  
 XX  
 PR 17-FEB-1999; 99US-00251652.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bednar MM, Gross CB, Thomas GR, Gross LJ;  
 XX  
 DR WPI; 2002-626528/67.





```
ABR42732
ID ABR42732 standard; protein; 107 AA.
XX
AC ABR42732;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-tissue factor humanized antibody light chain constant region.
XX
KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW antiinflammatory; mouse; human; hOAT.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FN WO2003037911-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034727.
XX
PR 29-OCT-2001; 2001US-0343306P.
PR 21-NOV-2001; 2001US-00990586.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
DR WPI; 2003-468399/44.
XX
PT New humanized antibody that binds specifically to human tissue factor,
PT useful for in vivo diagnostic methods, or for inhibiting blood
PT coagulation or blood clot formation, angiogenesis, tumor metastases or
PT inflammation in a mammal.
XX
PS Example 10; Fig 14A; 110pp; English.
XX
CC The present sequence is the protein sequence of the light chain constant
CC region of anti-human tissue factor (TF) humanized antibody hOAT
CC (humanised ch36-IgG1). Humanized antibodies of the invention provide
CC superior anticoagulant activity by binding native human TF with high
CC affinity and specificity. The antibodies bind human TF, either alone or
CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
CC Factor IX) binding to TF or the complex, and thereby reducing blood
CC coagulation. The humanized antibodies are useful for inhibiting blood
CC coagulation or blood clot formation, angiogenesis, tumour metastases or
CC inflammation in a mammal. They are also useful as drug carriers, as
CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
CC diagnosis
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 6 Gaps: 0

US-10-733-563-113 (1-321) x ABR42732 (1-107)
QY 1 CGTAGGGTGGACCATCTGTCTTCATCTCCGCCATCTGATGACAGTTGAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
QY 61 GGAAGTGGTGTGTGTGCTGCTGAATCACTTCTATCCAGAGGCCAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAnPheYrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAAGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCCACAGAGCAGGAC 180
Db 121 TGGAGGTGGATAAGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCCACAGAGCAGGAC 180

Db 41 TrpLysValAspAsnAlaLeuGlnSerClyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCGACCTTGAGCAAGACGACTTACCAG 240
Db 61 SerLysAspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrrGlu 80
QY 241 AAACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCTCACAAAG 300
Db 81 LysHisLysValTyrrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 9
ABR42734
ID ABR42734 standard; protein; 107 AA.
XX
AC ABR42734;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-tissue factor humanized antibody light chain constant region.
XX
KW Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW antiinflammatory; mouse; human; hOAT.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FN WO2003037911-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034727.
XX
PR 29-OCT-2001; 2001US-0343306P.
PR 21-NOV-2001; 2001US-00990586.
XX
PA (SUNO-) SUNOL MOLECULAR CORP.
XX
PI Jiao J, Wong HC, Nieves EL, Mosquera LA;
DR WPI; 2003-468399/44.
XX
PT New humanized antibody that binds specifically to human tissue factor,
PT useful for in vivo diagnostic methods, or for inhibiting blood
PT coagulation or blood clot formation, angiogenesis, tumor metastases or
PT inflammation in a mammal.
XX
PS Example 10; Fig 15A; 110pp; English.
XX
CC The present sequence is the protein sequence of the light chain constant
CC region of anti-human tissue factor (TF) humanized antibody hFAT
CC (humanised ch36-IgG4). Humanized antibodies of the invention provide
CC superior anticoagulant activity by binding native human TF with high
CC affinity and specificity. The antibodies bind human TF, either alone or
CC present in a TF:Factor VIIa complex, effectively preventing Factor X (or
CC Factor IX) binding to TF or the complex, and thereby reducing blood
CC coagulation. The humanized antibodies are useful for inhibiting blood
CC coagulation or blood clot formation, angiogenesis, tumour metastases or
CC inflammation in a mammal. They are also useful as drug carriers, as
CC cytotoxic agents, for reducing TF levels in mammals, and for in vivo
CC diagnosis
XX
SQ Sequence 107 AA;

Alignment Scores:
Pred. No.: 4.93e-55 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Mismatches: 0
```

Query Match: 98.05% Indels: 0  
DB: 6 Gaps: 0  
US-10-733-563-113 (1-321) x ABR42734 (1-107)  
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTCCAGAGCAGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAGGAGCAGCAGCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCCATCAGGCGCTGAGCTCGCCCGTCAAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107  
RESULT 10  
ABR55835  
ID ABR55835 standard; protein; 107 AA.  
AC ABR55835;  
XX  
XX  
DT 02-SEP-2003 (first entry)  
DE Anti-Ang-2 antibody kappa constant region.  
KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
KW angiogenesis; antibody.  
XX  
XX Homo sapiens.  
XX  
XX WO2003030833-A2.  
XX  
XX 17-APR-2003.  
XX  
XX 11-OCT-2002; 2002WO-US032613.  
XX  
XX 11-OCT-2001; 2001US-0328604P.  
XX 10-OCT-2002; 2002US-00269805.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Oliner JD;  
XX  
XX WPI; 2003-504963/47.  
XX  
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
XX for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
XX hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
XX  
XX Example 4; Page 96; 161pp; English.  
XX  
XX The invention relates to a specific binding agent, which comprises at  
XX least one peptide selected from any of 62 peptides (ABR55769-830) or its  
XX fragment. The binding agents are antibodies that recognize and bind to  
XX angiotensin-2 (Ang-2). The specific binding agent, particularly the  
XX antibody, is useful for inhibiting undesired angiogenesis, treating  
XX cancer, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
XX 2 activity, modulating vascular permeability or plasma leakage, or

CC treating a disease (e.g. ocular neovascular disease, obesity,  
CC haemangioma, haemangioma, arteriosclerosis, inflammatory disease,  
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
CC disease, bone-related disease, or psoriasis) in a mammal. The present  
CC sequence represents a human kappa constant region of an anti-Ang-2  
CC antibody  
XX  
SQ Sequence 107 AA;  
Alignment Scores: 4.93e-55 Length: 107  
Pred. No.: 553.00 Matches: 107  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 98.05% Gaps: 0  
DB: 6  
US-10-733-563-113 (1-321) x ABR55835 (1-107)  
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCAACTCGGTAACTCCAGGAGAGTGTCCAGAGCAGAC 180  
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAGGAGCAGCAGCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCCATCAGGCGCTGAGCTCGCCCGTCAAAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAsnArgGlyGluCys 107  
RESULT 11  
ADJ94622  
ID ADJ94622 standard; protein; 107 AA.  
XX  
XX AC ADJ94622;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human kappa chain (CK) constant region.  
XX  
XX humanised anti-CD20 monoclonal antibody; hCD20 monoclonal antibody; MAb;  
XX IV1AB variable region; B-cell lymphoma; leukaemia; autoimmune disease;  
XX thrombocytopenia; lupus; rheumatoid arthritis; kappa chain; human; CK;  
XX constant region.  
XX  
XX Homo sapiens.  
XX  
XX WO2003068821-A2.  
XX  
XX 21-AUG-2003.  
XX  
XX 14-FEB-2003; 2003WO-GB000665.  
XX  
XX 14-FEB-2002; 2002US-0356132P.  
XX 07-OCT-2002; 2002US-0416232P.  
XX  
XX (IMMU-) IMMUNOMEDICS INC.  
XX (MCCA/) MCCA J D.  
XX  
XX Hansen H, Qu Z, Goldenberg DM;

XX WPI; 2003-697522/66.  
DR N-PSDB; ADJ94621.  
XX  
XX  
PT New humanized anti-CD20 monoclonal antibody (MAb) that retains  
PT substantially the B-cell and B-cell lymphoma and leukemia cell targeting  
PT of the murine anti-CD20 MAB, useful for treating B-cell lymphoma,  
PT leukemia or an autoimmune diseases.  
XX  
XX Example 1; Fig 7B; 106pp; English.  
XX  
CC The invention comprises a humanised anti-CD20 (hCD20) monoclonal antibody  
CC (MAb) or its antigen-binding fragment containing the complementarity  
CC determining regions (CDRs) of at least one murine anti-CD20 MAB variable  
CC region and the framework regions (FRs) of at least one human IV1AB  
CC variable region. The antibodies of the invention are useful for  
CC diagnosing or preventing B-cell lymphoma, leukaemia or an autoimmune  
CC disease (e.g. thrombocytopenia, lupus or rheumatoid arthritis). The  
CC present amino acid sequence represents a human kappa chain (CK) constant  
CC region.  
XX  
XX Sequence 107 AA;  
SQ

Alignment Scores:  
Pred. No.: 4,93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x ADJ94622 (1-107)

QY 1 CGTACGGTGGCGACCACTCTCTTCATCTTCCCGCATCTGATGACGAGTTCGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCCTCTGTGTGTGCTGCTGTAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGATAAGCCCTCCCAATCGGTGTAATCTCCAGGAGAGTGTACAGACGAGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGCAGCAGCACCTACAGCCTCAGCAGCACCTGACCTGAGCAGCAAGCAGACTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCCCTGCGAAGTGCACCCATCAGGGCCTGAGCTGCCCGTCCACAAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 12  
ADF77161  
ID ADF77161 standard; protein; 107 AA.  
XX  
XX ADF77161;  
XX  
XX  
DT 26-FEB-2004 (first entry)  
XX  
XX  
DE Anti-VAP-1 monoclonal antibody L chain constant region.  
XX  
XX complementarity determining region; CDR; mouse;  
XX Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;  
XX chimeric; inflammatory disorder; rheumatoid arthritis;  
XX inflammatory bowel disease; autoimmune disease; psoriasis;  
XX immunoscintigraphic imaging.  
XX

AC ADL35096;  
 DT 03-JUN-2004 (first entry)  
 DE Human IgG4 (hFAT) kappa light chain constant domain protein SeqID 99.  
 KW antibody; variable domain; framework region; FR; huFR;  
 KW immune system molecule; kappa; anti-tissue factor; hFAT; human.  
 OS Homo sapiens.  
 PN WO2004020579-A2.  
 XX 11-MAR-2004.  
 XX 06-AUG-2003; 2003WO-US024637.  
 PR 29-AUG-2002; 2002US-00230880.  
 XX (SUNO-) SUNOL MOLECULAR CORP.  
 PA Wong HC, Stinson JR, Mosquera LA;  
 PI WPI; 2004-239169/22.  
 DR  
 XX Producing humanized antibodies for diagnostic and therapeutic purposes  
 PT comprises optimizing similarity between individual antibody framework  
 PT regions to help identify human framework regions suitable for making the  
 PT antibodies.  
 XX Disclosure; SEQ ID NO 99; 137pp; English.  
 XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all  
 CC humanised immune system molecules of interest. This polypeptide sequence  
 CC is the human IgG4 kappa light chain constant domain protein of the  
 CC invention.  
 XX Sequence 107 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 4.93e-55 Length: 107  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-733-563-113 (1-321) x ADL35096 (1-107)  
 QY 1 CGTACGGTGGCTGCACCATCTCTCTTCATCTCCGCCATCTGATGCGAGTTGAATCT 60  
 DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLysSer 20  
 QY 61 GGAACCTGCTCTGTGTGTGCTGCTGCTGAATACCTTCTATCCAGAGAGGCCAAAGTACAG 120  
 DB 21 GlyThrAlaSerValValCysLeuLeuAnanPheTyrProArgGluAlaLysValGln 40  
 QY 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAATCTCCAGAGAGAGTGTCCAGAGCAGAC 180  
 DB 121 TGGAAAGTGGATAACGCCCTCCAAATCGGGTAATCTCCAGAGAGAGTGTCCAGAGCAGAC 180

DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThrGluGlnAsp 60  
 QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCAGCACCTGACCCCTCAGCAAGCAGACTACGAG 240  
 DB 61 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrLeuSerLysAlaAspTyrGlu 80  
 QY 241 AAACACAAAGTCTACGCTTCGGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300  
 DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
 QY 301 AGCTTCAACAGCGGAGAGTGT 321  
 DB 101 SerPheAsnArgGlyGluCys 107  
 RESULT 14  
 ADL35094  
 ID ADL35094 standard; protein; 107 AA.  
 XX  
 AC ADL35094;  
 XX  
 DT 03-JUN-2004 (first entry)  
 DE Human IgG1 (hOAT) kappa light chain constant domain protein SeqID 97.  
 XX  
 DE antibody; variable domain; framework region; FR; huFR;  
 KW immune system molecule; kappa; anti-tissue factor; hOAT; human.  
 XX  
 OS Homo sapiens.  
 XX WO2004020579-A2.  
 PN 11-MAR-2004.  
 PD 06-AUG-2003; 2003WO-US024637.  
 XX 29-AUG-2002; 2002US-00230880.  
 XX (SUNO-) SUNOL MOLECULAR CORP.  
 PA Wong HC, Stinson JR, Mosquera LA;  
 PI WPI; 2004-239169/22.  
 DR  
 XX Producing humanized antibodies for diagnostic and therapeutic purposes  
 PT comprises optimizing similarity between individual antibody framework  
 PT regions to help identify human framework regions suitable for making the  
 PT antibodies.  
 XX Disclosure; SEQ ID NO 97; 137pp; English.  
 XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all  
 CC humanised immune system molecules of interest. This polypeptide sequence  
 CC is the human IgG1 kappa light chain constant domain protein of the  
 CC invention.  
 XX Sequence 107 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 4.93e-55 Length: 107  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-733-563-113 (1-321) x ADL35096 (1-107)

Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-113 (1-321) x ADL35094 (1-107)

Qy 1 CGTACGGTGGCTGACCATCTGTCTTCTATCTTCCGCCCATCTGATGACGAGTTGAAATCT 60  
Dd 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAAGTGCCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Dd 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGAGAGAGTGTCCACAGAGCAGGAC 180  
Dd 41 TrpLysValAlaPheAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGACCTTACAGCCTCAGCAGCAGCCTTGACCCCTGAGCAAGAGACTACAG 240  
Dd 61 SerLysAspSerThrTyrSerLeuSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AAACACAAAGTCTAGCCTGCGAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAAG 300  
Dd 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Dd 101 SerPheAsnArgGlyGluCys 107

RESULT 15  
ID ADM41539 standard; protein; 107 AA.  
XX AC ADM41539;  
XX DT 03-JUN-2004 (first entry)  
XX DE Anti-interleukin-1 receptor type 1 antibody kappa chain constant region.  
XX KW Human; monoclonal antibody; antibody; interleukin-1; receptor;  
XX KW antiasthmatic; antiinflammatory; dermatological; antiallergic;  
XX KW prozoocic; antirheumatic; antiarthritic; osteopathic; vasotropic;  
XX KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;  
XX KW anticonvulsant; dermatological; antigen; antiparkinsonian; antidiabetic;  
XX KW cystostatic.  
XX OS Homo sapiens.  
XX PN WO2004022718-A2.  
XX XX  
XX PD 18-MAR-2004.  
XX PP 05-SEP-2003; 2003WO-US027978.  
XX PR 06-SEP-2002; 2002US-0408719P.  
XX XX  
XX PA (AMGE-) AMGEN INC.  
XX XX  
XX PI Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;  
XX PI Elliott G;  
XX XX  
XX DR WPI; 2004-248462/23.  
XX DR N-PSDB; ADM41538.  
XX XX  
XX PT Isolated human antibody that specifically binds interleukin-1 receptor  
XX PT type 1 (IL-1RI) useful for treating IL-1 mediated diseases such as  
XX PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.  
XX XX  
XX PS Disclosure; SEQ ID NO 4; 179pp; English.  
XX XX

CC The present sequence is that of a human anti-interleukin-1 receptor type  
CC 1 (IL-1RI) monoclonal antibody (MAB) kappa chain constant region. Human  
CC MABs to IL-1RI were prepared using the HCo7 strain of transgenic mice,  
CC which expresses human antibody genes. These mice were immunised with  
CC purified recombinant IL-1RI, and splenocytes from immunised mice were  
CC fused to a mouse myeloma cell line to generate hybridomas. Hybridomas  
CC which secreted a MAb that bound with high avidity to IL-1RI were  
CC selected. The MABs inhibit IL-1 signalling by competing with IL-1beta and  
CC IL-1alpha binding to IL-1R. These MABs, as well as single chain  
CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies  
CC and (Fab')2 antibodies derived from them, are used in methods of treating  
CC IL-1 mediated diseases or for detecting the amount of IL-1RI in a sample.  
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral  
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,  
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,  
CC Clostridium associated illnesses, coronary conditions, cancer including  
CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,  
CC fibromyalgia, glomerulonephritis, graft versus host disease,  
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,  
CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,  
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,  
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,  
CC septic shock, side effects of radiation therapy, temporal mandibular  
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition  
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic  
CC surgery, infection or other disease processes.  
CC SQ Sequence 107 AA;

Alignment Scores:

Pred. No.: 4,93e-55 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 8 Gaps: 0

US-10-733-563-113 (1-321) x ADM41539 (1-107)

Qy 1 CGTACGGTGGCTGACCATCTGTCTTCTATCTTCCGCCCATCTGATGACGAGTTGAAATCT 60  
Dd 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
Qy 61 GGAAGTGCCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Dd 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
Qy 121 TGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGAGAGAGTGTCCACAGAGCAGGAC 180  
Dd 41 TrpLysValAlaPheAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
Qy 181 AGCAAGGACAGACCTTACAGCCTCAGCAGCAGCCTTGACCCCTGAGCAAGAGACTACAG 240  
Dd 61 SerLysAspSerThrTyrSerLeuSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
Qy 241 AAACACAAAGTCTAGCCTGCGAGTCAACCCATCAGGGCCTGAGCTCGCCGTCACAAAG 300  
Dd 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
Qy 301 AGCTTCAACAGGGGAGAGTGT 321  
Dd 101 SerPheAsnArgGlyGluCys 107

Search completed: January 28, 2006, 08:33:47  
Job time : 53.1261 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:20:11 ; Search time 8.75601 Seconds  
(without alignments)  
7054.719 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564

Sequence: 1 cgtacggtggtgcaccatc.....gcttcaacagggagagtgt 321

Scoring table: BLOSUM62

Gapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 568832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgm2\_1/USFPO\_spool\_p/US10733563/runat\_27012006\_180006\_4797/app\_query.fasta\_1.2716  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1 83 @runat\_27012006\_180006\_4797 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELCK=100 -LONGLOG  
-DEV\_TIMEOUT=1120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	553	98.0	215	2	JEO243	Ig kappa chain NIG
2	553	98.0	215	2	JEO244	Ig kappa chain NIG
3	553	98.0	215	2	JEO242	Ig kappa chain NIG
4	550	97.5	135	2	S52059	JC-kappa protein -
5	548	97.2	106	1	K3HU	Ig kappa chain C r
6	537	95.2	216	2	JEO241	Ig kappa chain Am3
7	520	92.2	215	2	A23746	Ig kappa chain V-1
8	513	91.0	99	2	A37927	Ig kappa chain C r
9	507	89.9	99	2	S26653	Ig kappa chain C r
10	372	66.0	240	2	S06084	Ig kappa chain C r
11	367	65.1	106	1	K1RTB	Ig kappa chain C r
12	366	64.9	178	2	PT0219	Ig kappa chain V-C
13	359	63.7	106	1	K1RTA	Ig kappa chain C r
14	358	63.5	217	2	S42772	Ig kappa chain - m

15	358	63.5	218	2	S68241	Ig kappa chain V r
16	358	63.5	219	2	S38865	Ig kappa chain - m
17	352	62.4	218	2	JCS810	monoclonal antibod
18	352	62.4	219	2	S52028	Ig kappa chain - m
19	352	62.4	219	2	PC4203	Ig kappa chain (no
20	352	62.4	219	2	S16112	Ig kappa chain V r
21	352	62.4	220	2	A31790	Ig kappa chain - m
22	352	62.4	225	2	S37484	Ig kappa chain V r
23	352	62.4	234	2	S14237	Ig kappa chain - m
24	352	62.4	234	2	S01320	Ig kappa chain pre
25	352	62.4	235	2	S25058	Ig kappa chain pre
26	350	62.1	106	1	K1MS	Ig kappa chain - m
27	350	62.1	126	2	I54782	gene Pvt-1a/Ig-Ck
28	348	61.7	225	2	JL0029	Ig kappa chain C r
29	345	61.2	230	2	S33161	Ig kappa chain pre
30	321	56.9	214	2	S68212	Ig kappa chain - a
31	321	55.3	210	2	A56169	Ig kappa chain (Ma
32	308.5	54.7	106	2	G20907	Ig kappa chain V r
33	306.5	54.3	106	1	K4RBBS	Ig kappa-B4 chain
34	277.5	49.2	229	2	A20969	Ig kappa-2 chain C
35	257.5	45.7	103	1	K4RB	Ig kappa chain pre
36	256	45.4	104	2	F53275	Ig kappa-B4 chain
37	246.5	43.7	104	1	K9RB	Ig kappa-1 chain C
38	245	43.4	238	2	A49633	Ig kappa-B9 chain
39	241	42.7	104	1	K9RBV	Ig lambda-like cha
40	237	42.0	118	2	A46518	Ig kappa chain C r
41	231	41.0	103	2	B26167	Ig L1 chain J-C re
42	231	41.0	213	2	A21177	Ig lambda chain C
43	225	39.9	108	1	K3FG	Ig light chain pre
44	223.5	39.6	103	1	K9RB	Ig light chain C r
45	222	39.4	197	2	S29593	Ig kappa-B5 chain
						Ig kappa chain (WM

ALIGNMENTS

RESULT 1

JEO243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JEO243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JEO243  
A:Accession: JEO243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Cross-references: UNIPARC:UPI0000176984  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 3.34e-47 Length: 215  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x JEO243 (1-215)

QY	1	CGTACGGTGGCGTGCACCATCTCTTCATCTTCGCCCATCTGATGACAGTTGAATCT	60
DB	109	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluLeuIysSer	128
QY	61	GGAACCTGCTCTGTGTGTGCTGCTGTAATAACTTCTATCCAGAGGCCAAAGTCAC	120
DB	129	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaIysValGln	148
QY	121	TGGAAGGTGGATAACGCCCTCAATCGGGTAACCTCCAGGAGAGTGTCCAGAGCAGAC	180
DB	149	TrpIysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp	168

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QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGAGCTACGAG 240
Db 169 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 188
QY 241 AAACACAAAGCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db 189 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 208
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 209 SerPheAenArgGlyGluCys 215
RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
A:Cross-references: UNIPARC:UPI0000176982
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 3,34e-47 Length: 215
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0
US-10-733-563-113 (1-321) x JE0244 (1-215)
QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 109 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 128
QY 61 GGAAGTGGTAACTGCTGCTGAATTAATCTTATCCAGAGAGGCCAAAGTACAG 120
Db 129 GlyThrAlaSerValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 148
QY 121 TGGAGGTGGATAACGCCCTCCAAATCGGTTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 149 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 168
QY 181 AGCAGGACAGCAGCTACAGCAGCAGCCCTGACCCCTGAGCAAGACGAGCTACGAG 240
Db 169 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 188
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db 189 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 208
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 209 SerPheAenArgGlyGluCys 215
RESULT 4
S52059
JC-kappa protein - human
C:Species: Homo sapiens (man)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C:Accession: S52059
R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;
EMBO J. 13, 5937-5943, 1994
A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c
A:Reference number: S52059; MUID:95112804; PMID:7813432
A:Accession: S52059
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <FRA>
A:Cross-references: UNIPARC:UPI00001184D0
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology
Alignment Scores:
Pred. No.: 6,81e-47 Length: 135
Score: 550.00 Matches: 106
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.07% Mismatches: 0
Query Match: 97.52% Indels: 0
DB: 2 Gaps: 0
US-10-733-563-113 (1-321) x S52059 (1-135)
QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 29 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 48
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QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAGACGAGCTACGAG 240
Db 169 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 188
QY 241 AAACACAAAGCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db 189 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 208
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 209 SerPheAenArgGlyGluCys 215
RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
A:Cross-references: UNIPARC:UPI0000176982
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
Alignment Scores:
Pred. No.: 3,34e-47 Length: 215
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0
US-10-733-563-113 (1-321) x JE0244 (1-215)
QY 1 CGTACGGTGGCTGCACCATCTGCTTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 109 ArgThrValAlaAlaProSerValPheilePheProSerAspGluGlnLeuLysSer 128
QY 61 GGAAGTGGTAACTGCTGCTGAATTAATCTTATCCAGAGAGGCCAAAGTACAG 120
Db 129 GlyThrAlaSerValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 148
QY 121 TGGAGGTGGATAACGCCCTCCAAATCGGTTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 149 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 168
QY 181 AGCAGGACAGCAGCTACAGCAGCAGCCCTGACCCCTGAGCAAGACGAGCTACGAG 240
Db 169 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 188
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db 189 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 208
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 209 SerPheAenArgGlyGluCys 215
RESULT 3
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossein, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
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QY 61 GGAACCTGCTCTGTGTGTGCTGCTGTAATACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db |||||ThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 68  
QY 121 TCGAAGGTGGATAACGCGCTCCAAATCGGTAACTCCAGAGAGTCTCACAGCAGGAC 180  
Db |||||TyrValValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 88  
QY 181 AGCAAGGACAGCACCTTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAAAGCAGATACAG 240  
Db |||||SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 108  
QY 241 AAACACAAAGTCTAGCCTGCGAAGTCAACCTCCAGGCTGAGTGGCCCTCACAAG 300  
Db |||||LysHisLysLeuTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 128  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
Db |||||SerPheAsnArgGlyGluCys 135  
RESULT 5  
K3HU  
Ig kappa chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02  
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc  
A:Reference number: A90562; MUID:71064023; PMID:5489770  
A:Contents: myeloma protein Eu  
A:Accession: B90562  
A:Molecule type: protein  
A:Residues: 1-106 <GOT>  
A:Cross-references: UNIPROT:P01834; UNIPARC:UPI000002F106  
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation: Eu, disulfide bonds  
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub  
A:Reference number: A91651; MUID:72188439; PMID:5027703  
A:Contents: Bence Jones protein Ti  
A:Accession: A91651  
A:Molecule type: protein  
A:Residues: 1-106 <SUT>  
A:Cross-references: UNIPARC:UPI000002F106  
R:Hietter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv  
A:Reference number: A90806; MUID:81042304; PMID:6775818  
A:Accession: A90806  
A:Molecule type: DNA  
A:Residues: 1-106 <HIE>  
A:Cross-references: UNIPARC:UPI000002F106; GB:J00241; NID:933140; PIDN:CAA23823.1; PID:9  
A:Note: the sequence was determined from the germline gene  
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
A:Reference number: A94417  
A:Contents: Bence Jones protein Roy  
A:Accession: A94417  
A:Molecule type: protein  
A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>  
A:Cross-references: UNIPARC:UPI000017376D  
A:Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu  
R:Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A:Title: Die vollständige Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).  
A:Reference number: A91639; MUID:68242259; PMID:5586923  
A:Contents: Bence Jones protein Cum

A:Accession: A91639  
A:Molecule type: protein  
A:Residues: 1-56, 'Q', 58-106 <H12>  
A:Cross-references: UNIPARC:UPI000017376E  
R:Tritani, K.; Shinoda, I.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete s  
A:Reference number: A92047; MUID:69234734; PMID:4893682  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <TIT>  
A:Cross-references: UNIPARC:UPI000017376F  
R:Köhler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507; PMID:5447531  
A:Contents: Waldenström's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <KOH>  
A:Cross-references: UNIPARC:UPI000017376F  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Cross-references: UNIPARC:UPI0000173770  
A:Note: allotype Inv(3)  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances thei  
A:Reference number: S02572; MUID:88005152; PMID:3115831  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-references: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp  
chain disulfide bonds; in some cases, such as IGA and IGH, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental  
Alignment Scores:  
Pred. No.: 1,09e-46 Length: 106  
Score: 548.00 Matches: 106  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.16% Indels: 0  
DB: 1 Gaps: 0  
US-10-733-563-113 (1-321) x K3HU (1-106)  
QY 4 ACGGTGGCTGCACCATCTGTCTTCATCTTCCGCGCATCTGTAGCAGTGTGAAATCTGGA 63  
Db |||||1 ThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSerGly 20  
QY 64 ACTGCCTCTGTGTGTGCTGCTCTGAATACTTCTATCCAGAGAGCCAAAGTACAGTGG 123  
Db |||||21 ThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTrp 40  
QY 124 AAGTGGATAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTCCACAGAGCAGCAGC 183  
Db |||||41 LysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAspSer 60  
QY 184 AAGGACAGCACCTTACAGCCTCAGCAGCACCCCTGAGCCCTGAGCAAGACAGACTTACCAGAAA 243  
Db |||||

Db 61 LysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGluLys 80  
Qy 244 CACAAAGTCTACGGCTCGAAGTCAACCATCGGCGCTGAGCTCGCCGCTCAAAAGAGC 303  
Db 81 HisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSer 100  
Qy 304 TTCACAGGGGAGAGTGT 321  
Db 101 PheAsnArgGlyGluCys 106  
RESULT 6  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: J050241  
F:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul  
A:Reference number: J050241  
A:Accession: J050241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
A:Cross-references: UNIPARC:UPI0000176981  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 1.33e-45 Length: 216  
Score: 537.00 Matches: 104  
Percent Similarity: 97.20% Conservative: 0  
Best Local Similarity: 97.20% Mismatches: 3  
Query Match: 95.21% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x J050241 (1-216)  
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGAGCAGTTGAATCT 60  
Db 110 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 129  
Qy 61 GGAATCGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 130 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 149  
Qy 121 TGAAGGTGGATAACGCTCCATTCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 150 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 169  
Qy 181 AGCAGGACACCTACAGCTCAGCAGCACCCTGAGCCCTGAGCAAGAGCAGTACGAG 240  
Db 170 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrSerLysAlaAspTyrGlu 189  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGCTCAAAAG 300  
Db 190 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 209  
Qy 301 AGCTTCACAGGGAGAGTGT 321  
Db 210 SerPheAsnArgGlyGluCys 216  
RESULT 7  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: A23746  
A>Status: preliminary

A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
A:Cross-references: UNIPARC:UPI0000176985  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 6.64e-44 Length: 215  
Score: 520.00 Matches: 104  
Percent Similarity: 98.11% Conservative: 0  
Best Local Similarity: 98.11% Mismatches: 2  
Query Match: 92.20% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x A23746 (1-215)  
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGAGCAGTTGAATCT 60  
Db 109 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 128  
Qy 61 GGAATCGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCAAAGTACAG 120  
Db 129 GlyThrAlaSerValValGlyLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 148  
Qy 121 TGAAGGTGGATAACGCTCCATTCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 149 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 168  
Qy 181 AGCAGGACACCTACAGCTCAGCAGCACCCTGAGCCCTGAGCAAGAGCAGTACGAG 240  
Db 169 SerLysAspSerThrTyrSerLeuSerSerThrThrLeuThrSerLysAlaAspTyrGlu 188  
Qy 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGCTCAAAAG 300  
Db 189 LysHisLysValTyrAlaGlyGluValThrHisGlnGlyLeuSerSerProValThrLys 208  
Qy 301 AGCTTCACAGGGAGAG 318  
Db 209 SerPheAsnArgGlyGlu 214  
RESULT 8  
A37927  
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772; PMID:1900145  
A:Accession: A37927  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
A:Cross-references: UNIPARC:UPI0000176ED6  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>  
Alignment Scores:  
Pred. No.: 3.45e-43 Length: 99  
Score: 513.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 98.99% Mismatches: 0  
Query Match: 90.96% Indels: 0  
DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x A37927 (1-99)  
Qy 25 TTCATCTTCGCCCATCTGATGAGCAGTTGAATCTGGAATCTGCTGTGTGTGCTG 84  
Db 1 PheIlePheProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeu 20

QY 85 CTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATTAACGCCCTCCAA 144  
 |||||  
 Db 21 LeuAsnAsnPhetyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGln 40  
 |||||  
 QY 145 TCGGGTAACTCCAGAGAGAGTGTCCAGAGCAGGACAGCAAGACAGCACTTACAGCTTC 204  
 |||||  
 Db 41 SerGlyAsnSerGlnGlnSerValThrGluGlnAspSerLysAspSerThrTrpSerLeu 60  
 |||||  
 QY 205 ACAGCACCCTGACCTCGAGCAAGACAGACTACGAGAAACACAAAGTCTACCGCTGCGAA 264  
 |||||  
 Db 61 SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysLeuTyrAlaCysGlu 80  
 |||||  
 QY 265 GTACCCATCAGGCGCTGAGCTGCGCCGCTCAAAAGAGCTTCAACAGGGGAGAGTGT 321  
 |||||  
 Db 81 ValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys 99  
 |||||  
 RESULT 9  
 S26653  
 Ig kappa chain C region - chimpanzee (fragment)  
 C:Species: Pan troglodytes (chimpanzee)  
 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
 C:Accession: S26653  
 R: Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
 Hum. Antibodies Hybridomas 1, 23-26, 1990  
 A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
 A:Reference number: S26652; MUID:91355693; PMID:2129418  
 A:Accession: S26653  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <EHR>  
 A:Cross-references: UNIPARC:UPI0000176BD5; EMBL:X65287  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 P:19-88/Domain: immunoglobulin homology <IMW>

Alignment Scores:  
 Pred. No.: 1.37e-42 Length: 99  
 Score: 507.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 89.8% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x S26653 (1-99)

QY 4 ACGGTGGCTGCACCATCTCTTCATCTTCCGCCATCTGTAGCAGTTCGAATCTCGA 63  
 |||||  
 Db 1 ThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSerGly 20  
 |||||  
 QY 64 ACTGCCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGGCCAAAGTACAGTGG 123  
 |||||  
 Db 21 ThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTrp 40  
 |||||  
 QY 124 AAGGTGATTAACGCCCTCAATCGGCTAACTCCAGGAGAGTGTACAGAGCAGCAGC 183  
 |||||  
 Db 41 LysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThrGluGlnAspSer 60  
 |||||  
 QY 184 AAGGACAGCAGCTCAGCCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACAGAA 243  
 |||||  
 Db 61 LysAspSerThrTyrSerLeuSerSerThrLeuThrHisGlnGlyLeuSerProValThrLys 80  
 |||||  
 QY 244 CACAAAGTCTAGCCTCGGAGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
 |||||  
 Db 81 HisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 99  
 |||||

RESULT 10

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 &lt;CRO&gt;

A:Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

P:1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

P:21-240/Product: Ig kappa chain #status predicted &lt;MAT&gt;

P:153-222/Domain: immunoglobulin homology &lt;IMW&gt;

Alignment Scores:

Pred. No.: 4.12e-29 Length: 240

Score: 372.00 Matches: 70

Percent Similarity: 77.57% Conservative: 13

Best Local Similarity: 65.42% Mismatches: 24

Query Match: 65.96% Indels: 0

DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x S06084 (1-240)

QY 1 CQTACGGTGGTGACCATCTCTCTTCATCTTCCGCCATCTGTAGCAGTTCGAATCT 60

|||

Db 134 ArgAlaAspAlaAlaProThrValSerIlePheProSerThrGluGlnLeuAlaThr 153

|||

QY 61 GGAAGTGGCTCTGTTGTGCTGCTGAATACTTCTATCCAGAGGCCAAAGTACAG 120

|||

Db 154 GlyGlyAlaSerValValCysLeuMetAsnAsnPheTyrProArgAspIleSerValLys 173

|||

QY 121 TGGAAAGTGGATAACGCCCTTCAATCGGCTAACTCCAGGAGAGTGTACAGAGCAGGAC 180

|||

Db 174 TrpLysIleAspGlyThrGluArgArgAspGlyValLeuAspSerValThrAspGlnAsp 193

|||

QY 181 AGCAAGGACAGCAGCTCAGCAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACGAG 240

|||

Db 194 SerLysAspSerThrTyrSerMetSerThrLeuSerLeuSerLysAlaAspTyrGlu 213

|||

QY 241 AAACACAAAGTCAAGCTGCGGAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300

|||

Db 214 SerHisAsnLeuTyrThrCysGluValValHisLysThrSerSerSerProValLys 233

|||

QY 301 AGCTTCAACAGCGGAGAGTGT 321

|||

Db 234 SerPheAsnArgAsnGluCys 240

|||

RESULT 11

KIRTB

Ig kappa chain C region (allele b) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004

C:Accession: A93901; A92807; A02117

R:Sheppard, H.W.; Gutman, G.A.

Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the lev

A:Reference number: A93901; MUID:82082587; PMID:6273908

A:Accession: A93901

A:Molecule type: DNA

A:Residues: 1-106 &lt;SHS&gt;

A:Cross-references: UNIPROT:P01835; UNIPARC:UPI000012DB83; GB:V01241; GB:J00745; GB:J025:

A:Experimental source: strain LOU

R:Starace, V.; Querinjean, P.

J. Immunol. 115, 59-62, 1975

A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation

A:Reference number: A92807; MUID:75212238; PMID:907630

A:Contents: Bence Jones protein S211

A:Accession: A92807

A:Molecule type: protein

A:Residues: 1, 'N', '3-29, 'K', '31-47, 49-78, 'Q', '80-86, 'Q', '88-98, 'W', '99, 'N', 101-106 &lt;STA&gt;

A:Cross-references: UNIPARC:UPI0000173771

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer

F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status predicted  
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Alignment Scores:

Pred. No.:	1.35e-28	Length:	106
Score:	367.00	Matches:	68
Percent Similarity:	78.85%	Conservative:	14
Best Local Similarity:	65.38%	Mismatches:	22
Query Match:	65.07%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-113 (1-321) x KIRTB (1-106)

QY	10	GCTGCACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCC	69
DB	3	AlaAlaProThrValSerIlePheProProSerThrGluGlnLeuAlaThrGlyGlyAla	22
QY	70	TCTGTGTGCTGCTGCTGAATACTTATCCAGAGAGCCAAAGTACAGTGGAGGTG	129
DB	23	SerValValCysLeuMetAsnAsnPheTyrProArgAspIleSerValIleTrpIle	42
QY	130	GATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGACGACGACGAGCAG	189
DB	43	AspGlyThrGluArgArgAspGlyValLeuAspSerValThrAspGlnAspSerIle	62
QY	190	AGCACCTACAGCCTCAGCAGACCTGACCTCGAGCAAGCAGACTACGAGAAACACAA	249
DB	63	SerThrTyrSerMetSerSerThrLeuSerThrIleValAlaAspTyrGluSerHis	82
QY	250	GTCTACGCTCGAAGTCAACCATCAGCGCTGAGCTCGCCGTCACAAAGAGTTCAC	309
DB	83	LeuTyrThrCysGluValValHisIleThrSerSerSerProValValIleSerPhe	102
QY	310	AGGGGAGAGTCT	321
DB	103	ArgAsnGluCys	106

RESULT 12

PT0219

Ig kappa chain V-C region (PIC18) - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jan-2000

C:Accession: PT0219

R:Lammers, B.M.; Beaman, K.D.; Kim, Y.B.

Mol. Immunol. 28, 877-880, 1991

A:Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.

A:Reference number: PT0219; MUID:91342694; PMID:1715030

A:Accession: PT0219

A:Molecule type: mRNA

A:Residues: 1-178 <LAM>

A:Cross-references: UNIPARC:UPI00001151A1; GB:M59321; NID:g164508; PIDN:AAA03520.1; PID:

A:Experimental source: spleen, strain Minnesota Miniature

A:Note: the authors translated the codon CTC for residue 141 as Ser

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-70/Domain: V region (fragment) <VRG>

F:12-18/Region: complementarity-determining 1

F:52-60/Region: complementarity-determining 2

F:61-70/Region: framework 2

F:71-178/Domain: C region <CRG>

F:96-156/Disulfide bonds: #status predicted

F:176/Disulfide bonds: interchain #status predicted

Alignment Scores:

Pred. No.:	1.66e-28	Length:	178
Score:	366.00	Matches:	69
Percent Similarity:	76.64%	Conservative:	13
Best Local Similarity:	64.49%	Mismatches:	25
Query Match:	64.89%	Indels:	0

DB: 2 Gaps: 0  
US-10-733-563-113 (1-321) x PT0219 (1-178)

QY	1	CGTAGCGTGGTGCACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCT	60
DB	70	ArgAlaAspAlaIlePheProSerValPheIlePheProSerIleGluGlnLeuAlaThr	89
QY	61	GGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTATCCAGAGAGCCAAAGTACAG	120
DB	90	ProThrValSerValCysLeuIleAsnAsnPhePheProArgGluIleSerValIle	109
QY	121	TGGAAGTGGATAAGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGACGAGCAG	180
DB	110	TrpIleValAspGlyValValGlnSerSerGlyHisProAspSerValThrGluGlnAsp	129
QY	181	AGCAAGGACACACCTACAGCCTCAGCAGACCTGACCCCTGAGCAAGACAGACTACGAG	240
DB	130	SerIleAspSerThrTyrSerLeuSerSerThrLeuSerLeuProThrSerGlnTyrLeu	149
QY	241	AAACACAAAGTCTACGCTGCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG	300
DB	150	SerHisAsnLeuTyrSerCysGluValThrHisIleThrLeuAlaSerProLeuValThr	169
QY	301	AGCTTCAACAGGGGAGAGTGT	321
DB	170	SerPheAsnArgAsnGluCys	176

RESULT 13

KIRTA

Ig kappa chain C region (allele a) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Aug-1982 #sequence\_revision 10-Sep-1982 #text\_change 09-Jul-2004

C:Accession: A02118

R:Sheppard, H.W.; Gutman, G.A.

Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the lev

A:Reference number: A93901; MUID:82082587; PMID:6273908

A:Accession: A02118

A:Molecule type: DNA

A:Residues: 1-106 <SHB>

A:Cross-references: UNIPROT:P01836; UNIPARC:UPI00001148A8; GB:J00745; NID:g204

A:Experimental source: strain DA

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer

F:19-88/Domain: immunoglobulin homology <IMM>

F:26-86/Disulfide bonds: #status predicted

F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Alignment Scores:

Pred. No.:	8.54e-28	Length:	106
Score:	359.00	Matches:	66
Percent Similarity:	78.85%	Conservative:	16
Best Local Similarity:	63.46%	Mismatches:	22
Query Match:	63.65%	Indels:	0
DB:	1	Gaps:	0

US-10-733-563-113 (1-321) x KIRTA (1-106)

QY	10	GCTGCACCATCTGCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCC	69
DB	3	AlaAlaProThrValSerIlePheProProSerMetGluGlnLeuThrSerGlyGlyAla	22
QY	70	TCTGTGTGCTGCTGCTGAATACTTATCCAGAGAGCCAAAGTACAGTGGAGGTG	129
DB	23	ThrValValCysPheValAsnAsnPheTyrProArgAspIleSerValIleTrpIle	42
QY	130	GATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGACGAGCAGCAGCAG	189
DB	43	AspGlySerGluGlnArgAspGlyValLeuAspSerValThrAspGlnAspSerIle	62



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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:19:11 ; Search time 49.2425 Seconds  
(without alignments)  
9198.340 Million cell updates/sec

Title: US-10-733-563-113  
Perfect score: 564  
Sequence: 1 cgtacggtggtgcaccatc.....gcttcacagggagagtgt 321

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DB=xlp  
-Q=/cgm2\_1/USPTO\_spool\_p/US10733563/runat\_27012006.180005.4782/app\_query.fasta\_1.2716  
-DB=UniProt -QMT=fascan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORES=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10733563 @CGN 1.1.632 @runat\_27012006.180005.4782 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT\_DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRAADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	98.0	120	Q6P5R5 HUMAN	Q6P5R5 homo sapien
2	553	98.0	234	Q6P5R5 HUMAN	Q6P5R5 homo sapien
3	553	98.0	234	Q6P5R5 HUMAN	Q6P5R5 homo sapien
4	553	98.0	235	Q6GMV9 HUMAN	Q6GMV9 homo sapien
5	553	98.0	235	Q6GMW0 HUMAN	Q6GMW0 homo sapien
6	553	98.0	235	Q6PJE2 HUMAN	Q6PJE2 homo sapien
7	553	98.0	236	Q6GMX0 HUMAN	Q6GMX0 homo sapien
8	553	98.0	236	Q6P5S8 HUMAN	Q6P5S8 homo sapien
9	553	98.0	236	Q6P5H4 HUMAN	Q6P5H4 homo sapien
10	553	98.0	236	Q6P5L8 HUMAN	Q6P5L8 homo sapien
11	553	98.0	236	Q6P5T5 HUMAN	Q6P5T5 homo sapien
12	553	98.0	236	Q6P5Y4 HUMAN	Q6P5Y4 homo sapien
13	553	98.0	236	Q6P5H7 HUMAN	Q6P5H7 homo sapien
14	553	98.0	236	Q6GMX9 HUMAN	Q6GMX9 homo sapien
15	553	98.0	236	Q6GMX8 HUMAN	Q6GMX8 homo sapien
16	553	98.0	236	Q6GMW1 HUMAN	Q6GMW1 homo sapien

17	553	98.0	236	2	Q502W4_HUMAN	Q502W4 homo sapien
18	553	98.0	239	2	Q6P491_HUMAN	Q6P491 homo sapien
19	553	98.0	239	2	Q8TCD0_HUMAN	Q8TCD0 homo sapien
20	553	98.0	240	2	Q6PIH6_HUMAN	Q6PIH6 homo sapien
21	549	97.3	239	2	Q8NEK0_HUMAN	Q8NEK0 homo sapien
22	548	97.2	106	1	KAC_HUMAN	P01834 homo sapien
23	548	97.2	234	2	Q569I9_HUMAN	Q569I9 homo sapien
24	369	65.4	234	2	Q4KM66_RAT	Q4KM66 rattus norv
25	369	65.4	234	2	Q5M838_RAT	Q5M838 rattus norv
26	367	65.1	106	1	KACB_RAT	P01835 rattus norv
27	359	63.7	106	1	KACA_RAT	P01836 rattus norv
28	358	63.5	219	2	Q5ZC00_MOUSE	Q5ZC00 mus musculus
29	352	62.4	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculus
30	352	62.4	235	2	Q5XFY8_MOUSE	Q5XFY8 mus musculus
31	352	62.4	235	2	Q58EV6_MOUSE	Q58EV6 mus musculus
32	352	62.4	236	2	Q7TS98_MOUSE	Q7TS98 mus musculus
33	352	62.4	236	2	Q52L95_MOUSE	Q52L95 mus musculus
34	352	62.4	237	2	Q569Y8_MOUSE	Q569Y8 mus musculus
35	352	62.4	238	2	Q66JS7_MOUSE	Q66JS7 mus musculus
36	352	62.4	238	2	Q58EU4_MOUSE	Q58EU4 mus musculus
37	352	62.4	239	2	Q58EU8_MOUSE	Q58EU8 mus musculus
38	352	62.4	240	2	Q52L64_MOUSE	Q52L64 mus musculus
39	352	62.4	241	2	Q53ZX4_MOUSE	Q53ZX4 mus musculus
40	350	62.1	106	1	KAC_MOUSE	P01837 mus musculus
41	306.5	54.3	106	1	KACB_RABIT	P01839 oryctolagus
42	292	51.8	189	2	Q569I7_HUMAN	Q569I7 homo sapien
43	259.5	46.0	116	2	Q6LEJ1_RABIT	Q6LEJ1 oryctolagus
44	259.5	46.0	116	2	Q6LEJ2_RABIT	Q6LEJ2 oryctolagus
45	257.5	45.7	103	1	KAC4_RABIT	P01840 oryctolagus

ALIGNMENTS

RESULT 1  
Q6P5R5 HUMAN  
ID Q6P5R5 HUMAN PRELIMINARY; PRT; 120 AA.  
AC Q6P5R5;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Glandular pool- thyroid;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Shat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.



RC TISSUE=glandular pool- thyroid;  
RG NIH MGC Project;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
CC histocompatibility complex class I molecules (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
DR EMBL; BC062732; AAC62732.1; -, mRNA.  
DR HSSP; P01837; 1KC1.  
DR SMR; Q6PSR3; 3-120.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; CI-set; 1.  
DR SMART; SM00407; IGcl; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
KW Immune response; Immunoglobulin domain; MHC I.  
SQ SEQUENCE 120 AA; 13153 MW; B42PA2928C5C8F1F CRC64;

Alignment Scores:  
Pred. No.: 1.24e-48 Length: 120  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PSR5\_HUMAN (1-120)

QY 1 CGTAGGGTGGCGACCATCTGCTTCATCTCCCGCCATCTGATGAGCGTTGAATCT 60  
Db 14 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 33  
QY 61 GGAATCGCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 34 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 53  
QY 121 TGGAGGTGGATAACGCTCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 54 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 73  
QY 181 AGCAAGGACACACCTACAGCTCAGCAGCACCTGACCCCTGAGCAGAGAGCTACAGAG 240  
Db 74 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 93  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
Db 94 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 113  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 114 SerPheAsnArgGlyGluCys 120

## RESULT 2

QSEPF6\_HUMAN  
ID QSEPF6\_HUMAN PRELIMINARY; PRT; 234 AA.  
AC QSEPF6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Anti-RHD monoclonal T125 kappa light chain precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Gaucher C., Klein P., Biliard R.;  
RT "Sequence determination of the recombinant human anti-RHD monoclonal  
RT antibody T125.";  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY894991; AA882027.1; -, mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; CI-set; 1.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
KW Signal.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 234 anti-RHD monoclonal T125 kappa light  
FT chain.  
SQ SEQUENCE 234 AA; 25698 MW; 866DCD1B4FD7D5EA CRC64;

## Alignment Scores:

Pred. No.: 1.35e-48 Length: 234  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x QSEPF6\_HUMAN (1-234)

QY 1 CGTAGGGTGGCGACCATCTGCTTCATCTCCCGCCATCTGATGAGCGTTGAATCT 60  
Db 128 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 147  
QY 61 GGAATCGCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 148 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 167  
QY 121 TGGAGGTGGATAACGCTCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGAC 180  
Db 168 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 187  
QY 181 AGCAAGGACACACCTACAGCTCAGCAGCACCTGACCCCTGAGCAGAGAGCTACAGAG 240  
Db 188 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 207  
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
Db 208 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 227  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 228 SerPheAsnArgGlyGluCys 234

## RESULT 3

Q7Z473\_HUMAN  
ID Q7Z473\_HUMAN PRELIMINARY; PRT; 234 AA.  
AC Q7Z473;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,



```

Db      149 GlyThrAlaSerValValCysLeuLeuAanPheTyrProArgGluAlaLysValGln 168
QY      121 TGGAGGTTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db      169 TrpLysValAspAanAlaLeuGlnSerGlyAanSerGlnGluSerValThrGluGlnAasp 188
QY      181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db      189 SerLysAaspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAaspTyrGlu 208
QY      241 AAACACAAAGTCTACGCCCTCGGAGCTCAGCCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db      209 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 228
QY      301 AGCTTCAACAGGGGAGAGTGT 321
Db      229 SerPheAanArgGlyGluCys 235

RESULT 5
Q6GMW0 HUMAN
ID Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC
OC
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073792; AAH73792.1; -; mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.

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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Alignment Scores:
Pred. No.: 1.36e-48 Length: 235
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6GMW0_HUMAN (1-235)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCATCTGTAGAGCAGTGAATCT 60
Db 129 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 148
QY 61 GGAATCGCTCTGTGTGTGCTCTCTGAATAACTTCTATCCAGAGGCGCAAGTACAG 120
Db 149 GlyThrAlaSerValValCysLeuLeuAanPheTyrProArgGluAlaLysValGln 168
QY 121 TGGAGGTTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 169 TrpLysValAspAanAlaLeuGlnSerGlyAanSerGlnGluSerValThrGluGlnAasp 188
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 189 SerLysAaspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAaspTyrGlu 208
QY 241 AAACACAAAGTCTACGCCCTCGGAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAACAAG 300
Db 209 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 228
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 229 SerPheAanArgGlyGluCys 235

RESULT 6
Q6PJF2 HUMAN
ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073792; AAH73792.1; -; mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.

```

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]

RT NUCLEOTIDE SEQUENCE.  
RC TISSUE=lung;  
RA Strausberg R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016380; AAH16380.1; -; mRNA.  
DR HSSP; P01837; 1KCU.  
DR SMR; Q6PJF2; 21-235.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
DR Hypothetical protein.  
KW SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;  
[2]

Alignment Scores:  
Pred. No.: 1,366-48 Length: 235  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PJF2\_HUMAN (1-235)

QY	1	CGTACGGTGGCTGCACCATCTCTTCATCTCCGCCCATCTGATGAGCAGTTGAATCT	60
Db	129	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer	148
QY	61	GGAACCTGCTCTGTGTGTGCTGCTGAATACTTCTATCCAGAGAGCCAAAGTACAG	120
Db	149	GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln	168
QY	121	TGGAAGTGGATAACGCCCTCCATCGGTAACTTCTATCCAGAGAGTGTCCACAGCAGGAC	180
Db	169	TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp	188
QY	181	AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGACCTGAGCAAGAGCAGTACGAG	240
Db	189	SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu	208
QY	241	AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCGCTCAACAAG	300
Db	209	LysHisLysValValAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys	228
QY	301	AGCTTCAACAGGGAGAGTGT 321	
Db	229	SerPheAsnArgGlyGluCys 235	

RESULT 7  
Q6GMX0\_HUMAN  
ID Q6GMX0\_HUMAN PRELIMINARY; PRT; 236 AA.  
AC Q6GMX0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]

RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073775; AAH73775.1; -; mRNA.  
DR SMR; Q6GMX0; 23-236.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
DR Hypothetical protein.  
KW SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;  
[2]

Alignment Scores:  
Pred. No.: 1,366-48 Length: 236  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6GMX0\_HUMAN (1-236)

QY	1	CGTACGGTGGCTGCACCATCTCTTCATCTCCGCCCATCTGATGAGCAGTTGAATCT	60
Db	130	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer	149
QY	61	GGAACCTGCTCTGTGTGTGCTGCTGAATACTTCTATCCAGAGAGTGTCCACAGCAGGAC	120
Db	150	GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln	169
QY	121	TGGAAGTGGATAACGCCCTCCATCGGTAACTTCTATCCAGAGAGTGTCCACAGCAGGAC	180
Db	170	TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp	189
QY	181	AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGACCTGAGCAAGAGCAGTACGAG	240
Db	190	SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu	209
QY	241	AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCGCTCAACAAG	300

Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCACAGGGAGAGTGT 321

Db 230 SerPheAsnArgGlyGluCys 236

RESULT 8

Q6P5S8 HUMAN

ID Q6P5S8\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6P5S8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Wozley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Glandular pool- thyroid;

RA Strausberg R.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC062704; AAH62704.1; -; mRNA.

DR HSSP; P01837; 1KCU.

DR SMR; Q6P5S8; 21-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig c1.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; C1-sect; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 2.

DR PROSITE; PS0290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.

SW SEQUENCE 236 AA; 25773 MW; 953E37BB8FF5F27 CRC64;

Alignment Scores:

Pred. No.:	1,36e-48	Length:	236
Score:	553.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.05%	Indels:	0
DB:	2	Gaps:	0

US-10-733-563-113 (1-321) x Q6P5S8\_HUMAN (1-236)

QY 1 CGTAGGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGACAGTGAATCT 60

Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAACTGCCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120

Db 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 169

QY 121 TGGAGGTGATTAACCGCCCTCCAATCGGTAACTCCAGAGAGAGTGTCCACAGAGCAGAC 180

Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189

QY 181 AGCAAGGACACACCTACAGCTCAGCAGCACCTGAGCACCTGAGCAAGAGCAGATACAG 240

Db 190 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 209

QY 241 AAACACAAAGTCTACGGCTCGAAGTCCACCATCAGGGCCCTGAGCTGCCCGTCCACAAAG 300

Db 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCACAGGGAGAGTGT 321

Db 230 SerPheAsnArgGlyGluCys 236

RESULT 9

Q6PIH4 HUMAN

ID Q6PIH4\_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC034146; AAH34146.1; -; mRNA.

DR HSSP; P01607; 1AR2.

DR SMR; Q6PIH4; 23-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06EBE26 CRC64;

Alignment Scores:  
 Pred. No.: 1,36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIH4\_HUMAN (1-236)

QY 1 CGTAGCGTGGCTGCACCATCTGCTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 120  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 169

QY 121 TGGAGGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 180  
 Db 170 TrpLysValAspAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 189

QY 181 AGCAAGGACAGCAGCCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
 Db 190 SerLysAspSerThrTyrSerLysSerSerThrLysLeuThrLysLeuSerLysAlaAspTyrGlu 209

QY 241 AAACACAAAGTCTAGCGCTCGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCAACAAG 300  
 Db 210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 230 SerPheAenArgGlyGlyCys 236

RESULT 10  
 Q6PIL8\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIL8;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marugina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032451; AAH32451.1; -; mRNA.  
 DR HSP; P01837; 1KCU.  
 DR SMR; Q6PIL8; 21-236.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Alignment Scores:  
 Pred. No.: 1,36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIL8\_HUMAN (1-236)

QY 1 CGTAGCGTGGCTGCACCATCTGCTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
 Db 130 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 149

QY 61 GGAAGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 120  
 Db 150 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 169

QY 121 TGGAGGTGGTAAAGCGCTCAATCGGTAACTCTATCCAGAGAGTGTCCAGAGCAGGAC 180  
 Db 170 TrpLysValAspAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 189

QY 181 AGCAAGGACAGCAGCCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
 Db 190 SerLysAspSerThrTyrSerLysSerSerThrLysLeuThrLysLeuSerLysAlaAspTyrGlu 209

QY 241 AAACACAAAGTCTAGCGCTCGAAGTCAACCCATCAGGCGCTGAGCTCGCCCTCAACAAG 300  
 Db 210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229

QY 301 AGCTTCAACAGGGAGAGTGT 321  
 Db 230 SerPheAenArgGlyGlyCys 236

RESULT 11  
 Q6PIT5\_HUMAN PRELIMINARY; PRT; 236 AA.  
 ID Q6PIT5\_HUMAN PRELIMINARY;  
 AC Q6PIT5;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)







Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q723V4\_HUMAN (1-236)

QY 1 CGTACGGTGGCTGCACCATCTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
 |||||  
 DB 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 149  
 |||||

QY 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
 |||||  
 DB 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 169  
 |||||

QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAATCCAGGAGAGTGTCCAGAGCAGGAC 180  
 |||||  
 DB 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
 |||||

QY 301 AGCTTCAACAGGGAGAGTGT 321  
 |||||  
 DB 230 SerPheAsnArgGlyGluCys 236  
 |||||

RESULT 13

Q6PIH7\_HUMAN  
 ID Q6PIH7\_HUMAN PRELIMINARY; PRT; 236 AA.  
 AC Q6PIH7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE IGKC protein.  
 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Trichman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC034141; AAH34141.1; -; mRNA.  
 DR HSP; P01607; 1AR2.  
 DR SMR; Q6PIH7; 23-236.  
 DR Ensembl; ENSG00000163245; Homo sapiens.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig.MHC.  
 DR InterPro; IPR003596; Ig.V.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN 1.  
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;

Alignment Scores:  
 Pred. No.: 1.36e-48 Length: 236  
 Score: 553.00 Matches: 107  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.05% Indels: 0  
 DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x Q6PIH7\_HUMAN (1-236)

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 DB 130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 149  
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QY 61 GGAACCTGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120  
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 DB 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyProArgGluAlaLysValGln 169  
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QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAATCCAGGAGAGTGTCCAGAGCAGGAC 180  
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 DB 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
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QY 181 AGCAGGAGCAGCCTCAGCAGCCTCAGCAGCAGCCTGAGCCCTGAGCAAGCAGACTACAG 240  
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 DB 190 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 209  
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QY 241 AAACACAAAGTCTACGCTCGGAAGTACCCCATCAGGCGCTGAGCTCGCCGTCACAAG 300  
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 DB 210 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229  
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QY 301 AGCTTCAACAGGGAGAGTGT 321  
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RESULT 14

Q6GMX9\_HUMAN  
 ID Q6GMX9\_HUMAN PRELIMINARY; PRT; 236 AA.  
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 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
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 GN Name=IGKC;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Trichman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RG NIH MGC Project;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Primary B-Cells;  
RC NIH MGC Project;  
RG Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073763; AAH73763.1; -; mRNA.  
DR SMR; Q6GMX9; 23-236.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25924 MW; FD2E093DC560CF7 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.36e-48 Length: 236  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-113 (1-321) x Q6GMX9\_HUMAN (1-236)  
  
Qy 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACGAGTGAATCT 60  
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130 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 149  
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Qy 61 GGAAGTGGATACGCCCTCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGAC 180  
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|||  
170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThrGluGlnAsp 189  
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181 AGCAAGGACACACCTACAGCTCAGCAGCAGCCCTGACCTGACGACGACGACGACGAC 240  
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241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCCATCAGGCGCTGAGCTCCCGCTCACAAAG 300  
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210 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 229  
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230 SerPheAsnArgGlyGluCys 236  
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RESULT 15  
Q6GMX8\_HUMAN

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE IGKC protein.  
GN Name=IGKC;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
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RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
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RP TISSUE=Primary B-Cells;  
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RL EMBL; BC073764; AAH73764.1; -; mRNA.  
DR SMR; Q6GMX8; 24-235.  
DR Ensembl; ENSG00000163245; Homo sapiens.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
  
Alignment Scores:  
Pred. No.: 1.36e-48 Length: 236  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-733-563-113 (1-321) x Q6GMX8\_HUMAN (1-236)  
  
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Db 150 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 169  
QY 121 TCGAAGGTGGATAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTCAACAGAGCAGGAC 180  
Db 170 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 189  
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACCCCTGAGCAAGCAGACTACGAG 240  
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Db 230 SerPheAsnArgGlyGluCys 236

Search completed: January 28, 2006, 08:44:12  
Job time : 51.2425 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:22:17 ; Search time 12.6922 Seconds  
(without alignments)  
4181.924 Million cell updates/sec

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Perfect score: 564  
Sequence: 1 cgtacgtggtgcaccatc.....gcttcaacaggaggagtgt 321

Scoring table: BLOSUM62

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          Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/ptodata/1/iaa/RE COMB.pcp:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	553	98.0	107	1	US-08-422-091-8
3	553	98.0	107	1	US-08-422-092-8
4	553	98.0	107	1	US-08-788-800-5
5	553	98.0	107	2	US-08-422-093-8
6	553	98.0	107	2	US-08-422-112-8
7	553	98.0	107	2	US-09-301-593-20
8	553	98.0	212	2	US-10-011-125A-5
9	553	98.0	213	2	US-08-630-820-6
10	553	98.0	213	2	US-08-397-411-12
11	553	98.0	213	2	US-09-273-453-6
12	553	98.0	213	2	US-09-996-288-209

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21	553	98.0	213	2	US-09-996-288-227
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35	553	98.0	213	2	US-09-996-288-257
36	553	98.0	213	2	US-09-996-265-209
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45	553	98.0	213	2	US-09-996-265-227

ALIGNMENTS

RESULT 1  
US-08-422-101-8  
; Sequence 8, Application US/08422101  
; Patent No. 5739277  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedcor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,101  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881

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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-101-8

Alignment Scores:
Pred. No.: 2.07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-101-8 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATGCTCTGTGTGTGCTGCTGAATACTTATCCAGAGAGGCCAAAGTACAG 120
DB 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAAAGTGGATACGGCTCCATCGGTAACCTCCAGAGAGAGTGTCCAGAGCAGGAC 180
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCCAGCAGGAGTGTCCAGAGCAGGAC 240
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCCATCAGGCGCTGAGCTCCGCCGTCACAAAG 300
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGTGCT 321
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 2
US-08-422-091-8
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
```

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; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-091-8

Alignment Scores:
Pred. No.: 2.07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-091-8 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
DB 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATGCTCTGTGTGTGCTGCTGAATACTTATCCAGAGAGGCCAAAGTACAG 120
DB 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAAAGTGGATACGGCTCCATCGGTAACCTCCAGAGAGAGTGTCCAGAGCAGGAC 180
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTCCAGCAGGAGTGTCCAGAGCAGGAC 240
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCCATCAGGCGCTGAGCTCCGCCGTCACAAAG 300
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGTGCT 321
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08-788-800
; FILING DATE: 22-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 932-4
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-092-8

Alignment Scores:
Pred. No.: 2,078-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-422-092-8 (1-107)
QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTCCCGCATCTGATGAGCAGTTGAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheilePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAasp 60
QY 181 AGCAGGAGCAGCACCCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAAAAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Arntell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-5

Alignment Scores:
Pred. No.: 2,078-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 1 Gaps: 0

US-10-733-563-113 (1-321) x US-08-788-800-5 (1-107)
QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTCCCGCATCTGATGAGCAGTTGAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheilePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAasp 60
QY 181 AGCAGGAGCAGCACCCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 61 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrglu 80
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCATCAGGCGCTGAGCTCCGCCGTCAAAAG 300
Db 81 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 5
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.093
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-093-8

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Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

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US-10-733-563-113 (1-321) x US-08-422-093-8 (1-107)

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Qy 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTCCAGAGCGAC 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTCCAGAGCGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGCAGCAGCAGCCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

```

RESULT 6

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; Sequence 8, Application US/08422112
; Patent No. 6121022
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.112
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-112-8

```

```

Alignment Scores:
Pred. No.: 2,07e-59 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

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US-10-733-563-113 (1-321) x US-08-422-112-8 (1-107)

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Qy 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCGGCCATCTGATGACGAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
Qy 61 GGAAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTCCAGAGCGAC 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGTGGTAAACGGCTCCATCGGTAACTCCAGGAGAGTGTCCAGAGCGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGCAGCAGCAGCCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

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RESULT 7

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US-09-301-593-20
; Sequence 20, Application US/09301593A
; Patent No. 6455877
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier

```

APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-20

Alignment Scores:  
Pred. No.: 2,076-59 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-301-593-20 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAAGTGGCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCGCAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40  
QY 121 TGAAGGTGGATAACGCCCTCCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCAGCAAGCAGCTACAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCTCCCAATCGGGTAACTCCAGGAGAGTGTACAGAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 8  
US-10-011-125A-5  
Sequence 5, Application US/10011125A  
Patent No. 6828121  
GENERAL INFORMATION:  
APPLICANT: Chen, Christina Yu-Ching  
TITLE OF INVENTION: BACTERIAL HOST STRAINS  
FILE REFERENCE: P1804R1  
CURRENT APPLICATION NUMBER: US/10/011,125A  
CURRENT FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: US 60/256,162  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 5  
LENGTH: 212  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sequence is synthesized.  
Patent No. 6828121  
US-10-011-125A-5

APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

Alignment Scores:  
Pred. No.: 2,626-59 Length: 212  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-10-011-125A-5 (1-212)

QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGAGCAGTTGAAATCT 60  
DB 106 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 125  
QY 61 GGAAGTGGCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCGCAAGTACAG 120  
DB 126 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 145  
QY 121 TGAAGGTGGATAACGCCCTCCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
DB 146 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 165  
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCCTGAGCAGCAAGCAGCTACAG 240  
DB 166 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 185  
QY 241 AAACACAAAGTCTAGCCTCGCAAGTCAACCTCCCAATCGGGTAACTCCAGGAGAGTGTACAGAG 300  
DB 186 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 205  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
DB 206 SerPheAsnArgGlyGluCys 212

RESULT 9  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-820-6

Alignment Scores:
Pred. NO.: 2.63e-59 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-08-630-820-6 (1-213)
Qy 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCGCCCATCTGATGACGAGTTCGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126
Qy 61 GGAATCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 146
Qy 121 TGGAAAGTGGATACGCCCTCCATCGGGTAACCTCCAGAGAGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
Qy 181 AGCAAGGACACACCTACAGCCTCAGCAGCACCTGACCCCTGAGCGCTGAGTCCGCCGTCA 240
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
Qy 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCCATCAGGCGCTGAGTCCGCCGTCA 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 10
US-08-397-411-12
; Sequence 12, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-12

Alignment Scores:
Pred. No.: 2.63e-59 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-08-397-411-12 (1-213)
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Db 127 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 146
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Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
Qy 181 AGCAAGGACACACCTACAGCCTCAGCAGCACCTGACCCCTGAGCGCTGAGTCCGCCGTCA 240
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
Qy 241 AAACACAAAGTCTACGGCTCGGAAGTCAACCCATCAGGCGCTGAGTCCGCCGTCA 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213

RESULT 11
US-09-273-453-6
; Sequence 6, Application US/09273453
; Patent No. 6602688
; GENERAL INFORMATION:
; APPLICANT: Oppen, Martin
; APPLICANT: Bosslet, Klaus
; APPLICANT: Czech, Joerg
; TITLE OF INVENTION: CYTOLASMIC EXPRESSION OF ANTIBODIES,
; ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
; IN E. COLI
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/273,453  
FILING DATE: 22-Mar-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,820  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-273-453-6

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

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QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206

RESULT 12  
US-09-996-288-209  
Sequence 209, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 211  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-209

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

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QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206

RESULT 12  
US-09-996-288-209  
Sequence 209, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 209  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-209

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-209 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
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QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCAACAAG 300  
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206

QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

RESULT 13  
US-09-996-288-211  
Sequence 211, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 211  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-211

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-211 (1-213)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTCCGCCCATCTGATGACAGTTGAAATCT 60  
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146  
QY 121 TGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240  
Db 167 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186  
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QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

RESULT 12  
US-09-996-288-209  
Sequence 209, Application US/09996288  
Patent No. 6818216  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1

Db 107 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 126  
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QY 121 TGGAGGTGGATAACGCCCTCCATTCGGGTAACCTCCAGAGAGGTGCACAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
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QY 241 AAACACAAAGTCTAGCCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 187 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

## RESULT 14

US-09-996-288-213  
; Sequence 213, Application US/09996288  
; Patent No. 6818216

; GENERAL INFORMATION:  
; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 213

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-213

Alignment Scores:  
Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

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QY 121 TGGAGGTGGATAACGCCCTCCATTCGGGTAACCTCCAGAGAGGTGCACAGCAGGAC 180  
Db 147 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 166  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 186  
QY 241 AAACACAAAGTCTAGCCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
Db 187 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206

QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

## RESULT 15

US-09-996-288-215  
; Sequence 215, Application US/09996288  
; Patent No. 6818216

; GENERAL INFORMATION:  
; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 215

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-215

Alignment Scores:

Pred. No.: 2,63e-59 Length: 213  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 2 Gaps: 0

US-10-733-563-113 (1-321) x US-09-996-288-215 (1-213)

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QY 121 TGGAGGTGGATAACGCCCTCCATTCGGGTAACCTCCAGAGAGGTGCACAGCAGGAC 180  
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QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCCCTGACCCCTGAGCAAAAGCAGACTACAG 240  
Db 167 SerLysAspSerThrTySerLeuSerSerThrLeuThrLeuSerLysAlaAspTyGlu 186  
QY 241 AAACACAAAGTCTAGCCTGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
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QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 207 SerPheAenArgGlyGluCys 213

Search completed: January 28, 2006, 08:48:59

Job time : 13.6922 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 28, 2006, 08:44:22 ; Search time 39.2012 Seconds  
(without alignments)  
6842.811 Million cell updates/sec

Title: US-10-733-563-113

Perfect score: 564

Sequence: 1 cgtacggtggtgcaccatc.....gcttcacagggagagtgt 321

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	553	98.0	107	3	US-09-990-586-99
5	553	98.0	107	4	US-10-121-464-18
6	553	98.0	107	4	US-10-269-805-67
7	553	98.0	107	4	US-10-159-006-20
8	553	98.0	107	4	US-10-310-113-166
9	553	98.0	107	4	US-10-310-113-168
10	553	98.0	107	4	US-10-230-880-97
11	553	98.0	107	4	US-10-230-880-99

12	553	98.0	107	4	US-10-366-709-54	Sequence 54, Appl
13	553	98.0	107	4	US-10-404-286-5	Sequence 5, Appl1
14	553	98.0	107	4	US-10-656-769-4	Sequence 4, Appl1
15	553	98.0	107	4	US-10-679-620-60	Sequence 60, Appl
16	553	98.0	107	4	US-10-733-563-112	Sequence 112, App
17	553	98.0	107	5	US-10-815-449-10	Sequence 10, Appl
18	553	98.0	107	5	US-10-684-957-4	Sequence 4, Appl1
19	553	98.0	107	5	US-10-886-838-8	Sequence 8, Appl1
20	553	98.0	107	5	US-10-822-300-9	Sequence 9, Appl1
21	553	98.0	107	5	US-10-687-118-9	Sequence 9, Appl1
22	553	98.0	107	5	US-10-872-932A-41	Sequence 41, Appl
23	553	98.0	107	5	US-10-891-658-8	Sequence 8, Appl1
24	553	98.0	107	5	US-10-937-596-29	Sequence 29, Appl
25	553	98.0	107	5	US-10-893-576-44	Sequence 44, Appl
26	553	98.0	107	5	US-10-810-881A-40	Sequence 40, Appl
27	553	98.0	107	5	US-10-981-936-40	Sequence 40, Appl
28	553	98.0	107	6	US-11-001-980-4	Sequence 4, Appl1
29	553	98.0	107	6	US-11-001-980-8	Sequence 8, Appl1
30	553	98.0	107	6	US-11-132-143-60	Sequence 60, Appl
31	553	98.0	107	6	US-11-102-403-23	Sequence 23, Appl
32	553	98.0	109	4	US-10-272-899A-12	Sequence 12, Appl
33	553	98.0	109	4	US-10-733-563-116	Sequence 116, App
34	553	98.0	134	4	US-10-272-899A-66	Sequence 66, Appl
35	553	98.0	212	4	US-10-011-125-5	Sequence 5, Appl1
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37	553	98.0	212	5	US-10-867-506-77	Sequence 77, Appl
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41	553	98.0	213	3	US-09-796-848A-44	Sequence 44, Appl
42	553	98.0	213	3	US-09-796-848A-46	Sequence 46, Appl
43	553	98.0	213	3	US-09-796-848A-48	Sequence 48, Appl
44	553	98.0	213	3	US-09-796-848A-50	Sequence 50, Appl
45	553	98.0	213	3	US-09-796-848A-52	Sequence 52, Appl

#### ALIGNMENTS

RESULT 1  
US-09-301-593-20  
; Sequence 20, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John B.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-20

Alignment Scores:  
Pred. No.: 5.01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-301-593-20 (1-107)

QY 1 CGTACGGTGGCTGCACCAATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCCAAGTACAG 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGATACGCCCTTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCACCTTGACCTGAGCAAGCAGACTACAG 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAG 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
101 SerPheAenArgGlyGluCys 107

## RESULT 2

US-09-811-384-5  
; Sequence 5, Application US/09811384  
; Patent No. US20020081294A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/811,384  
; FILING DATE: 20-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788800  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1729C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

## Alignment Scores:

Pred. No.: 5.01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-811-384-5 (1-107)

QY 1 CGTACGGTGGCTGCACCAATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCCAAGTACAG 120  
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGATACGCCCTTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180  
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCACCTTGACCTGAGCAAGCAGACTACAG 240  
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAG 300  
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGAGAGTGT 321  
Db 101 SerPheAenArgGlyGluCys 107

## RESULT 3

US-09-990-586-97  
; Sequence 97, Application US/09990586  
; Publication No. US20030109680A1  
; GENERAL INFORMATION:  
; APPLICANT: JIAO, JIN-AN  
; APPLICANT: WONG, HING C.  
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS  
; TITLE OF INVENTION: OF USE THEREOF  
; FILE REFERENCE: 71758/46943-CIP2  
; CURRENT APPLICATION NUMBER: US/09/990,586  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-990-586-97

## Alignment Scores:

Pred. No.: 5.01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-990-586-97 (1-107)

QY 1 CGTACGGTGGCTGCACCAATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60  
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20  
QY 61 GGAACCTGCTCTGTTGTGCTGCTGCTGAATACTTCTATCCAGAGAGCCCAAGTACAG 120  
|||



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Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TCGAAGTGGATAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGACCTACAGCTCAGCAGCACCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 4
US-09-990-586-99
; Sequence 99, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-99

Alignment Scores:
Pred. No.: 5,016-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 3 Gaps: 0

US-10-733-563-113 (1-321) x US-09-990-586-99 (1-107)
QY 1 CGTACGGTGGCTGACCACTCTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheLeuPheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TCGAAGTGGATAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGACCTACAGCTCAGCAGCACCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 5
US-10-121-464-18
; Sequence 18, Application US/10121464
; Publication No. US20030103968A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies
; FILE REFERENCE: 1-1203ff
; CURRENT APPLICATION NUMBER: US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/283,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
; OTHER INFORMATION: sequence
US-10-121-464-18

Alignment Scores:
Pred. No.: 5,016-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-121-464-18 (1-107)
QY 1 CGTACGGTGGCTGACCACTCTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheLeuPheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAATCGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TCGAAGTGGATAACGCCCTCCAAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db 41 TrpLysValAspAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGACCTACAGCTCAGCAGCACCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGCTCGCAAGTCAACCATCAGGCGCTGAGCTCGCCCTCAAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 6
US-10-269-805-67
; Sequence 67, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-67

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-269-805-67 (1-107)

QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
QY 61 GGAAGTGGTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCTGACCCCTGACCAAGAGCAGCTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGGCTCGAAGTACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 7
US-10-159-006-20
; Sequence 20, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: Fc $\gamma$ 2b-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-20

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-159-006-20 (1-107)

QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
QY 61 GGAAGTGGTCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGCCCAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAAAGTGGATAACGCCCTCCCAATCGGTAACTCCAGGAGAGTGTCCAGAGCAGGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
QY 181 AGCAAGGACAGCAGCTACAGCCTCAGCAGCAGCCTGACCCCTGACCAAGAGCAGCTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTACGGCTCGAAGTACCCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAsnArgGlyGluCys 107

RESULT 8
US-10-310-113-166
; Sequence 166, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-310-113-166 (1-107)

QY 1 CGTACGGTGGTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 20
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QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTGAATCTCCAGGAGAGTGTACAGAGGAGC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 60
QY 181 AGCAAGGAGCAGCACCTTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCACAGGGGAGAGTGT 321
Db 101 SerPheAenAArgGlyGluCys 107
RESULT 9
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168
Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-113 (1-321) x US-10-310-113-168 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTGAATCTCCAGGAGAGTGTACAGAGGAGC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 60
QY 181 AGCAAGGAGCAGCACCTTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCACAGGGGAGAGTGT 321
Db 101 SerPheAenAArgGlyGluCys 107
RESULT 11
US-10-733-563-113 (1-321) x US-10-733-563-113 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 1 ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer 20
QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTGAATCTCCAGGAGAGTGTACAGAGGAGC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 60
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QY 181 AGCAAGGAGCAGCACCTTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCACAGGGGAGAGTGT 321
Db 101 SerPheAenAArgGlyGluCys 107
RESULT 10
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97
Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0
US-10-733-563-113 (1-321) x US-10-230-880-97 (1-107)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
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QY 61 GGAACCTGCTCTGTGTGCTGCTGAATAACTTCTATCCAGGAGAGGCCAAAGTACAG 120
Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTGAATCTCCAGGAGAGTGTACAGAGGAGC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAep 60
QY 181 AGCAAGGAGCAGCACCTTACAGCCTTCAGCAGCACCCCTGACCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
QY 241 AAACACAAAGTCTAGCCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCTCACAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
QY 301 AGCTTCACAGGGGAGAGTGT 321
Db 101 SerPheAenAArgGlyGluCys 107
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US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

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Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGTAACGCCCTCCAAATCGGTAACCTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCCGCTCAAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 12
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
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; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Alignment Scores:
Pred. No.: 5,01e-51 Length: 107
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 4 Gaps: 0

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Db 21 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAGGTGGTAACGCCCTCCAAATCGGTAACCTCCAGAGAGAGTGTACAGAGCAGAC 180
Db 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTAGCGCTCGGAAGTCAACCATCAGGCGCTGAGCTCCCGCTCAAAAG 300
Db 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGAGAGTGT 321
Db 101 SerPheAenArgGlyGluCys 107

RESULT 13
US-10-404-286-5
; Sequence 5, Application US/10404286
; Publication No. US20040057951A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/811384
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; FILING DATE: 20-DEC-2000  
; APPLICATION NUMBER: 09/251652  
; FILING DATE: 17-FEB-2000  
; APPLICATION NUMBER: 08/788800  
; FILING DATE: 22-JAN-1997  
; APPLICATION NUMBER: 60/093038  
; FILING DATE: 23-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, David W.  
; REGISTRATION NUMBER: NONE  
; REFERENCE/DOCKET NUMBER: P1729C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1739  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-404-286-5

Alignment Scores:  
Pred. No.: 5,01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
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DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
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DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

## RESULT 14

US-10-656-769-4  
; Sequence 4, Application US/10656769  
; Publication No. US2004009712A1  
; GENERAL INFORMATION:  
; APPLICANT: Varnum, Brian  
; APPLICANT: Witte, Allison  
; APPLICANT: Vezina, Chris  
; APPLICANT: Wong, Lu Min  
; APPLICANT: Qian, Xueming  
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody  
; FILE REFERENCE: 01,1554  
; CURRENT APPLICATION NUMBER: US/10/656,769  
; PRIORITY FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4

; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-656-769-4

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Pred. No.: 5,01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservatives: 0  
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DB 21 GlyThrAlaSerValValCysLeuLeuAenPheTyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGATAAGCCCTCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACCTGAGCAAAAGCAGACTACGAG 240  
DB 61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80  
QY 241 AAACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCGTCACAAAG 300  
DB 81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

## RESULT 15

US-10-679-620-60  
; Sequence 60, Application US/10679620  
; Publication No. US20040110930A1  
; GENERAL INFORMATION:  
; APPLICANT: Large Scale Biology  
; APPLICANT: Reinel, Stephen J.  
; APPLICANT: Edwards, Patricia C.  
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING  
; FILE REFERENCE: 34150-004A  
; CURRENT APPLICATION NUMBER: US/10/679,620  
; PRIORITY FILING DATE: 2003-10-03  
; PRIOR APPLICATION NUMBER: 60/415,940  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 60  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: huscFabmia6, see Example 15  
US-10-679-620-60

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Pred. No.: 5,01e-51 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservatives: 0  
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DB: 4 Gaps: 0

US-10-733-563-113 (1-321) x US-10-679-620-60 (1-107)

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Qy 61 GGAATGCTCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
21 GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln 40
Qy 121 TGGAAGGTGGATTAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
41 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 60
Qy 181 AGCAAGGACAGCACCTACAGCTCAGCAGCACCCCTGACCCCTGAGCAGCAAGCAGACTACGAG 240
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61 SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 80
Qy 241 AAACACAAAGTCTAGCCCTGCGAAGTCAACCCATCAGGGCCCTGAGCTCGCCCGTCACAAAG 300
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81 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100
Qy 301 AGCTTCAACAGGGAGAGTGT 321
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101 SerPheAsnArgGlyGluCys 107
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Job time : 41.2012 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Run on: January 28, 2006, 08:46:13 ; Search time 4.09685 Seconds  
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Title: US-10-733-563-113

Perfect score: 564

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Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications AA\_New:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	553	98.0	107	7	US-11-025-712-5
5	553	98.0	107	7	US-11-075-351-61
6	553	98.0	107	7	US-11-061-821-40
7	553	98.0	107	7	US-11-102-621-29
8	553	98.0	110	7	US-11-024-251-27
9	553	98.0	213	7	US-11-172-320-4
10	553	98.0	213	7	US-11-172-320-8

11	553	98.0	213	7	US-11-174-186-42	Sequence 42, Appl
12	553	98.0	213	7	US-11-120-338-13	Sequence 13, Appl
13	553	98.0	213	7	US-11-120-338-16	Sequence 16, Appl
14	553	98.0	213	7	US-11-173-969-4	Sequence 4, Appl
15	553	98.0	213	7	US-11-173-969-8	Sequence 8, Appl
16	553	98.0	213	7	US-11-102-621-118	Sequence 118, App
17	553	98.0	213	7	US-11-102-621-135	Sequence 135, App
18	553	98.0	213	7	US-11-107-028-31	Sequence 31, Appl
19	553	98.0	213	7	US-11-107-028-44	Sequence 44, Appl
20	553	98.0	213	7	US-11-106-820-24	Sequence 24, Appl
21	553	98.0	213	7	US-11-106-820-29	Sequence 29, Appl
22	553	98.0	213	7	US-11-106-820-44	Sequence 44, Appl
23	553	98.0	213	7	US-11-158-505-34	Sequence 34, Appl
24	553	98.0	214	7	US-11-025-712-11	Sequence 11, Appl
25	553	98.0	214	7	US-11-094-625-9	Sequence 9, Appl
26	553	98.0	214	7	US-11-102-621-129	Sequence 129, App
27	553	98.0	214	7	US-11-128-900-71	Sequence 71, Appl
28	553	98.0	214	7	US-11-154-337-14	Sequence 14, Appl
29	553	98.0	214	7	US-11-154-337-16	Sequence 16, Appl
30	553	98.0	215	7	US-11-102-621-141	Sequence 141, App
31	553	98.0	215	7	US-11-166-906-2	Sequence 2, Appl
32	553	98.0	218	6	US-10-923-327-6	Sequence 6, Appl
33	553	98.0	218	6	US-10-923-327-8	Sequence 8, Appl
34	553	98.0	218	6	US-10-923-327-10	Sequence 10, Appl
35	553	98.0	218	6	US-10-923-327-12	Sequence 12, Appl
36	553	98.0	218	6	US-10-923-327-17	Sequence 17, Appl
37	553	98.0	218	7	US-11-084-554-11	Sequence 11, Appl
38	553	98.0	218	7	US-11-158-505-4	Sequence 4, Appl
39	553	98.0	218	7	US-11-158-505-28	Sequence 28, Appl
40	553	98.0	218	7	US-11-004-590-229	Sequence 229, App
41	553	98.0	219	7	US-11-080-587-8	Sequence 8, Appl
42	553	98.0	232	7	US-11-106-820-23	Sequence 23, Appl
43	553	98.0	233	7	US-11-128-900-15	Sequence 15, Appl
44	553	98.0	233	7	US-11-128-900-67	Sequence 67, Appl
45	553	98.0	234	7	US-11-128-900-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-999-866-40

; Sequence 40, Application US/10999866

; Publication No. US20050266004A1

; GENERAL INFORMATION:

; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann

; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND

; FILE REFERENCE: CEN5042NP

; CURRENT APPLICATION NUMBER: US/10/999,866

; CURRENT FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: 60/527,794

; PRIOR FILING DATE: 2003-12-08

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 40

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC\_FEATURE

; LOCATION: (1)..(107)

; OTHER INFORMATION: Light chain kappa constant region (IgKc)

US-10-999-866-40

Alignment Scores:			
Pred. No.:	8.09e-49	Length:	107
Score:	553.00	Matches:	107
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.05%	Indels:	0
DB:	6	Gaps:	0

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Db	1	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuIysSer	20
Qy	61	GGAACGCGCTCTGTGTGTGGCTGCTGTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG	120
Db	21	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaIysValGln	40
Qy	121	TGGAAGGTGGATAACGCCCTCCAAATCGGTACTCCAGGAGAGTCTCACAGGCAGGAC	180
Db	41	TrpIysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGlnSerValThrGluGlnAsp	60
Qy	181	AGCAAGAGACAGCACCTCACAGCTTCAGCAGCACCTCGACCTCAGCAAAACAGCATACGAG	240
Db	61	SerIysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerIysAlaAspTyrGlu	80
Qy	241	AAACACAAAGTCTACGCTCGGAAGTCACCCATCAGGGCGCTGAGCTCGCCCGCTCACAAAG	300
Db	81	LysHisIysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrIys	100
Qy	301	AGCTTCAACACGGGGAGAGTGT	321
Db	101	SerPheAsnArgGlyGluCys	107

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RESULT 2
US-10-886-383-8
; Sequence 8, Application US/10886383
; Publication No. US2006005571A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,383
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-8

```

Alignment Scores:	
Pred. No.:	8.09e-49
Score:	553.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	98.05%
DB:	6
	6
	Gaba:
	0
	Indels:
	0
	Mismatches:
	0
	Conservative:
	0
	Matches:
	107
	Length:
	107

**US-10-733-563-113 (1-321) x US-10-886-383-8 (1-107)**

Qy	<b>1</b>	CGTACGGTGGCTGCACCATCGTCGTTCACTCCCGC CATCTGATGAGCAGTGGAATCT	60
Dbb	<b>1</b>	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLysSer	20
Qy	<b>61</b>	GGAACTGCCTCTGTTGTGCTGTGTAATAA CTCTATCCAGAGAGGCCAAAGTACAG	120
Dbb	<b>21</b>	GlyThrAlaSerValValCyslLeuLeuAanPheTy rProArgGluAlaLysValGln	40
Qy	<b>121</b>	TGGAAGGTGGATAACGCCCTCCAATCGGGT AACTCCCAGAGAGGTGTACAGAGCAGGAC	180
Dbb	<b>41</b>	TrpLysValAspAenAlaLeuGlnSerGlyA enSerGinGluSerValThrGluGlnAsp	60
Qy	<b>181</b>	AGCAAAGACAGCACCTACAGCCTCAGCAG CACCCGTGACCCTCAGACAAGCAGCATACGAG	240
Dbb	<b>61</b>	SerLysAspSerThryrSerLeuSerSerThr LeuthrLeuSerLysAlaAspTyrGlu	80
Qy	<b>241</b>	AACACAAAAGTCTTAGCCTCGGAAGTC ACCCATCAGGCGCTGAGCTCGCCCCGTACAAAG	300

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Db      81  LyshisLysValTyAlaCysGluValThrHisGlnGlyLeuSerProValThrLys 100

Qy      301  AGCTTCAACAGCGGAGAGTGT 321
          |||||
Db      101  SerPheAsnArgGlyGluCys 107

RESULT 3
US-10-988-207-21
; Sequence 21, Application US/10988207
; Publication No. US2006008457A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OF B-CLL
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988,207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab TGN1412 constant region light chain
US-10-988-207-21

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Alignment Scores:	
Pred. No.:	8,098-49
Score:	553.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	98.05%
DB:	6
	DB:
	Gaps:
	Indels:
	Mismatches:
	Conservative:
	Matches:
	Length:
	107
	107

US-10-733-563-113 (1-321) x US-10-988-207-21 (1-107)

Qy	1	CGTACGGTGGCTGCACCACTCTGTCTTTCATCTCCCGCATCTGATGACGAGTGGAAATCT	60
Db	1	ArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGlnLeuLeuSer	20
Qy	61	GGAACTGCCTCTGTTGTGTGCTGCTGAATTAACCTTATCCACAGAGAGGCCAAAGTACAG	120
Db	21	GlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAlaLysValGln	40
Qy	121	TGGAGGTGGATAACGCCCTCCATCCGGTTAACTCCACGAGGAGTGTCCACAGAGCAGGAC	180
Db	41	TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp	60
Qy	181	AGCAAGGACGAGCACCTACAGCTCAGCAGCACCTGACCCCTGAGCAAGCAGACTACGAG	240
Db	61	SerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrGlu	80
Qy	241	AAACACAAAGTCTACGCCCTGGGAAAGTCAACCATCAGGGCCTGAGCTGCCCGTCACAAAG	300
Db	81	LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys	100
Qy	301	AGCTTCAACAGGGGAGAGTGT	321
Db	101	SerPheAsnArgGlyGluCys	107

RESULT 4  
US-11-025-712-5  
; Sequence 5, Application US/11025712  
; Publication No. US20050255108A1  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; Thomas, G. Roger  
; Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE



; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(107)  
; OTHER INFORMATION: Light chain kappa constant region (IgKc)  
US-11-061-821-40

Alignment Scores:  
Pred. No.: 8.09e-49 Length: 107  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-061-821-40 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCCGCCATCTGATGAGCAGTTCGAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheilePheProProSerAspGluGlnLeuLysSer 20  
QY 61 GGAAGTGGCTGCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGTAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGACACACCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACGAG 240  
DB 61 SerLysAspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
DB 81 LysHisLysValTyrrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 7

US-11-102-621-9  
; Sequence 9, Application US/11102621  
; Publication No. US20050276799A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs, Inc.  
; APPLICANT: Hinton, Paul R.  
; APPLICANT: Tsurushita, Naoya  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Vaquez, Maximiliano  
; TITLE OF INVENTION: ALTERATION OF FC $\gamma$ R BINDING AFFINITIES OR SERUM HALF-LIVES OF  
; FILE REFERENCE: 05882.0039.00PC03  
; CURRENT APPLICATION NUMBER: US/11/102,621  
; PRIOR FILING DATE: 2005-04-08  
; PRIOR APPLICATION NUMBER: US 10/822,300  
; PRIOR FILING DATE: 2004-04-09  
; NUMBER OF SEQ ID NOS: 146  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody  
US-11-102-621-9

Alignment Scores:  
Pred. No.: 8.09e-49 Length: 107  
Score: 553.00 Matches: 107

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-102-621-9 (1-107)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCCGCCATCTGATGAGCAGTTCGAATCT 60  
DB 1 ArgThrValAlaAlaProSerValPheilePheProProSerAspGluGlnLeuLysSer 20  
QY 61 GGAAGTGGCTGCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
DB 21 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 40  
QY 121 TGGAGGTGGTAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180  
DB 41 TrpLysValAspAsnAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAsp 60  
QY 181 AGCAAGACACACCTACAGCTCAGCAGCAGCCCTGAGCCCTGAGCAAGACGACTACGAG 240  
DB 61 SerLysAspSerThrTyrrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyrrGlu 80  
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAG 300  
DB 81 LysHisLysValTyrrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 100  
QY 301 AGCTTCAACAGGGGAGAGTGT 321  
DB 101 SerPheAsnArgGlyGluCys 107

RESULT 8

US-11-024-251-27  
; Sequence 27, Application US/11024251  
; Publication No. US20050266425A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Paris, Mark  
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies  
; FILE REFERENCE: 1843.0230001  
; CURRENT APPLICATION NUMBER: US/11/024,251  
; CURRENT FILING DATE: 2004-12-29  
; PRIOR APPLICATION NUMBER: 60/533,241  
; PRIOR FILING DATE: 2003-12-31  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: cLambda Constant Domain  
US-11-024-251-27

Alignment Scores:

Pred. No.: 8.1e-49 Length: 110  
Score: 553.00 Matches: 107  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.05% Indels: 0  
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-024-251-27 (1-110)

QY 1 CGTACGGTGGCTGCACCATCTGCTTCATCTTCCCGCCATCTGATGAGCAGTTCGAATCT 60  
DB 4 ArgThrValAlaAlaProSerValPheilePheProProSerAspGluGlnLeuLysSer 23  
QY 61 GGAAGTGGCTGCTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120  
DB 24 GlyThrAlaSerValValCysLeuLeuAsnAsnPhetyrProArgGluAlaLysValGln 43  
QY 121 TGGAGGTGGTAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTCCAGAGCAGGAC 180

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Db 44 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 63
QY 181 AGCAAGGACAGCAGCTACAGCCCTCAGCAGCAGCCCTGACCCCTGAGCAAGCAGACTACGAG 240
Db 64 SerLysAspSerThrTySerLysSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 83
QY 241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTCAGCTCGCCCTCAAAAG 300
Db 84 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 103
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 104 SerPheAsnArgGlyGluCys 110
RESULT 9
US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-10-733-563-113 (1-321) x US-11-172-320-4 (1-213)
Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-113 (1-321) x US-11-172-320-4 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGCTTCTATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnPheTyrProArgGluAlaLysValGln 146
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTACTCCAGGAGAGTGTCCACAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
QY 181 AGCAAGGACAGCAGCTACAGCCCTCAGCAGCAGCCCTGATCCAGAGGCCAAAGTACAG 240
Db 167 SerLysAspSerThrTySerLysSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
QY 241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTCAGCTCGCCCTCAAAAG 300
Db 104 SerPheAsnArgGlyGluCys 110
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 104 SerPheAsnArgGlyGluCys 110
RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
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Db 187 LysHisLysValTyAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213
RESULT 10
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-11-172-320-8
Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
US-10-733-563-113 (1-321) x US-11-172-320-8 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGCTTCTATCTTCCGCCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAspGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAsnPheTyrProArgGluAlaLysValGln 146
QY 121 TGGAGGTGGATAACGCCCTCCAATCGGTACTCCAGGAGAGTGTCCACAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
QY 181 AGCAAGGACAGCAGCTACAGCCCTCAGCAGCAGCCCTGATCCAGAGGCCAAAGTACAG 240
Db 167 SerLysAspSerThrTySerLysSerSerThrLeuThrLeuSerLysAlaAspTyrGlu 186
QY 241 AAACACAAAGTCTAGCCTCGGAGTCAACCCATCAGGGCCTCAGCTCGCCCTCAAAAG 300
Db 104 SerPheAsnArgGlyGluCys 110
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAsnArgGlyGluCys 213
RESULT 11
US-11-174-186-42
; Sequence 42, Application US/11174186
```

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; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42

Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-174-186-42 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAsePheGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCCACAGCAGGAC 180
Db 147 TrpLysValAseAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAse 166
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 167 SerLysAsePheThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAsePheTyrGlu 186
US-10-733-563-113 (1-321) x US-11-174-186-42 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAsePheGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCCACAGCAGGAC 180
Db 147 TrpLysValAseAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAse 166
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 167 SerLysAsePheThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAsePheTyrGlu 186
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCTCCAGGAGAGTGTCCACAGCAGGAC 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAenArgGlyGluCys 213
RESULT 12
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-16

Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-120-338-16 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-13

Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0

US-10-733-563-113 (1-321) x US-11-120-338-13 (1-213)
QY 1 CGTACGGTGGCTGCACCATCTGTCTTCATCTCCCGCCATCTGATGAGCAGTTGAAATCT 60
Db 107 ArgThrValAlaAlaProSerValPheIlePheProSerAsePheGluGlnLeuLysSer 126
QY 61 GGAATCGCTCTGTGTGCTGCTGCTGAATACTTCTATCCAGAGAGGCCAAAGTACAG 120
Db 127 GlyThrAlaSerValValCysLeuLeuAenAenPheTyrProArgGluAlaLysValGln 146
QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTCCACAGCAGGAC 180
Db 147 TrpLysValAseAenAlaLeuGlnSerGlyAenSerGlnGluSerValThrGluGlnAse 166
QY 181 AGCAAGGACAGCAGCTACAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 167 SerLysAsePheThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAsePheTyrGlu 186
QY 241 AAACACAAAGTCTACGCTCGGAAGTCAACCTCCAGGAGAGTGTCCACAGCAGGAC 300
Db 187 LysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLys 206
QY 301 AGCTTCAACAGGGGAGAGTGT 321
Db 207 SerPheAenArgGlyGluCys 213
RESULT 13
US-11-120-338-16
; Sequence 16, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 16
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-16

Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0

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QY 121 TGAAGGTGGATAACGCCCTCCAAATCGGGTAACCTCCAGAGAGGTGTCCAGAGCAGGAC 180
Db 147 TrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThrGluGlnAsp 166
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QY 301 AGCTTCAACAGGGGAGAGTGT 321
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RESULT 14
US-11-173-969-4
; Sequence 4, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf. G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: 4
US-11-173-969-4
Alignment Scores:
Pred. No.: 8,45e-49 Length: 213
Score: 553.00 Matches: 107
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.05% Indels: 0
DB: 7 Gaps: 0
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QY 301 AGCTTCAACAGGGGAGAGTGT 321
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Search completed: January 28, 2006, 09:32:26  
Job time : 6.09685 secs

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